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<td><strong>Tuesday, July 29</strong></td>
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<td>Special Presentation by Jon Lorsch, Director of the National Institute</td>
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<td>How to Get Published Presentation</td>
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Conference Organizers
Trisha Davis, Chair
Mike Snyder, Co-chair

Program Committee
Karen Arndt        Leonid Kruglyak        Dave Toczyski
Sue Biggins            Michael Lichten          Phong Tran
Orna Cohen-Fix          Vicki Lundblad        Olga Troyanskaya
Liz Conibear           Mike McMurray          Toshi Tsukiyama
Maitreya Dunham          Yoshi Ohya            Fred van Leeuwen
Richard Gardner          Steve Oliver           Eric Weiss
Tim Hughes

Mobile website:  http://y.gsaconf.org
Follow the conference on Twitter: #YEAST14
The Genetics Society of America is pleased to be working with the yeast community to support the Yeast Genetics Meeting.

Founded in 1931, the Genetics Society of America (GSA) is a professional scientific society with more than 5,000 members worldwide working to deepen our understanding of the living world by advancing the field of genetics, from the molecular to the population level. GSA represents the collective interests of the genetics and model organism communities in advocating support for research, educating students and the public about the importance of genetics, and providing a respected and authoritative voice on genetic issues increasingly in the public eye.

GSA promotes research and fosters communication through a number of GSA conferences including regular meetings that focus on cross-cutting areas of genetics and particular model organisms including C. elegans, Chlamydomonas, ciliates, Drosophila, fungi, mice, Xenopus, yeast, and zebrafish.

GSA publishes two peer-edited scholarly journals:

- **GENETICS**, which has published high quality original research across the breadth of the field since 1916, and
- **G3: Genes|Genomes|Genetics**, an open-access journal launched in 2011 to disseminate high quality foundational research in genetics and genomics.

The Society has a deep commitment to fostering the next generation of scholars in the field, through providing career development activities and resources and offering travel grant programs including the GSA Undergraduate Travel Awards and DeLill Nasser Awards for Professional Development in Genetics.

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<td></td>
<td><strong>Trisha Davis</strong>, Meeting Organizer, University of WA, Seattle</td>
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<td><strong>Adam Fagen</strong>, Executive Director, Genetics Society of America</td>
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<td><strong>Mark Johnston</strong>, Editor, GENETICS</td>
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<td><strong>Brenda Andrews</strong>, Editor, G3: Genes, Genome, Genetics</td>
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<td>7:15 pm - 8:15 pm</td>
<td><strong>Ira Herskowitz Award Lecture</strong></td>
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<td><strong>Olga Troyanskaya, Princeton University</strong></td>
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<td>Introduction by Chad Myers</td>
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<td>Introduction by Mike Snyder</td>
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<td>12:15 pm - 2:00 pm</td>
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<td>2:00 pm - 3:30 pm</td>
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<td><strong>Chair</strong>: Toshi Tsukiyama</td>
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<td>4:00 pm - 5:30 pm</td>
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<td>** Trafficking and Cellular Architecture**</td>
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<td><strong>Chair</strong>: Liz Conibear</td>
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<td>10:30 am - 12:00 noon</td>
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<td><strong>Chair</strong>: Aimee Dudley</td>
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<td>1:30 pm - 3:00 pm</td>
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<td><strong>Organizer</strong>: Judy Berman</td>
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| 3:15 pm – 4:45 pm  | **Advocacy Presentation**  
Organizer: Adam Fagen                                               | Kane Hall Room 210     |
| 6:00 pm - 7:30 pm  | Dinner  
GSA Career Dinner                                                 | HUB Den                |
| 7:30 pm – 11:00 pm | **Poster Session 2 and Exhibits**                                    | HUB Grand Ballroom     |

**Friday, August 1**

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<td>Registration</td>
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</table>
| 8:30 am - 10:00 am | **Chromosome Dynamics**  
*Chair*: Bonny Brewer                                                 | Meany Theater          |
| 10:30 am - 11:15 am| **Aging**  
*Chair*: Martha Cyert                                                 | Meany Theater          |
| 11:15 am - 12:00 noon | **Lifetime Achievement Award**  
Jeremy Thorner, University of California, Berkeley  
Introduction by Martha Cyert   | Meany Theater          |
| 12:15 pm - 2:00 pm | Lunch                                                                | Lander Hall, Local Point Dining |
| 2:00 pm - 3:30 pm  | **Next Generation Genetics**  
*Chair*: Vivien Measday                                                | Meany Theater          |
| 4:00 pm - 5:30 pm  | **Epigenetics and Post-Transcriptional Regulation**  
*Chair*: Fred Winston                                                 | Meany Theater          |
| 5:15 pm – 5:30 pm  | **Tribute to Fred Sherman**  
by Sue Liebman                                                          | Meany Theater          |
| 6:00 pm - 7:30 pm  | Dinner                                                               | HUB Den                |
| 7:30 pm - 11:00 pm | **Poster Session 3 and Exhibits**                                    | HUB Grand Ballroom     |

**Saturday, August 2**

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<td>8:15 am - 12:00 noon</td>
<td>Registration</td>
<td>Meany Theater Lobby</td>
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</tbody>
</table>
| 8:30 am - 10:00 am | **Spatial Relationships**  
*Chair*: Yoshi Ohya                                                      | Meany Theater          |
| 10:30 am - 12:00 noon | **Chromosome Rearrangements and Polyploidy**  
*Chair*: Audrey Gasch                                                  | Meany Theater          |
| 2:00 pm - 3:30 pm  | **New Technologies**  
*Chair*: Sue Jaspersen                                                   | Meany Theater          |
| 4:00 pm - 5:30 pm  | **Yeast and Human Disease**  
*Chair*: Jasper Rine                                                      | Meany Theater          |
| 5:30 pm - 5:45 pm  | **GSA Awards**  
Presentation of Edward Novitski Prize to Charlie Boone  
Presentation of Elizabeth W. Jones Award for Excellence in Education to Malcolm Campbell | Meany Theater          |
| 6:00 pm - 12:00 am | Banquet,  
**Winge-Lindegren Address**  
**Anita Hopper, Ohio State University**  
Introduction by Ben Hall  
Conference Party | HUB Grand Ballroom          |

**Sunday, August 3**

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<th>Time</th>
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| 9:00 am - 11:00 am | **Genomics and Proteomics**  
*Chair*: Corey Nislow                                                  | Meany Theater          |
General Information

Registration Desk Hours:

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Mobile Web Site
Bookmark the mobile website on your web enabled mobile device: ygsaconf.org

Follow the conference on Twitter: #YEAST14

Platform Presenter Instructions
All platform authors should load their presentations onto the conference computer 45 minutes before the start of their session. A computer technician will be available to assist you in Meany Theater. Speakers should go into the theater, proceed to the front of the room and enter the door on the left to access the stage.

Posters
All posters will be displayed in the Husky Union Building (HUB) Grand Ballroom. Presenters may begin posting their presentations on Wednesday, July 30 at 9:00 am and should be in place by 7:00 pm on Wednesday evening. Authors will present according to the following schedule:

**Wednesday, July 30**

**Poster Session 1**

- Authors of even numbered “A” posters will present 7:30 pm – 8:30 pm
- Authors of odd numbered “A” posters will present 8:30 pm – 9:30 pm
- Open Viewing 9:30 pm – 11:00 pm

**Thursday, July 31**

**Poster Session 2**

- Authors of even numbered “B” posters will present 7:30 pm – 8:30 pm
- Authors of odd numbered “B” posters will present 8:30 pm – 9:30 pm
- Open Viewing 9:30 pm – 11:00 pm

**Friday, August 1**

**Poster Session 3**

- Authors of even numbered “C” posters will present 7:30 pm – 8:30 pm
- Authors of odd numbered “C” posters will present 8:30 pm – 9:30 pm
- Open Viewing – ALL POSTERS REMOVED by 11:15 pm 9:30 pm – 11:00 pm

Posters must be removed from their boards by 11:15 pm on Friday, August 1, to prepare the room for the dinner/party on Saturday night. POSTERS NOT RETRIEVED BY THIS TIME WILL BE DISCARDED. The GSA Administrative Office staff, Univ. of WA staff and the personnel taking down the boards will not be responsible for posters left by the authors.

Poster Legend

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<td>Gene Expression: 274A – 330C</td>
<td>Late Posters: 466 - 471</td>
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Photography
Absolutely no photography is allowed in the poster display areas.

Messages and Notices Boards
Boards for messages, employment notices and conferences are located in HUB Grand Ballroom.
General Information

Meals

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<td>Lander Hall, Local Point</td>
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<tr>
<td>Dinner</td>
<td>6:00 pm – 7:30 pm</td>
<td>Husky Union Building, Den</td>
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Social Events

Tuesday First Time Attendees Social: Members of the Organizing Committee and other leaders in the field want to personally welcome you to the meeting. All first time attendees are invited for a cookies and coffee social in the Meany Hall Lobby at 6:00 pm.

Tuesday Opening Mixer: Catch up with old friends or meet new people at the Opening Mixer. Beer and wine from local microbrews and wineries will be served in addition to soft drinks and light appetizers.

Wednesday, Thursday and Friday evenings: A hosted bar will be open from 8:00 pm until 11:00 pm each evening in the Grand Ballroom. Be sure to stop by and visit the exhibits. Beer and wine from local microbrews and wineries will be served in addition to soft drinks and snacks.

Saturday evening: A banquet and party is planned from 6:00 pm until 12:30 am in the HUB Grand Ballroom. The GSA Poster Awards will be presented. Anita Hopper, University of Ohio, will present the Winge-Lindegren Address. Following the presentation, there will be a DJ and a hosted bar.

Annual Yeast Genetics Meeting Awards and Special Presentations

The following awards and special presentations will be given:

Ira Herskowitz Award: Olga Troyanskaya, Princeton University
Lee Hartwell Lecture: George Church, Harvard University
Lifetime Achievement Award: Jeremy Thorner, University of California, Berkeley
Winge-Lindegren Address: Anita Hopper, Ohio State University

How to Get Published: Process and Tips from the GSA Journals GENETICS and G3

Wednesday, July 30: 6:00 pm – 7:30 pm, HUB, Room 250
Join GENETICS and G3 journal editors as they discuss the ins and outs of publishing. Enjoy an opportunity to ask questions and learn more about publishing your articles. Topics may include: the peer-review process, open access, writing to get published, where and how your work can have the most impact, revisions and editing, ethical issues in publishing, journal data policies, and more. All are invited to attend, but students, postdocs, and newer faculty members may find the event most useful. After going through the buffet line in the Husky Den, participants should proceed to Room 250, with their dinner, for the presentation and to meet with the editors.

Advocacy Presentation

Thursday, July 31, 3:15 pm – 4:45 pm, Kane Hall, Room 210
The GSA Executive Director will discuss the latest policy and legislative news affecting funding for NIH, describe why it is important for scientists to speak out about issues that affect their grants and research, and share tips for engaging in advocacy.
Tuesday, July 31

GSA Trainee Boot Camp (advance registration required)
11:00 am – 5:00 pm, HUB, Room 340
The boot camp, which is only open to graduate students and postdocs, will cover the following areas: finding funding, getting published, navigating academia and beyond traditional academia.

GSA Education Special Interest Group Mixer/Pedagogy Workshop
5:00 pm – 6:30 pm, HUB, Room 337
Faculty with a passion for genetics education are encouraged to attend this event, where they can mix and mingle with other educators. Current members of the Education SIG can catch up on actions taken by GSA with regards to the education initiative, and those who are not yet SIG members can learn about the Education SIG.

Wednesday, July 30

Genetics Conference Experience: 8:30 am – 12:30 pm
The GSA Genetics Conference Experience provides students at local undergraduate institutions without strong research programs with the unique opportunity to observe distinguished career scientists present their current research in a conference setting. The students will receive a background lecture and participate in an interactive discussion before attending part of a plenary session. This program gives students a glimpse into the real world of genetics research and provides them the opportunity to learn about scientific research outside of a textbook, witness the communication of scientific research first-hand, and ideally will foster an interest in furthering their science education. Invitation-only.

Undergraduate Dinner
6:00 pm – 7:00 pm, HUB Den
Undergraduate researchers attending the conference will network on their own forming a peer-group that will help provide lasting support for the remainder of the conference. After going through the buffet line, participants should go to the tables designated “Undergraduate Researchers”.

Thursday, August 2

Plenary and Workshop for Undergraduate Researchers
1:30 pm – 3:00 pm, Kane Hall, Room 210
Undergraduate conference attendees will attend a plenary session with two talks presented at a level appropriate for an undergraduate audience. Participants will then have a chance to talk to a panel of graduate students about applications, interviewing, admission, choosing a lab and quality of life in graduate school.

GSA Career Dinner
6:00 pm – 7:30 pm, HUB, Den
The GSA Career Dinner is an excellent opportunity for undergraduates, graduate students, and postdoctoral fellows to have informal conversations with senior career scientists regarding the unique challenges and rewards of a scientific career. The dinner is organized by topic table. Topics may include: transition to independence, work-family balance, teaching at undergraduate institutions, non-academic careers for scientists, the job search, the postdoc search, etc. After going through the buffet line, participants should look for the topic tables.
Exhibits will be open during the poster sessions in the HUB Grand Ballroom. Registrants are encouraged to visit the exhibits.

**Carl Zeiss Microscopy**
Thornwood, NY
Website: www.zeiss.com/microscopy
Email: micro@zeiss.com

As the world's only manufacturer of light, X-ray and electron/ion microscopes, ZEISS offers tailor-made microscope systems for 3D imaging in biomedical research, life sciences and healthcare. A well-trained sales force, an extensive support infrastructure and a responsive service team enable customers to use their ZEISS microscopes to their full potential.

**EMD Millipore Corporation**
Billerica, MA
Website: www.emdmillipore.com
Email: james.fell@merckgroup.com

**Formedium**
Norkolk, United Kingdom
Website: www.Formedium.com
Email: Julia.grant@formedium.com

Specialist manufacturer of media for Yeast and Pombe systems. Extensive ranges of all Drop- Out Supplements and formulations. Cost effective custom made Yeast media formulations. Guaranteed reliability with outstanding value. For stock items delivery 3 days, custom made media delivery 6 days. Formedium - dedicated to research to optimize your results.

**Genetics Society of America**
Bethesda, MD
Website: www.genetics-gsa.org
Email: society@genetics-gsa.org

Come explore the resources and opportunities that GSA has to offer including education, career development and policy, meet members of the GSA staff and leadership; and find out about publishing in *GENETICS* and *G3: Genes|Genomes|Genetics*.

**M2P Labs**
Baesweiler, Germany
Website: www.m2p-labs.com
Email: katz@m2p-labs.com

m2p-labs is a worldwide leading supplier of microbioreactor systems. The company focuses on microreactor systems and automated solutions for screening and bioprocess development. The BioLector® represents the core technology and based on this, m2p-labs also provides enhanced automated microbioreactor systems like the RoboLector®, which offers even more bioprocessing capabilities at the microscale.

**SGD**
Stanford, CA
Website: www.yeastgenome.org
Email: Costanzo@stanford.edu

The *Saccharomyces* Genome Database (SGD, [http://www.yeastgenome.org](http://www.yeastgenome.org)) is the community resource for the budding yeast *Saccharomyces cerevisiae*, providing encyclopedic information about the yeast genome and its genes, proteins, and other encoded features. SGD is freely accessible to students, researchers, and educators worldwide.

**Singer Instrument Company**
Somerset, United Kingdom
Website: www.singerinst.co.uk
Email: yeast@singerinst.co.u

Singer Instruments have been making scientific instruments since 1934 and have brought speed, convenience, automation, reliability, technology and ergonomics to yeast tetrad dissection to over 400 labs in 50 countries. Singers Instruments also make the ROTOR HDA; a small, fast, high-density pinning and arraying robot for yeast, bacteria, and fungi research.

**Sunrise Science Products**
San Diego, CA
Website: www.sunrisescience.com
Email: lkylin@sunrisescience.com

Sunrise Science Products manufactures hundreds of selective and non-selective yeast media formulations, and custom recipes for any organism are quickly produced. We are also proud to distribute yeast antibodies, products for protein expression in E. coli and unique magnetic devices for efficient isolation of DNA, RNA and proteins.
Welcome and Opening Remarks

Trisha Davis, Meeting Organizer, University of Washington, Seattle
Adam Fagen, Executive Director Genetics Society of America
Mark Johnston, GENETICS Editor and Brenda Andrews, G3: Genes, Genome, Genetics Editor

Ira Herskowitz Award Lecture
Olga Troyanskaya
Princeton University

Introduction by Chad Myers

Cell Cycle Transitions
Chair: Mark Rose

1 - 8:30

2 - 8:45
Morphogenesis checkpoint kinase Swe1 is the executor of lipolysis-dependent cell cycle progression. Sepp D. Kohlwein, Neha Chauhan, Myriam Visram.

3 - 9:00
Compartmentalization of G1/S regulators allows signaling information to traverse a switch-like transition. Andreas Doncic, Jan M. Skotheim.

4 - 9:15
Coordination of cell cycle-regulated gene expression by Cdk1. Benjamin Landry, Claudine Mapa, Heather Arsenault, Kristin Poti, Jennifer Benanti.

5 - 9:30
Understanding the Regulation, Composition and Function of P bodies and Stress Granules in Quiescent Cells. Khyati H. Shah, Paul K. Herman.

6 - 9:45
Novel pathways of transcription regulation during the transition from growth to quiescence. Shawna Miles, Amali P. Abeysinghe, Linda L. Breeden.
Platform and Workshop Session Listings

Wednesday, July 30 10:30 am–12:00 noon
Meany Theater

Environmental Sensing Networks
Chair: Brenda Andrews

7 - 10:30
The inferred stress-activated signaling network from yeast: coordination, interconnectivity, and a novel NaCl network hub, Cdc14 phosphatase. Yi-Hsuan Ho, Deborah Chasman, Matthew MacGilvray, James Hose, Anna Merrill, Joshua Coon, Mark Craven, Audrey Gasch.

8 - 10:45
An integrated ‘omics approach to large-scale quantitative analysis of cellular metabolic regulation. Sean Hackett, Vito Zanotelli, David Perlman, Joshua Rabinowitz.

9 - 11:00

Lee Hartwell Lecture
George Church
Harvard University

Introduction by Mike Snyder

Wednesday, July 30 2:00 pm–3:30 pm
Meany Theater

Temporal and Spatial Control of Chromatin
Chair: Toshi Tsukiyama

10 - 2:00
Heritable capture of heterochromatin dynamics in Saccharomyces cerevisiae. Anne Dodson, Ryan Janke, Kathryn Sieverman, Jasper Rine.

11 - 2:15
Dissecting the crosstalk between histone H2B ubiquitination and histone H3 methylation. Hanneke Vlaming, Tibor van Welsem, Erik de Graaf, Maarten Altelaar, David Ontoso, Pedro San-Segundo, Fred van Leeuwen.

12 - 2:30
Identification of a nucleosome patch required for conserved histone modifications. Christine Cucinotta, Alexandria Young, Karen Arndt.

13 - 2:45
Mitochondrial feedback control through global H3K4 demethylation. Maria Soloveychik, Mengshu Xu, Ashruti Narula, Adam Rosebrock, Amy Caudy, Marc Meneghini.

14 - 3:00
Role of ATP-dependent chromatin remodeling enzyme Fun30 in co-transcriptional pre-mRNA splicing. Qiankun Niu, Wei Wang, Boseon Byeon, Yong Li, Asim Bikas Das, Wei-Hua Wu.

15 - 3:15
Platform and Workshop Session Listings

Wednesday, July 30 4:00 pm–5:30 pm
Meany Theater

Special Presentation by Jon Lorsch, Director of the National Institute of General Medical Sciences, NIH

Thursday, July 31 8:30 am–10:00 am
Meany Theater

Trafficicking and Cellular Architecture
Chair: Liz Conibear

16 - 8:30
The budding yeast polo kinase, Cdc5, is a regulator of nuclear morphology. Alison D. Walters, Christopher K. May, Emma Dauster, Bertrand P. Cinquin, Elizabeth A. Smith, Carolyn A. Larabell, Orna Cohen-Fix

17 - 8:45
Surveying the Inner Nuclear Membrane Landscape. Christine J. Smoyer, Jennifer Gardner, Sreenivasulu Santharam Katta, Brian Slaughter, Jay Unruh, Dan Bradford, Scott McCroskey, Sue Jaspersen.

18 - 9:00
SNAREs and the Dsl1 tethering complex mediate an alternative, Sey1p-independent ER fusion pathway. Jason V. Rogers, Conor McMahon, Anastasia Baryshnikova, Michael Costanzo, Charles M. Boone, Frederick M. Hughson, Mark D. Rose.

19 - 9:15

20 - 9:30
Elucidating the architecture and function of the yeast exocyst complex. Mary Munson, Margaret Heider, Caroline Duffy, Zhanna Hakhverdyan, Raghav Kalia, Nicholas Farrall, Michael Rout, Adam Frost.

21 - 9:45
The molecular architecture of the Target Of Rapamycin Complex 2 reveals why it is insensitive to rapamycin. C. Gaubitz, T. Maia de Oliveira, Manoël Prouteau, A. Leitner, M. Karuppasamy, D. Rispal, S. Eltschinger, G. Robinson, G. Konstantinidou, S. Thore, R. Aebersold, R. Loewith, C. Schaffitzel

Thursday, July 31 10:30 am–12:00 noon
Meany Theater

Dissecting Complex Traits
Chair: Aimee Dudley

22 - 10:30
Higher-order epistasis between a mutation and four or more segregating variants generates a 'new' phenotype in a cross. Matthew Taylor, Ian Ehrereich.

23 - 10:45
A quantitative study of whether the HSP90 chaperone modulates robustness to new mutations, recombination, and standing variation in yeast. Kerry A. Geiler-Samerotte, Mark L. Siegal.

24 - 11:00
Diversity across the Saccharomyces genus and the genomic tools to tap it. Chris Todd Hittinger, William G. Alexander, Drew T. Doering, David Peris, Kayla Sylvester, Diego Libkind, Paula Gonçalves, José Paulo Sampaio.

25 - 11:15
High-throughput functional screening of driver mutations. Celia Payen, Anna Sunshine, Giang Ong, Wei Zhao, Maitreya Dunham.

26 - 11:30

27 - 11:45
Analysis of transcription activation distance as a polygenic trait in Saccharomyces cerevisiae. Caitlin Reavey. Mark Hickman, David Botstein, Fred Winston.
Thursday, July 31 1:30 pm–3:00 pm
Kane Hall, Room 120

**Beyond Cerevisiae**
Chair: Judy Berman

*Saccharomyces cerevisiae* is arguably the most powerful eukaryotic model system for molecular genetics and genomics. The increased accessibility of technologies such as whole genome sequencing has made analysis of closely related and more distantly related species much more feasible. In this workshop, speakers will introduce the organism or organisms they are studying and the reasons for studying them. They will then provide insights into the types of studies they are performing, and highlight the results they are obtaining, to better understand these organisms. We will start with a focus on comparisons between the species and then highlight more distantly related organisms including important human pathogens.

1:30
Comparative Genomics of Yeast Genome Conformation and Functional Annotation by Multiplexed Hi-C
*Ivan Liachko*, Joshua Burton, Jay Shendure, Maitreya Dunham, Genome Sciences

1:45
Investigating reticulate evolution in the *Saccharomyces* genus and repeating it for the bioethanol industry.
*David Peris Navarro*, Kayla Sylvester, Maria Sardi, William Alexander, Diego Libkind, Paula Gonçalves, José Sampaio, Lucas Parreiras, Trey Sato, Chris Hittinger.

2:00
Evolutionary genomics of ecological speciation in *Saccharomyces paradoxus*. Jean-Baptiste Leducq, Lou Nielly-Thibaut, Guillaume Charron, Christian Landry.

2:15
Genome-wide patterns of genetic variation reveal chromosome-scale heterogeneous evolution in a protoploid yeast. Anne Friedrich, Paul Jung, Cyrielle Reisser, Gilles Fischer, Joseph Schacherer.

2:30
The development of molecular tools facilitates functional comparisons between *Saccharomyces cerevisiae* and the related pathogenic yeast *Candida glabrata*.
*Lauren Ames*, Hsueh-lui Ho, Jane Usher and Ken Haynes.

2:45
**A Tetraploid Intermediate Precedes Aneuploid Formation in Yeasts Exposed to Fluconazole.** Benjamin Harrison, Maayan Bibi, Rebecca Pulver, Melanie Wellington, Jordan Hashemi, Guillermo Sapiro, Judith Berman.

Thursday, July 31 1:30 pm–3:00 pm
Kane Hall, Room 220

**Computational Tools at SGD**
Chair: Maria Costanzo

In the *Saccharomyces* Genome Database workshop, we’ll be talking about ways that you can get more out of SGD. We’ll focus on our incredibly powerful tool, YeastMine, that lets you ask virtually any question about yeast data. We’ll also discuss recent improvements to SGD, and have time for questions.

- S. cerevisiae Strains and Sequences
- The Awesome Power of YeastMine
- New Features Coming Soon to SGD
- Open Q&A

Thursday, July 31 1:30 pm–3:00 pm
Kane Hall, Room 210

**Plenary and Workshop for Undergraduate Researchers**
Chair: Beth Ruedi

Undergraduate conference attendees will attend a plenary session with two talks presented at a level appropriate for an undergraduate audience. Participants will then have a chance to talk to a panel of graduate students about applications, interviewing, admission, choosing a lab and quality of life in graduate school.

Thursday, July 31 3:15 pm–4:45 pm
Kane Hall, Room 220

**Advocacy Presentation**
Chair: Adam Fagen

We will discuss the latest policy and legislative news affecting funding for NIH, describe why it is important for scientists to speak out about issues that affect their grants and research, and share tips for engaging in advocacy.
<table>
<thead>
<tr>
<th>Listing</th>
<th>Time</th>
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<tbody>
<tr>
<td>28 - 8:30</td>
<td>Mapping Recombination in Single Meiotic Cells Reveals that Tel1/ATM Controls the Positioning and Fate of DNA Double-Strand Breaks. Carol Anderson, Ashwini Oke, Phoebe Yam, Jennifer Fung.</td>
</tr>
<tr>
<td>29 - 8:45</td>
<td>RAD51 and the DNA damage checkpoint are essential for increased chromosome mobility after DNA damage in diploid S. cerevisiae. Michael J. Smith, Fraulin Joseph, Marina Ermakova, Ignacio Izeddin, Vincent Recamier, Xavier Darzacq, Judith Mine-Hattab, Rodney Rothstein.</td>
</tr>
<tr>
<td>30 - 9:00</td>
<td>A combined genetic and biochemical analysis of yeast telomerase. Johnathan W. Lubin, Timothy M. Tucey, Lisa Nguyen, Vicki Lundblad</td>
</tr>
<tr>
<td>31 - 9:15</td>
<td>The FACT complex interacts with the E3 ubiquitin ligase Psh1 to prevent ectopic localization of CENP-A. Gary M. Deyter, Sue Biggins.</td>
</tr>
<tr>
<td>32 - 9:30</td>
<td>Reconstitution of strong kinetochore attachments requires more than the microtubule binding components of the kinetochore. Emily M. Mazanka, Neil T. Umbreit, Alex Zelter, Daniel R. Gestaut, Charles L. Asbury, Trisha N. Davis.</td>
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**Friday, August 1 10:30 am–12:00 noon**

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<tr>
<th>Listing</th>
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<tbody>
<tr>
<td>34 - 10:30</td>
<td>An Asymmetric Competition for Protons Promotes Aging but Facilitates Rejuvenation. Kiersten A. Henderson, Adam L. Hughes, Daniel E. Gottschling. Basic Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA.</td>
</tr>
<tr>
<td>36 - 11:00</td>
<td>Translocation of cyclin C to the mitochondria mediates stress-induced fission and programmed cell death. Randy S. Strich, Katrina F. Cooper.</td>
</tr>
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**Lifetime Achievement Award**

Jeremy Thorner, University of California, Berkeley

Introduction by Martha Cyert
Friday, August 1 2:00 pm–3:30 pm
Meany Theater

Next Generation Genetics
Chair: Vivien Measday

37 - 2:00
Engineering of alcohol and stress tolerance traits in *Saccharomyces cerevisiae* using a novel synthetic biology approach for producing genetic diversity.
Sabrina German, Biranchi N. Patra, Animesh Ray, Helge Zieler.

38 - 2:15

39 - 2:30

40 - 2:45
Global analysis of HAT and HDAC substrates in vivo. David Paul Toczyski, Michael Downey.

41 - 3:00
Protein localization re-patterning during DNA replication stress. Nikko P. Torres, Grant W. Brown.

42 - 3:15
High dimensional phenotyping reveals remarkable extent of haploinsufficiency in essential genes. Shinsuke Ohnuki, Yoshikazu Ohya.

Friday, August 1 4:00 pm–5:30 pm
Meany Theater

Epigenetics and Post-Transcriptional Regulation
Chair: Fred Winston

43 - 4:00
Intrinsically disordered proteins drive heritable epigenetic switches that transform the phenotypic landscape of *S. cerevisiae*. Sohini Chakrabortee, James Byers, Susan Lindquist, Daniel Jarosz.

44 - 4:15
Cheaters Do Prosper: Reciprocal cheating drives epigenetic switching of facultative multicellularity. Sorna Kamara, Randal Halfmann.

45 - 4:30
The PUF Protein Puf3 Toggles the Translational Fate of Bound mRNAs to Regulate Mitochondrial Biogenesis. Chien-Der Lee, Benjamin Tu.

46 - 4:45
Genome-wide screen identifies pathways that govern tRNA splicing and intron turnover in *Saccharomyces cerevisiae*. Jingyan Wu, Yao Wan, Anita Hopper.

47 - 5:00
Heritable variation of mRNA decay rates in yeast. Jennifer M. Andrie, Jon Wakefield, Joshua M. Akey.

Tribute to Fred Sherman

Given by Sue Liebman
Platform and Workshop Session Listings

Saturday, August 2 8:30 am–10:00 am
Meany Theater

Spatial Relationships
Chair: Yoshi Ohya

48 - 8:30
A Stable Quasi-Filamentous Growth Pattern in Budding Yeast. Junwon Kim, Mark D. Rose.

49 - 8:45

50 - 9:00
Spatial control of microtubule length and lifetime by opposing stabilizing and destabilizing functions of Kinesin-8. Yusuke Fukuda, Anna Luchniak, Erin Murphy, Mohan Gupta.

51 - 9:15
Polarization of the Endoplasmic Reticulum by ER-Septin Tethering. Jesse T. Chao, Andrew K. O. Wong, Shabnam Tavassoli, Barry P. Young, Adam Chruscicki, Nancy N. Fang, LeAnn J. Howe, Thibault Mayor, Leonard J. Foster, Christopher J. R. Loewen

52 - 9:30
Coordination between terminal septin subunits: both Cdc11 and Shs1 promote bud neck recruitment of the myosin II-binding factor Bni5. Gregory C. Finnigan, Julie Tagaki, Christina Cho, Elizabeth Booth, Jeremy Thorner.

53 - 9:45
A cytosolic chaperone network mediates quality control of higher-order septin assembly. C. Johnson, A. Weems, J. Brewer, J. Thorner, M. McMurray.

Saturday, August 2 10:30 am–12:00 noon
Meany Theater

Chromosome Rearrangements and Polyploidy
Chair: Audrey Gasch

54 - 10:30

55 - 10:45
The impact of polyploidy on the rate and dynamics of adaptation. Anna M. Selmecki, Yosef E. Maruvka, Philip A. Richmond, Marie Guillet, Noam Shoresh, Amber Sorenson, Subho De, Roy Kishony, Franziska Michor, Robin Dowell, David Pellman.

56 - 11:00
Polyploidy drives population heterogeneity through random and stepwise chromosome loss. Meleah A. Hickman, Carsten Paulson, Judith Berman.

57 - 11:15

58 - 11:30
Sexual conflicts and chromosome rearrangements drive infertility. Sarah E. Zanders, Michael Eickbush, Jonathan Yu, JiWon Kang, Gerry Smith, Harmit Malik.

59 - 11:45
3D structure of yeast synthetic chromosomes. Heloise Muller, Axel Cournac, Romain Koszul.
Saturday, August 2 2:00 pm–3:30 pm
Meany Theater

New Technologies
Chair: Sue Jaspersen

60 - 2:00

61 - 2:15

2:30
Judit Villen, Title unavailable at time of print

63 - 2:45
The use of fluorescence cross-correlation spectroscopy to assay information about protein complexes in yeast. Brian Slaughter, Jay Unruh, Christine Smoyer, Sue Jaspersen.

2:55
ŠTULIPs: tunable, light-controlled interacting protein tags for cell biology. Eric Weiss

3:05
N-terminal
An all-in-one yeast library - creating a new toolbox for studying the proteome. Uri Weill, Ido Yofe, Maya Schuldiner.

3:15
High level of chromosomal mosaicism in supposedly clonal yeast cell populations. Alexandre Gillet-Markowska, Gilles Fischer.

Saturday, August 2 4:00 pm–5:30 pm
Meany Theater

Yeast and Human Disease
Chair: Jasper Rine

64 - 4:00
Quantifying the functional impact of all possible missense variants of BRCA1. Lea Starita, Jacob Kitzman, Justin Gullingsrud, Jeffrey Parvin, Jay Shendure, Stanley Fields.

65 - 4:15
Using DNA Repair Mutants for Cancer Drug Discovery and Identifying Chemoresistance Targets. Irene Ojini, Alison Gammie.

66 - 4:30

67 - 4:45

68 - 5:00
Orphan Diseases: Identifying Genes and NovelTherapeutics to Enhance Treatment (IGNITE). Christopher McMaster.

69 - 5:15
Chromosome instability and synthetic cytotoxicity in yeast and cancer. Philip A. Hieter, Derek van Pel, Hunter Li, Noushin Moshgabadi, Melanie Bailey, Nigel O'Neil.

GSA Awards

Presentation of
Edward Novitski Prize to
Charlie Boone, University of Toronto

Presentation of
Elizabeth W. Jones Award for Excellence in Education to
Malcolm Campbell, Davidson College
Sunday, August 3 9:00 am–11:00 pm
Meany Theater

Genomics and Proteomics
Chair: Corey Nislow

9:00 am
Determination of in vivo RNA kinetics using RATE-seq.
David Gresham

9:15 am
Proteomic approach to predicting regulators of yeast response to 4MCHM. Jennifer Gallagher

9:30 am
Profiling the RNA maturation landscape in yeast. John Aitchison

9:45 am
Mapping the cellular response to small molecules using chemogenomic fitness signature, Guri Giaver

10:00 am
A Chemical-Genetic Matrix Strategy for Directed Discovery of Small Molecule Synergizers. Mike Tyers

10:15 am
Improving the yeast metabolic model using LOPIT proteomic data. Stephen Oliver

10:30 am
Extensive diversity in the transcriptional output from the yeast genome. Lars Steinmetz
Cell Biology: Cell cycle/Growth control/Metabolism

70A
Understanding the regulation of motor proteins in cdc15-2 cells recovering from spindle damage. Beryl Augustine, Foong May Yeong. Dept of Biochemistry, Yong Loo Lin School of Medicine, National University of Singapore, Singapore.

71B

72C
A cell separation checkpoint ensures proper order of late cytokinetic events. Jennifer L. Brace, Matthew Doerfler, Eric L. Weiss. Molecular Biosciences, Northwestern Univ, Evanston, IL.

73A
Respiro-fermentative differentiation in yeast colonies. Michal Cap1, Libuse Vachova2, Zdena Palkova1. 1) Department of Genetics and Microbiology, Faculty of Science, Charles University, 128 44 Prague, Czech Republic; 2) Institute of Microbiology of the ASCR, v.v.i., 142 20 Prague 4, Czech Republic.

74B

75C
The metabolic response to acetic acid stress in Saccharomyces cerevisiae. Yachen Dong, Zhihua Jiao, Jin Cai, Ruosi Fang, Qihe Chen. Department of Food Science and Nutrition, Zhejiang University, Hangzhou, China.

76A

77B
Quantifying Condition-Dependent Intracellular Protein Levels Enables High-Precision Fitness Estimates. Kerry A. Geier-Samerotte, Tatsu Hashimoto, Mike Dion, Bogdan Budnik, Ed Biohl, D. Allan Drummond. 1) Center for Genomics and Systems Biology, New York University, New York, NY; 2) Department of Biochemistry and Molecular Biology, University of Chicago, Chicago, IL 60637, USA; 3) Department of Statistics, Harvard University, Cambridge, MA 02138, USA; 4) FAS Center for Systems Biology, Harvard University, Cambridge, MA 02138, USA.

78C

79A

80B
Untargeted metabolomics reveals the rate of secondary mutations causing metabolic phenotypes. Julia A. Hanchard, Adam P. Rosebrock, Amy A. Caudy. 1) Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 2) Donnelly Center for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario, Canada.

81C
Functions of genes typical of structured colony morphology. Otakar Hlavacek1, Vratislav Stovicek2, Libuse Vachova1, Zdena Palkova2. 1) Laboratory of Cell Biology, Institute of Microbiology, ASCR, v.v.i., 142 20 Prague 4, Czech Republic; 2) Department of Genetics and Microbiology, Faculty of Science, Charles University in Prague, 128 44 Prague 2, Czech Republic.

82A

83B
SUN Family Proteins Sun4p, Uth1p and Sim1p are efficiently secreted out of the Saccharomyces cerevisiae cells and regulated differently during development of yeast cultures. Evgeny Kuznetsov1, Helena Kucerova2, Zdena Palkova1, Libuse Vachova2. 1) Department of Genetics and Microbiology, Charles University in Prague, Czech Republic; 2) Institute of Microbiology of the ASCR.
84C The Npr2 complex regulates a metabolic switch that controls TORC1 dependent proliferation during amino acid limited growth. Sunil Laxman, Benjamin Sutter, Lei Shi, Benjamin Tu. Biochemistry, UT Southwestern Medical Center, Dallas, TX.

85A Role for alkaline ceramidase and its products sphingoid bases in the oxidative stress response. Jae Kyo Yi, Ruijuan Xu, EunMi Jeong, Cungui Mao. The Department of Medicine and Cancer Center, Stony Brook University, Stony Brook, NY.


87C Measurement of thiamine vitamers and ethanol/CO2 in C. glabrata. Erin M. Neal, Christine L. Kerwin-Iosue, Dennis Wykoff. Biology Department, Villanova University, Villanova, PA.

88A Identification of regulators of riboneogenesis by high-throughput metabolomic and expression screens. Yoomi Oh1,2, Adam Rosebrock1, Amy Caudy1,2. 1) Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario, Canada; 2) Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada.

89B The fourth function of the cell wall. Hiroki Okada, Shinsuke Ohnuki, Yoshikazu Ohya. Integrated Biosciences, University of Tokyo, Kashiwa, Chiba, Japan.

90C Roles of four putative Cyk3-binding proteins in coordination of cleavage-furrow ingression and abscission during cytokinesis. Masayuki Onishi, Meng Wang, John Pringle. Dept Gen, Stanford Univ, Stanford, CA.

91A Contribution of metabolic adaptation and chronological aging to cell differentiation within yeast colonies. Zdena Palkova1, Libuse Vachova2, Michal Cap1, Marcela Hejlova2. 1) Department of Genetics and Microbiology, Charles University in Prague, 128 44 Prague 2, Czech Republic, zdenap@natur.cuni.cz; 2) Institute of Microbiology of the ASCR, v.v.i., 142 20 Prague 4, Czech Republic.

92B Roles of FMS1 (orf19.4589) and CBP1 (orf19.7323) genes in the de novo beta-alanine synthesis pathway from polyamines in Candida albicans. Ruvini U. Pathirana1, Dhammika H. M. L. P. Navarathna2, Kenneth W. Nickerson1. 1) School of Biological Sciences, University of Nebraska - Lincoln, Lincoln, NE; 2) Laboratory of Pathology, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, Maryland.

93C Revisiting the myth of trehalose in the heat shock response: The Tps1 protein, and not trehalose, protected yeast cells from losing viability at high temperature. M. Petitjean, MA. Teste, JL. Parrou. Laboratoire d’Ingénierie des Systèmes Biologiques et des Procédés, UMR-CNRS5504 & UMR-INRA 792 & INSA & Université de Toulouse, Toulouse, France.

94A Revisiting the role of TPS1 encoding trehalose 6-P synthase in the regulation of yeast glycolysis. M. Petitjean, A. Vax, MA. Teste, JL. Parrou, JM. François. Laboratoire d’Ingénierie des Systèmes Biologiques et des Procédés, UMR-CNRS5504, UMR-INRA 792, INSA, Toulouse, France.

95B Specific histone residues mediate RTS1 rescue of gcn5A growth under stress. Emily L. Petty1,2, Shannon M. Tomlinson1, Anne Lafon1, Bryce Mendelsohn1, Kristofer Webb1, Eric J. Bennett1, Lorraine Pillus1,2. 1) Division of Biological Sciences, UCSD, La Jolla, CA; 2) Moores Cancer Center Institute, UCDSD, La Jolla, CA; 3) Institut Curie, Paris; 4) Department of Pediatrics, Division of Medical Genetics, UCSF, San Francisco, CA.

96C Characterization of double budding in wild-type Saccharomyces cerevisiae. Angela L. Piotrowski, Robert M. Seiser. Roosevelt University, Schaumburg, IL.

97A Ubiquitylation may promote the Glc7 activity opposing Ipl1 kinase during mitosis. R. Ravindran1, P. Polk2, L. C. Robinson1, K. Tatchell1. 1) Biochemistry and Molecular Biology, LSUHSC, Shreveport, LA; 2) Research Core Facility, LSUHSC, Shreveport, LA.

98B The efflux pump MlcE from the Penicillium solitum compactin biosynthetic gene cluster increases Saccharomyces cerevisiae resistance to natural statins. Ana Rens, Rasmus John Normand Frandsen. DTU Systems Biology, Technical University of Denmark, Kongens Lyngby, Denmark.
Poster Session Listings

99C Determining the adaptive landscape of the SUL1 promoter. Matthew S. Rich1, Celia Payen1, Maitreya J. Dunham1, Stanley Fields1,2,3. 1) Department of Genome Sciences, University of Washington, Seattle, WA; 2) Department of Medicine, University of Washington, Seattle, WA; 3) Howard Hughes Medical Institute, University of Washington, Seattle, WA.

99D Physiological role of nitric oxide as a signaling molecule in the regulation of sporulation in Saccharomyces cerevisiae. Kyohei Saiki1, Akira Nishimura, Iwao Ohtsu, Daisuke Watanabe, Hiroshi Takagi. NAIST, Nara, Japan.

100A New insights into glucose sensing by S. cerevisiae. Kobi Simpson-Lavy1, Mark Johnston. Biochemistry and Molecular Genetics, CU-Denver School of Medicine, Aurora, CO, 80045.

100B A minimal glycolytic pathway in Saccharomyces cerevisiae. D. Solis-Escalante1, N. Barrajón Simancas1, N. G. Kuijpers1, J. T. Pronk1,2, JM. Daran1,2, P. Daran-Lapujade1. 1) Department of Biotechnology, Delft University of Technology, Delft, The Netherlands; 2) Platform Green Synthetic Biology, Delft, The Netherlands.


102C Feral strains forming biofilm colonies are derived from domesticated strains under stress conditions. Libuse Vachova1, Zdena Palkova2, Vratislav Stovic2, Marketa Begany1. 1) Institute of Microbiology of the ASCR, v.v.i., 142 20 Prague 4, Czech Republic, vachova@biomed.cas.cz; 2) Department of Genetics and Microbiology, Charles University in Prague, 128 44 Prague 2, Czech Republic.

103A Linker scanning mutagenesis of microtubule nucleating components Spe97 and Spe98. Kimberly Fong1, Jerry Tien1, Celia Payen1, Alex Zelter1, Beth Graczky1, Maitreya Dunham2, Trisha Davis1. 1) Department of Biochemistry, University of Washington, Seattle, WA; 2) Department of Genome Sciences, University of Washington, Seattle, WA.

104A Linker scanning mutagenesis of microtubule nucleating components Spe97 and Spe98. Kimberly Fong1, Jerry Tien1, Celia Payen1, Alex Zelter1, Beth Graczky1, Maitreya Dunham2, Trisha Davis1. 1) Department of Biochemistry, University of Washington, Seattle, WA; 2) Department of Genome Sciences, University of Washington, Seattle, WA.

105A Identification of yeast Greatwall kinase Rim15p as a novel negative regulator for alcoholic fermentation. Daisuke Watanabe1,2, Yan Zhou3, Aiko Hirata3, Yoshikazu Ohya3, Takeshi Akao2, Hitoshi Shimo2, Hiroshi Takagi1. 1) NAIST, Nara, Japan; 2) NRIB, Hiroshima, Japan; 3) University of Tokyo, Kashiwa, Japan.


107A An "oncometabolite" in yeast: 2-hydroxyglutarate accumulates in response to altered mitochondrial and central carbon metabolism. Olga Zaslaver1,2, Adam Rosebrock1, Amy Caudy1,2. 1) Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON, Canada; 2) Department of Molecular Genetics, University of Toronto, Toronto, ON, Canada.

Cell Biology: Cytoskeleton

108A Quality Control of Higher-order Septin Assembly: Mapping the Septin Proteostasis Network in vivo. Andrew Weems, Michael McMurray. Cell and Developmental Biology, University of Colorado Anschutz Medical Campus, Aurora, CO.

109A Linker scanning mutagenesis of microtubule nucleating components Spe97 and Spe98. Kimberly Fong1, Jerry Tien1, Celia Payen1, Alex Zelter1, Beth Graczky1, Maitreya Dunham2, Trisha Davis1. 1) Department of Biochemistry, University of Washington, Seattle, WA; 2) Department of Genome Sciences, University of Washington, Seattle, WA.

110A Kinetochores require oligomerization of the Dam1 complex to maintain microtubule attachments against tension during biorientation. Neil Umbreit1, Matthew Miller3, Jérôme Cattin-Ortolà1, Jerry Tien1, Charles Asbury1, Trisha Davis1. 1) Department of Biochemistry, University of Washington, Seattle, WA; 2) Division of Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA; 3) Department of Physiology and Biophysics, University of Washington, WA.

111A Identification of yeast Greatwall kinase Rim15p as a novel negative regulator for alcoholic fermentation. Daisuke Watanabe1,2, Yan Zhou3, Aiko Hirata3, Yoshikazu Ohya3, Takeshi Akao2, Hitoshi Shimo2, Hiroshi Takagi1. 1) NAIST, Nara, Japan; 2) NRIB, Hiroshima, Japan; 3) University of Tokyo, Kashiwa, Japan.

112A Crosslinking analysis identifies hundreds of distance constraints in protein complexes. Alex Zelter1, Michael Hoopman2, Richard Johnson3, Michael MacCoss3, Robert Moritz2, Trisha Davis1. 1) Department of Biochemistry University of Washington, Seattle, WA; 2) Institute for Systems Biology, Seattle, WA; 3) Department of Genome Sciences, University of Washington, Seattle, WA.
Cell Biology: Mating/Sporulation/Meiosis

113B Regulation of the Ndc80 complex during meiosis in budding yeast. Jingxun Chen1, Angelika Amon2, Elcin Unal1. 1) Department of Molecular and Cell Biology, University of California, Berkeley, Berkeley, CA; 2) Department of Biology, Massachusetts Institute of Technology, Cambridge, MA.

114C To What Extent Does Homologous Chromosome Pairing Depend on Recombination-Independent Chromosome Interactions? S. Cheng, A. MacQueen. Wesleyan University, Middletown, CT.

115A Regulation of nuclear shape in response to mating pheromone. Alison Walters, Emma Dauster, Orna Cohen-Fix. NIDDK/NIH, LCMB, Bethesda, MD.


120C Translational regulation determines gene insulation during yeast meiosis. Liang Jin, Rolf Stenzel, Aaron Neiman. Department of Biochemistry and Cell Biology, Stony Brook University, Stony Brook, NY.

121A Multiple MAPK cascades regulate the transcription of IME1, the master transcriptional activator of meiosis in Saccharomyces cerevisiae. Yona Kassir1, Smadar Kahana-Edwin1, Michal Stark2. 1) Dept Biol, Technion Inst, Haifa, Israel; 2) Cancer Research Center, Sheba Medical Center, Tel-Hashomer, Israel 52621.

122B Schizosaccharomyces japonicus provides the second example where chirality of DNA strands causes sister-sister cells developmental asymmetry. Amar J. S. Klar. Gene Reg & Chromosome Biol Lab, NCI-Frederick Cancer Res Fac, Frederick, MD.

123C A mating pathway deficiency as a reproductive barrier between Saccharomyces cerevisiae and Saccharomyces paradoxus. Camille Meslin, Allyson O'Donnell1, Nathan Clark' 1) Computational and Systems Biology, University of Pittsburgh, Pittsburgh, PA; 2) Cell Biology, University of Pittsburgh, PA.


125B SPS1 and SPO77 act together to regulate prospore membrane closure during sporulation in S. cerevisiae. Scott Paulissen. Christian Slubowski, Linda Huang. Biology, University of Massachusetts Boston, Boston, MA.

126C Characterizing the function of Kar5p during inner nuclear membrane fusion during yeast mating. Jason V. Rogers. Mark D. Rose. Department of Molecular Biology, Princeton University, Princeton, NJ.

127A Quantification of Meiotic Chromosome Mis segregation Frequency in Natural Isolates of Saccharomyces cerevisiae. Amy Carol Sirr, Gareth Cromie, Aimée Dudley. Pacific Northwest Diabetes Research Inst, Seattle, WA.

128B Kel1p collaborates with Fus2p for yeast cell fusion. Jean Smith, Richard Stein, Mark Rose. Molecular Biology, Princeton University, Princeton, NJ.

129C KAR4 has separable functions in mating and multiple steps of meiosis. Abigail J. Sporer, Mark D. Rose. Molecular Biology, Princeton University, Princeton, NJ.
### Poster Session Listings

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<tr>
<td>130A</td>
<td>Unprogrammed presentation number</td>
<td>Kelsey Van Dalfsen, Gloria Brar. Molecular and Cell Biology, UC-Berkeley, Berkeley, CA.</td>
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<tr>
<td>132C</td>
<td>Mitochondrial ribosome function/assembly: Regulation by accessory factors in <em>Saccharomyces cerevisiae</em>.</td>
<td>Kaustuv Datta, Jaswinder Kaur, Dharmendra Pandey. Department of Genetics, University of Delhi South Campus, New Delhi, India.</td>
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<td>133A</td>
<td>PEP3 overexpression protects yeast from acid stress by promoting vacuolar biogenesis.</td>
<td>J. Ding1,2, G. Holzwarth3, S. Bradford3, B. Cooley4, A. Yoshinaga5, J. Patton-Vogt4, H. Abeliovich6, M. Penner7, A. Bakalinsky1,2.</td>
<td>Department of Biochemistry &amp; Biophysics, Oregon State University, Corvallis, OR, USA; 2) Department of Food Science &amp; Technology, Oregon State University, Corvallis, OR, USA; 3) Environmental &amp; Molecular Toxicology, Oregon State University, Corvallis, OR, USA; 4) Biological Sciences, Duquesne University, Pittsburgh, PA, USA; 5) Department of Microbiology, Oregon State University, Corvallis, OR, USA; 6) Department of Biochemistry and Food Science, Hebrew University, Rehovot, Israel.</td>
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<td>134B</td>
<td>Ysp1 homologous proteins participate in responses to membrane stress in <em>S. cerevisiae</em> and <em>S. pombe</em>.</td>
<td>Vladimir Sirokin1, Michael James1, Elizabeth Bonarigo6, Gary Franke2, Kelly Hopkins2, Scott Erdman1,2.</td>
<td>1) Dept of Cell and Developmental Biology, SUNY Upstate School of Medicine, Syracuse, NY; 2) Dept Biol, Syracuse Univ, Syracuse, NY.</td>
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<td>135C</td>
<td>Elucidation of the Mitochondrial Protein-Protein Interaction Network.</td>
<td>Matthew G. M. Jessulat1, Hiroyuki Aoki1, Zoran Minic3, James Vlasblom2, Sadhana Phanse1,3, Zhaolei Zhang2, Jodi Nunnari3, Mohan Babu1.</td>
<td>1) Department of Chemistry and Biochemistry, University of Regina, Regina, Saskatchewan, Canada; 2) Department of Chemistry, University of Toronto, Toronto, Canada; 3) Banting and Best Department of Medical Research, Donnelly Center, University of Toronto, Toronto, Ontario, Canada; 4) Department of Microbiology and Molecular Genetics, University of California Davis, California, USA.</td>
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<td>MTG3, a putative GTPase that regulates mitochondrial ribosome function in <em>Saccharomyces cerevisiae</em>.</td>
<td>Upasana Mehra, Yash Verma, Kaustuv Datta. Department of Genetics, University of Delhi, New Delhi, India.</td>
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<td>138C</td>
<td>A genetic screen for suppressors of the age-associated decline of mitochondrial membrane potential.</td>
<td>NH Thayer1,2, MA Borden3, AL Hughes4, D. Lindstrom3, FS Vizeacoumar4, C. Boone4, DE Gottschling1.</td>
<td>1) Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Molecular and Cellular Biology Program, University of Washington, Seattle, WA; 3) Current Location: Biological Chemistry, University of Utah, Salt Lake City, UT; 4) University of Toronto, Toronto, ON.</td>
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<td>Membrane insertion mechanisms of mitochondrially-encoded proteins by the Oxa1 homolog, Cox18.</td>
<td>Mei-Yi Zheng, Heather L. Fiumera. Dept. of Biological Sciences, Binghamton University, Binghamton, NY.</td>
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### Cell Biology: Mitochondria/Vacuoles/Peroxisomes

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### Cell Biology: Protein Sorting and Turnover

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142A
Stress conditions promote Gap1 permease ubiquitylation and downregulation via the arrestin-like Bul and Aly proteins. M. Crapeau, A. Merhi, B. Andre. IBMM, Free University of Brussels, Gosselies, Belgium.

143B
The protein quality control machinery regulates its misassembled proteasome subunits, and distinguishes them from proteasome storage granules. S. Ben-Aroya, L. Peters, O. Yogev, R. Hazan. Bar-Ilan University, Ramat-Gan, Israel.

144C
Cdc48-Shp1 chaperone promotes structural integrity of protein phosphatase 1 holoenzyme. You-Liang Cheng, Rey-Huei Chen1,2. 1) Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan; 2) Graduate Institute of Life Sciences, National Defense Medical Center, Taipei, Taiwan.

145A
The Yeast Biogenesis of Lysosome Related Organelle (BLOC) Complex interacts with ESCRT to regulate endosomal trafficking. Lauren E. Dalton1, Matthew Jessulat2, Viktor Deineko3, Jeffery Tong1, Mohan Babu2, Elizabeth Conibear1. 1) Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC, Canada; 2) Department of Biochemistry, Research and Innovation Centre, University of Regina, Regina, Saskatchewan, Canada.

146B
Identifying new protein trafficking networks using evolutionary rate covariation (ERC). Zelia A. Ferreira1, Allyson F. O’Donnell1, Nathan L. Clark1. 1) Computational and Systems Biology, University of Pittsburgh, 15260, Pittsburgh, PA; 2) Dept. of Cell Biology, Univ. of Pittsburgh, 15260, Pittsburgh, PA.

147C
Hsp31 is a Stress-response Chaperone that Prevents α-Synuclein Aggregation. Chai-jui Tsai1, Kiran Aslam1, Holli Brendel2, Josephat Asiago1, Kourtney Fultz1, Jean-Christophe Rochet1, Tony Hazbun1. 1) Department of Medicinal Chemistry and Molecular Pharmacology, Purdue University, West Lafayette, IN; 2) Department of Medical and Molecular Genetics, Indiana University School of Medicine, Indianapolis, IN.

148A
Degeneracy of parameters underlying partitioning of macromolecular content upon yeast cell division. Ali Kinkhabwala1, Anton Khmelinskii1, Michael Knop1. 1) ZMBH, University of Heidelberg, Heidelberg, Germany; 2) Max Planck Institut of molecular Physiology, Dortmund, Germany.

149B
Vps13 plays a role at the early and late endosomes. Kathleen L. Kolehmainen1,2, Elizabeth Conibear1. 1) Biochemistry and Molecular Biology, University of British Columbia, Vancouver, British Columbia, Canada; 2) Centre for Molecular Medicine and Therapeutics, Vancouver, British Columbia, Canada.

150C

151A
Impairment of translocon-associated protein degradation under conditions of endoplasmic reticulum stress. Eric M. Rubenstein1, Mark Hochstrasser2. 1) Department of Biology, Ball State University, Muncie, IN; 2) Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT.

152B
Substrate-induced ubiquitylation and endocytosis of Gap1 and Can1 permeases: role of arrestin-like proteins. Elie Saliba1, Kassem Gheddar1, Ahmad Merhi1, Eva-Maria Krammer2, Martine Prévost1, Bruno André1. 1) Molecular Physiology of the Cell, Université Libre de Bruxelles, IBMM, 6041 Gosselies, Belgium; 2) Structure and Function of Biological Membranes, Université Libre de Bruxelles, Campus Plaine, 1050 Brussels, Belgium.

153C

154A
A direct role of HRD3 in ER associated degradation (ERAD). Nidhi Vashista1, Sarah Carroll1, Randolph Hampton1. 1) Cell and Developmental Biology, University of California San Diego, La Jolla, CA; 2) University of Washington, Seattle, WA.

155B
The alternate clathrin adaptor complex subunit Apm2 works with Imalp in a distinct protein transport pathway. Shawn T. Whitfield1,2, Helen E. Burston3, Nandini Raghuram1, Elizabeth Conibear1. 1) Biochemistry and Molecular Biology, University of British Columbia, Vancouver, British Columbia, Canada; 2) Centre for Molecular Medicine and Therapeutics, Vancouver, British Columbia, Canada.
Cell Biology: Signal Transduction

156C
Non-Preferred Carbon Source Utilization Induces Snf1p- and ER Stress-Dependent Activation of the High Osmolarity Glycerol (HOG) Pathway. Hema Adhikari, Paul Cullen. Department of Biological Sciences at SUNY-Buffalo, NY 14260-1300.

157A
ER Stress Stimulates Mucin Receptor Signaling From the Secretory Pathway. Hema Adhikari1, Nadia Vadaie1, Jacky Chow1, Christopher Stefan2, Jason MacGurn2, Paul Cullen1. 1) Department of Biological Sciences at SUNY-Buffalo, 14260-1300; 2) Weill Institute for Cell and Molecular Biology & Department of Molecular Biology and Genetics Cornell University Ithaca NY 14853-7202.

158B
Quantifying the effect of coding sequence variation in human orthologs of Saccharomyces cerevisiae Bim1 on the pheromone response. D. Britain1,2, W. Peria1, G. Pesce1, R. Brent1,2,5. 1) Division of Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Department of Bioengineering, University of Washington, Seattle, WA; 3) Department of Biochemistry, University of Washington, Seattle, WA; 4) The Molecular Sciences Institute, Berkeley, CA; 5) Department of Genome Sciences, University of Washington, Seattle, WA.

159C

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161B
The Cdc42-Interacting Protein Bem4 Regulates the Filamentous Growth Pathway. Colin A. Chavel1, Andrew Pitoniak1, Jeremy Smith1, Diawoye Camara1, Jacky Chow1, Sheelaranji Karunanithi1, Ken Wolfe2, Paul Cullen1. 1) University at Buffalo, SUNY, 337 Cooke Hall, North Campus, Buffalo, NY 14260; 2) Smurfit Institute of Genetics, Trinity College, University of Dublin, Dublin 2, Ireland.

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163A
Tor1 and PKA downregulation in stationary phase rely on Mtl1 to preserve mitochondrial integrity and cell survival. Venkatraghavan Sundaran1, Mima Petkova1, Nuria Pujol-Carrion1, Jordi Boada2, Maria Angeles de la Torre-Ruiz1. 1) Basic Medical Sciences-IRBLLeida, University of Lleida, LLEIDA, Spain; 2) Experimental Biology-IRBLLeida, University of Lleida, Lleida, Spain.

164B
Calcineurin regulates the yeast synaptojanin Inp53/Sjl3 during membrane stress. Evan Guiney1, Joshua Elias2, Martha Cyert1. 1) Biology, Stanford University, Stanford, CA; 2) Chemical and Systems Biology, Stanford University, Stanford, CA.

165C
TOR Complex 1 is a direct target of amino acid sensor Gcn2. Wenjie Yuan, Yu Jiang. Department of Pharmacology and Chemical Biology, Univ Pittsburgh, Pittsburgh, PA.

166A
Protein-Protein Interactions of the Yak1 Kinase. Adeline Boettcher, Scott Blaszak, Samantha J. DeWerff, Stephen D. Johnston. Department of Biology, North Central College, Naperville, IL.

167B
Endolysosomal membrane trafficking complexes drive nutrient-dependent TORC1 signaling to control cell growth in Saccharomyces cerevisiae. Joanne M. Kingsbury, Neelam D. Sen, Maria E. Cardenas. Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, NC.

168C
Membrane fluidity and temperature sensing are coupled via circuitry comprised of Ole1, Rps5, and Hsf1 in Candida albicans. Michelle Leach1,2, Leah Cowen1. 1) Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 2) Aberdeen Fungal Group, University of Aberdeen, Institute of Medical Sciences, Aberdeen, UK.

169A
Regulation of the essential protein kinase Ypk1 by the TORC2 complex. Kristin Leskoske, Françoise Roelants, Jeremy Thorner. Div. of Biochemistry, Biophysics and Structural Biology, Dept. of Molecular and Cell Biology, Univ. of California, Berkeley, CA 94720-3202 USA.
170B

171C
The phosphorylation state of *Saccharomyces cerevisiae* signaling proteins varies in a stress-dependent fashion. Matthew MacGilvray¹, Anna Larson², David Berry³, Josh Coon⁴, Audrey Gasch⁵. 1) Laboratory of Genetics, University of Wisconsin-Madison, Madison, WI; 2) Department of Chemistry, University of Wisconsin-Madison, Madison, WI; 3) Institute for Neurodegenerative Disease, UCSF School of Medicine, San Francisco, CA.

172A
Substrate sequence specificity and catalytic properties of the signaling Ssy5 endoprotease. Antonio Martins, Per Ljungdahl. Department of Molecular Biosciences, The Wenner-Gren Institute, Stockholm University, Stockholm, Sweden.

173B
TORC1 regulates the yeast lipin Pah1 via the Nem1/Spo7 protein phosphatase complex. Emmanuelle Dubots, Stéphanie Cottier, Marie-Pierre Péli-Gulli, Malika Jaquenoud, Sérénine Bontron, Marta Moreno Torres, Roger Schneider, Claudio De Virgilio. Department of Biology, Unit of Biochemistry, University of Fribourg, Fribourg, Switzerland.

174C
TORC2-dependent Protein Kinase Ypk1 Phosphorylates Ceramide Synthase Components Lag1 and Lac1 to Stimulate Sphingolipid Synthesis. Alexander Muir, Subramaniam Ramachandran, Françoise Roclants, Garrett Timmons, Jeremy Thorner. Department of Molecular and Cell Biology, University of California, Berkeley, Berkeley, CA.

175A
Target of rapamycin-responsiveness on the GATA-family transcription activator Gln3. Rajendra Rai¹, Jennifer J. Tate¹, Karthik Shannunganatham², Martha M. Howe³, Terrance G. Cooper¹. 1) Dept. Microbiol., Immunol. and Biochem., Univ. Tennessee, Memphis, TN; 2) Dept. Infectious Disease, St. Jude Children's Research Hospital, Memphis, TN.

176B

177C
Functional characterization of protein interactors of Wsc1p and Mid2p stress sensors and PKC1 signaling in *Saccharomyces cerevisiae*. Ednalise Santiago-Cartagena¹, Vladimir Vélez-Segarra¹, Igor Stagljar¹, Brian C. Rymond³, José R. Rodríguez-Medina¹. 1) Biochemistry, University of Puerto Rico- Medical Sciences Campus, San Juan, PR; 2) Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Canada; 3) University of Kentucky, Lexington, KY.

178A

179B
Role of the Glc7-Reg1/2 phosphatase in the control of the Mig1 transcriptional repressor. Sviatlana Shashkova¹, Raul Garcia-Salcedo³, Loubna Bendrioua¹, Timo Lubitz², Niek Welkenhuysen¹, Edda Klipp², Stefan Hohmann¹. 1) Chemistry and Molecular Biology, University of Gothenburg, Sweden; 2) Theoretical Biophysics, Humboldt-Universität zu Berlin, Germany.

180C
Components of the Vid30 complex participates in the transcriptional regulation of glucose-repressed genes in *Saccharomyces cerevisiae*. Angus Ross, Chris Snowdon, Andrew Fletcher, George van der Merwe. Department of Molecular & Cellular Biology, University of Guelph, Guelph, Canada.

181A
Dynamics of MAPK signaling in *Saccharomyces cerevisiae*. Sarah Weisser¹,², Konstanze Bandmann¹,², Julia van der Felden¹,², Peter Lenz¹,², Hans-Ulrich Mösch¹,². 1) Department of Genetics, Philipps-Universität Marburg, Karl-von-Frisch-Straße 8, 35043 Marburg, Germany; 2) Department of Physics, Philipps-Universität Marburg, Renthof 6, 35032 Marburg, Germany; 3) LOEWE-Center for Synthetic Microbiology (SYNMIKRO), Hans-Meerwein-Straße, 35043 Marburg.

182B
Glucose derepression via Snf1-Mig1 is controlled at different levels. Niek Welkenhuysen, Tian Ye, Raul Garcia-Salcedo, Stefan Hohmann. Department of Chemistry and Molecular Biology, University of Gothenburg, Gothenburg, Sweden.

183C
Dissecting the role of calcineurin and protein kinase C signalling in Hsp90-dependent caspofungin tolerance. Jinglin L. Xie¹, Michelle D. Leach¹,², Leah E. Cowen¹. 1) Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 2) Aberdeen Fungal Group, School of Medical Sciences, Institute of Medical Sciences,
University of Aberdeen, Foresterhill, Abderdeen, United Kingdom.

**184A**
TORC1 and TORC2 regulate Rps6 phosphorylation via Ypk1/2/3 in budding yeast. Seda Yerlikaya¹, Madeleine Meusburger¹, Alexandre Huber², Dorothea Anrather³, Gustav Ammerer², Robbie Loewith¹. 1) Molecular Biology, University of Geneva, Geneva, Switzerland; 2) Max F. Perutz Laboratories, Department of Biochemistry, University of Vienna, Dr. Bohrgasse 9, A1030 Vienna, Austria; 3) Swiss National Centre for Competence in Research Programme Chemical Biology, Geneva 1211, Switzerland.

**185B**
Mechanisms of nitrogen in regulating cAMP signal in Saccharomyces cerevisiae. Y. Li¹, A. Zhang¹,², H. Jin¹. 1) Hebei University of Technology, No8 Guangrong Road, Hongqiao District, Tianjin, China; 2) Tianjin University, No92 Weijin Road, Nankai District, Tianjin, China.

**186C**
Characterization of the Recruitment of Casein Kinase 1 to P Bodies. Bo Zhang, Khyati Shah, Qian Shi, Paul Herman. Molecular Genetics, The Ohio State University, Columbus, OH 43210.

**Cell Biology: Other**

**187A**
An overexpression suppressor screen to identify genes that are effectors of nuclear morphology in Saccharomyces cerevisiae. James T. Arnone, Orna Cohen-Fix. Laboratory of Cell and Molecular Biology, NIDDK/NIH, Bethesda, MD.

**188B**
A cell biological screen for age dependent changes in lipid metabolic pathways reveals changes in sphingolipid pathways. Anthony O. Beas, Karen L. Zhao, Daniel E. Gottschling. Division of Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA.

**189C**
Molecular switches of Golgi size control. Madhura D. Bhave, Prasanna Iyer, Bhawik Jain, Dibyendu Bhattacharyya. Bhattacharyya lab, Advanced Centre for Treatment, Research & Education in Cancer (ACTREC), Tata Memorial Centre, Kharghar, Sector 22, Navi Mumbai-410 210. MH INDIA.

**190A**
The osmotolerant yeast *Zygosaccharomyces rouxii* possesses two differently regulated glycerol transporters. Michala Bubnová¹, Hana Sychrová¹, Candida Lucas². 1) Department of Membrane Transport, Institute of Physiology Academy of Sciences of the Czech Republic, v.v.i, Prague, Czech Republic; 2) Department of Biology, University of Minho, Campus de Gualtar, Braga, Portugal.

**191B**
A conserved role for GSK3β in regulating lipid homeostasis through lipins. Leslie J. Chan¹,², Jennifer McQueen¹,³, Timothy R. Peterson²,³, Meredith Briggs¹, David M. Sabatini²,³, Vivien Measday⁴, Christopher J. R. Loewen¹. 1) Department of Cellular and Physiological Sciences, University of British Columbia, Vancouver, British Columbia, V6T 1Z3, Canada; 2) Whitehead Institute for Biomedical Research, Cambridge, MA 02142, USA; 3) Wine Research Centre, Faculty of Land and Food Systems, University of British Columbia, Vancouver, British Columbia, V6T 1Z3, Canada; 4) Howard Hughes Medical Institute; 5) These authors contributed equally to this work.

**192C**

**193A**
The JmjC Domain-containing Regulator Gis1 is Regulated by Levels of Heme and Oxygen Independently. Jonathan M. Comer, Ajit Shah, Sneha Lal, Thai Cao, Jagmohan Hooda, Li Zhang. Molecular and Cell Biology, University of Texas at Dallas, Richardson, TX.

**194B**
Characterization of the CIA complex in maintaining genome stability. Lilach Emuna, Marina Volpe, Galit David Kadoch, Shay Ben A. roya. Faculty of Life Science, Bar-Ilan University, Ramat-Gan, Israel.

**195C**

**196A**
The Role of Phosphorylation in Ribosomal Protein L4. Jesse Michael Fox, Lasse Lindahl. Biological Sciences, University of Maryland, Baltimore County, Baltimore, MD.
197B
Understanding the role of the translation factor eIF5A through genetic interaction network of different mutants. Fabio C. Galvao¹, Sara Sharifpoor², Danuza Rossi¹, PPaulo E. G. Boldrin³, Natalia M. Barboas¹, Brenda J. Andrews², Cleslei F. Zanelli¹, Sandro R. Valentini¹. 1) Biological Science, UNESP-Univ. Estadual Paulista, Araraquara, São Paulo, Brazil; 2) Department of Molecular Genetics, The Donnelly Centre for Cellular and Biomolecular Research, University of Toronto.

198C
Allele-specific SGA screening to identify functions for ER polarization. Analise K. Hofmann, Andrew K. O. Wong, Christopher J. R. Loewen. 2350 Health Sciences Mall University of British Columbia Vancouver, B. C. Canada V6T 1Z3.

199A
YlSnf1 Affects the Production of Omega-3 Fatty Acids from Yarrowia lipolytica. J. Seip, R. Jackson, H. He, Q. Zhu, S.-P. Hong. Biotechnology, DuPont Central R&D, Wilmington, DE.

200B
PM - ER Membrane Tethering Complexes and Non-vesicular Sterol Transport. Jesper Johansen¹, Evan Quon¹, Yves Sere², Anant K. Menon¹, Christopher T. Beh¹. 1) Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, British Colombia, Canada; 2) Department of Biochemistry, Weill Cornell Medical College, New York, NY.

201C
Hsp104 as stress indicator in hybrids of the Saccharomyces sensu stricto complex. Claudia Kempf, Jürgen Wendland. Carlsberg Laboratory, Copenhagen, Denmark.

202A
Roles of the Yap1 Transcription Factor and Antioxidants in Saccharomyces cerevisiae’s Tolerance to Furfural and 5-Hydroxymethylfurfural, which Function as Thiol-Reactive Electrophiles Generating Oxidative Stress. Dahee Kim, Ji-Sook Hahn. Chemical and Biological engineering, Seoul National University, Seoul, South Korea.

203B
A metabolic strategy to enhance long-term survival by Phx1 through stationary phase-specific pyruvate decarboxylases in fission yeast. Eun Jung Kim, Ji Yoon Kim, Jung Hye Roe. School of Biological Sciences, Seoul National University, Seoul, Korea.

204C
Evaluation of cytotoxicity caused by the strong expression of GFPs with various localization signals. R. Kintaka, K. Makanae, H. Moriya. RCIS, Okayama University, City of Okayama, Japan.

205A
Swi3, a novel regulator of aerobic respiration genes and oxygen metabolism in Saccharomyces cerevisiae. Sneha Lal, Jagmohan Hooda, Md Maksudul Alam, Ajit Shah, Thai Cao, Li Zhang. Molecular and Cell Biology, University of Texas at Dallas, Richardson, TX.

206B
Mechanism of Non-Genetic Heterogeneity in Growth Rate of Saccharomyces cerevisiae. Shuang Li, Mark Siegal. Department of Biology, New York University, New York, NY.

207C
Heavy Water Promotes Longevity in Yeast. Xiyan Li, Michael Snyder. Genetics, Stanford University, Stanford, CA.

208A

209B
Changes in transcription and metabolism during the early stage of replicative cellular senescence in budding yeast. Yukio Mukai¹, Yuka Kamei¹, Yoshihiro Tamada², Yasumune Nakayama³, Eiichiro Fukusaki³. 1) Department of Bioscience, Nagahama Institute of Bio-Science and Technology, 1266 Tamura-cho, Nagahama, Shiga 526-0829, Japan; 2) Department of Biotechnology, Graduate School of Engineering, Osaka University, 2-1 Yamadaoka, Suita, Osaka 565-0871, Japan.

210C
Changes in intracellular abundance and localization of Saccharomyces cerevisiae Hsp31p under various environmental stresses suggest its role in neutralizing the effects of oxidative stress insult. Urszula Natkanska¹, Adrianna Skoneczna², Marek Skoneczny¹. 1) Department of Genetics, Institute of Biochemistry and Biophysics Polish Academy of Sciences, Warszawa, Poland; 2) Laboratory of Mutagenesis and DNA Repair, Institute of Biochemistry and Biophysics Polish Academy of Sciences, Warszawa, Poland.

211A
Cell wall architecture in wine yeast: Compositional and physiological analysis of yeast cell walls having varying impact on wine protein stability. Thulile Ndlovu, Florian F. Bauer. Institute for Wine Biotechnology, Faculty of AgriSciences, South Africa, Western Cape, South Africa.
212B
Elucidating the Effects of Human Genetic Variation On Vitamin D Signaling. Lauren Richardson, Jasper Rine. QB3, University of California, Berkeley, Berkeley, CA.

213C
The stress response pathway is activated in siw14 mutants. Elizabeth Steidle, Daisy Walker, Ronda J. Rolfe. Biology, Georgetown University, Washington, DC.

214A
Inducible and rapid depletion of proteins in S. cerevisiae. Fabian Rudolf, Gintautas Vainorius, Moritz Lang, Joerg Stelling. D-BSSE, ETH Zurich, 4058 Basel, Switzerland.

215B

216C
Selection for strains of Saccharomyces cerevisiae with enhanced Ochratoxin-A detoxification capabilities. Aaron Welch. Chaplin School of Hospitality and Tourism, Florida International University, North Miami, FL.

217A
Identifying biomarkers of extended chronological lifespan through comparative gene expression profiling. Margaret B. Wierman, Mirela Matecic, Veena Valsakumar, Daniel L. Smith, Stefan Bekiranov, Jeffrey S. Smith. Department of Biochemistry and Molecular Genetics, University of Virginia, Charlottesville, VA.

218B
An ER-Septin Diffusion Barrier Polarizes the Endoplasmic Reticulum. Andrew K. O. Wong1, Jesse T. Chao1, Shahnam Tavassoli1, Barry P. Young1, Adam Chrusciicki2, Nancy N. Fang2,3, LeAnn J. Howe2, Thibault Mayor2,3, Leonard J. Foster2,3, Christopher J. R. Loewen1. 1) Cellular and Physiological Sciences, University of British Columbia, Vancouver, British Columbia, Canada; 2) Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, British Columbia, Canada; 3) Centre for High-Throughput Biology, University of British Columbia, Vancouver, British Columbia, Canada.

219C
Structural and functional analysis of Saccharomyces cerevisiae cell surface adhesins. N. Wozniak, H.-U. Mösch. Philippus University Marburg, Department of Genetics, Karl-von-Frisch-Straße 8, 35043 Marburg, Germany.

220A
Chromatin regulation of pericentric non-coding RNA in S. cerevisiae affects chromosome stability. Julia Allison Gallo, Jen Gallagher. Biology, West Virginia University, Morgantown, WV.

221B
Dynamic Regulation of the Cnn1-Ndc80 Kinetochore Interaction During Mitosis. Kriti Shrestha1, Amanda Oldani2, Cinzia Pagliuca2, Peter De Wulf2, Tony Hazbun1. 1) Dept MCMP, Purdue Univ, West Lafayette, IN; 2) European Institute of Oncology, Department of Experimental Oncology, Milan, 20139, Italy.

222C

223A
Regulation of centromeric nucleosome localization by the E3 ubiquitin ligase Psh1. Erica Marie Hildebrand1,2, Sue Biggins1. 1) Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Molecular and Cellular Biology, University of Washington, Seattle, WA.

224B
Development of an in vitro kinetochore assembly assay to investigate kinetochore function and two alternate assembly pathways. Jackie Lang1,2, Sue Biggins1,2. 1) Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Molecular and Cellular Biology, University of Washington, Seattle, WA.

225C
Molecular Basis of Deleterious Pericentric Recombination during Meiosis. Mridula Nambiar, Gerald Smith. Division of Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA.

226A
Mutations in histones H3 and H4 define nucleosome regions essential for chromosome segregation. Payel Chaudhuri, Ines Pinto. Dept Biological Sciences, University of Arkansas, Fayetteville, AR.


Chromosome Dynamics: Chromosome Structure

227B
The stromalin conservative domain in the Sec3 subunit of cohesin mediates the interaction with both Mcd1 and the loading complex. Ola Origil 1, Avi Matityahu 1, Thomas Eng 2, Vincent Guacci 2, Douglas Koshland 2, Itay Onn 1. 1) Faculty of Medicine, Bar-Ilan University, Safed, Israel; 2) Molecular and Cell Biology Dept, University of California, Berkeley, Berkeley, CA USA.

228C
Stability of a Large Amplification in Saccharomyces cerevisiae. Jamie Pogachar, Celia Payen, Maitreya Dunham. Genome Sciences, University of Washington, Seattle, WA.

229A
Chromosome Breakage at Potential Fragile Sites in Retrotransposon Overdose Strains. Cristina M. Lanzilotta 1, Samantha Minikel 1, Nicholas Monteleone 1, Bracha Erlanger 2, Sarah J. Wheelan 2, Lisa Z. Scheifele 1. 1) Department of Biology, Loyola University Maryland, Baltimore, MD; 2) Department of Oncology, Division of Biostatistics and Bioinformatics, Center for Computational Genomics, Johns Hopkins School of Medicine, Baltimore, MD.

230B
Interface between a two-cohesin complex model of cohesion and DNA replication. Kevin Tong, Soumya Rudra, Robert V. Skibbens. Biological Sciences, Lehigh University, Bethlehem, PA.

Chromosome Dynamics: Mutagenesis/Repair

231C
Systematic gene over-expression screen for increased mutation rate in Saccharomyces cerevisiae. Jonathan S. Ang 1, Supipi Duffy 1, Peter C. Stirling 2, Phil Hieter 1. 1) University of British Columbia, Vancouver, Canada; 2) Terry Fox Laboratory, BC Cancer Agency, Vancouver, Canada.

232A

233B
The State of the Rfa2 N-Terminus Affects Rfa1-Protein Interactions that Map Outside of the Rfa1 N-Terminus. Kaitlin M. Dailey, Erica N. Mueller, Gunjan Piya, Stuart J. Haring. Chemistry and Biochemistry, North Dakota State University, Fargo, ND.

234C

235A
Distinct Roles for the Rfa2 N-Terminus in the DNA Damage Response and Adaptation in Saccharomyces cerevisiae. Padmaja L. Ghospurkar 1, Timothy M. Wilson 1, Amber L. Severson 1, Sarah J. Klein 2, Sakina K. Khaku 1, Andre P. Walther 2, Stuart J. Haring 1. 1) Department of Chemistry and Biochemistry, North Dakota State University, Fargo, ND; 2) Biological Sciences, Cedar Crest College, Allentown, PA.

236B
The application of glucose starvation as a selective force for the study of adaptive mutations in yeast. Maria Hubmann, Petra Dorninger, Agnes Civegna, Erich Heidenreich. Institute of Cancer Research, Dep. of Medicine I, Medical University of Vienna, Vienna, Austria.

237C
Volatility of mutator phenotypes at single cell resolution. Alan Herr, Scott Kennedy, Eric Schultz, Thomas Chappell, Gary Knowels, Brendan Kohrn. Department of Pathology, University of Washington, Seattle, WA.

238A
An experimental system to investigate large-scale CAG/CTG trinucleotide repeat expansions. Jane C. Kim, Samantha T. Harris, Kartik A. Shah, Sergei M. Mirkin. Biology, Tufts University, Medford, MA.

239B
Stimulation of RNA Polymerase II ubiquitination by yeast RNA 3' processing factors is a conserved DNA damage response in eukaryotes. Jason N. Kuehner 1, Hilary Duffy 1, Claire Moore 2. 1) Department of Biology, Emmanuel College, Boston, MA; 2) Department of Developmental, Molecular, and Chemical Biology, Tufts University School of Medicine, Boston, MA.

240C
Two structurally separable functions of Ctp1 in the early steps of DSB repair. L. Ma, M. Nambar, N. Milman, GR. Smith. Basic Science Division, Fred Hutchinson Cancer Research Center, Seattle, WA.
241A
Cancer-associated exosome mutations cause DNA:RNA hybrids in yeast. K. Milbury1, Y. Chan1, V. Mathew1, P. Hieter2,3, P. Stirling1,4. 1) Terry Fox Laboratory, BC Cancer Research Centre, Vancouver, British Columbia, Canada; 2) Genome Science and Technology, University of British Columbia, Vancouver, British Columbia, Canada; 3) Michael Smith Laboratories, University of British Columbia, Vancouver, British Columbia, Canada; 4) Department of Medical Genetics, University of British Columbia, Vancouver, British Columbia, Canada.

242B
Numerous extrachromosomal circular DNA elements in Saccharomyces cerevisiae. Henrik D. Møller1, Lance Parsons2, David Botstein2, Birgitte Regenberg1. 1) Department of Biology, University of Copenhagen, Copenhagen, Copenhagen Ø, Denmark; 2) Lewis-Sigler Institute for Integrative Genomics, Princeton University, USA.

243C
The Role of DNM1 in Mitochondrial Genome Stability in Budding Yeast. Christopher T. Prevost, Deanna Pedeville, Rey A. Sia. Dept. of Biology, The College at Brockport-SUNY, Brockport, NY.

244A
Dbf4-dependent kinase regulates both spontaneous and induced mutagenesis by binding to and phosphorylating the Rev7 subunit of DNA polymerase ζ. Robert A. Sclafani1, Luis Brandao1, Rebecca Ferguson1, Irma Santoro3,4, Sue Jinks-Robertson2,4. 1) Dept Biochem, Molec Gen, Univ Colorado Denver, Aurora, CO; 2) Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, NC; 3) Department of Biology, 7300 Reinhardt Circle, Reinhardt University, Waleska, GA; 4) Department of Biology, Emory University, Atlanta, GA.

245B
Structure-function analysis of the yeast ELG1 gene. Keren Shemesh, Martin Kupiec. Department of Molecular Microbiology and Biotechnology, Tel Aviv University, Ramat Aviv, Israel.

246C
The dark side of Swi6; genomic screen for mutants hypersensitive to double strand breaks reveals Swi6 indispensability for genome integrity and maintaining of cellular ploidy. Izabela Brozda1, Paulina Adamus1, Kamil Krol1, Marek Skoneczny2, Adrianna Skoneczna1. 1) Laboratory of Mutagenesis and DNA Repair, Institute of Biochemistry and Biophysics, PAS, Warsaw, Poland; 2) Department of Genetics, Institute of Biochemistry and Biophysics, Polish Academy of Science, Warsaw, Poland.

247A
Genomic screen for mutations conferring zeocin hypersensitivity reveals diverse roles of vesicular trafficking paths in genotoxic stress protection and in genome preservation. Kamil Krol1, Izabela Brozda1, Marek Skoneczny2, Maria Bremer3, Adrianna Skoneczna1. 1) Laboratory of Mutagenesis and DNA Repair, Institute of Biochemistry and Biophysics, PAS, Warsaw, Poland; 2) Department of Genetics, Institute of Biochemistry and Biophysics, PAS, Warsaw, Poland; 3) Faculty of Chemistry, Warsaw University of Technology, Warsaw, Poland.

248B

249C
Localization to the nuclear pore complex is required for stabilizing CAG repeats. Xiaofeng Su1, Vincent Dion1, Susan M. Gasser3, Catherine H. Freudreich1. 1) Biology, Tufts University, Medford, MA, USA; 2) Center for Integrative Genomics, University of Lausanne, Lausanne, Switzerland; 3) Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland.

250A
Interchangeable Parts: Determining Rpa2 N-Terminal and Loop 3-4 Function through the Use of Human/Yeast Rpa2 Hybrid Proteins. Timothy M. Wilson, Kaiithlin M. Dailey, Anna Herauf, Jenna Steffes, Erica N. Mueller, Padmaja L. Ghospurkar, Stuart Haring. Chemistry and Biochemistry, North Dakota State University, Fargo, ND.

Chromosome Dynamics: Recombination

251B
The role of nucleoporins, specifically Nup2, during meiosis in budding yeast. Daniel Chu, Sean Burgess. MCB, UC Davis, Davis, CA.

252C
253A

254B
A potential novel mechanism for DNA double-strand break repair pathway choice. Tatsuya Ii, Hiromi Ando, Melanie Alvarado, Miki Ii. Biological Sciences, University of Alaska Anchorage, Anchorage, AK.

255C

256A
Redefining the M26 hotspot. Walter Steiner, Chelsea Recor, Bethany Zakrzewski. Dept Biol, Niagara Univ, Lewiston, NY.

257B
The Schizosaccharomyces pombe mitochondrial recombination junction-resolving enzyme is functionally homologous to Cce1p of Saccharomyces cerevisiae. Stephan Zweifel, Cody Finke, Kristin Andrykovich, Margaret Alexander, Jean Bower. Department of Biology, Carleton College, Northfield, MN.

Chromosome Dynamics: Telomeres

258C
Ku primarily impacts telomere length in Saccharomyces cerevisiae via Est1 recruitment to the telomere. Laramie Lemon, Jaime Williams, Faissal Ouenzar, Pascal Chartrand, Alison Bertuch. 1) Department of Pediatrics, Baylor College of Medicine, Houston, TX; 2) Department of Biochemistry, Université de Montréal, Quebec, Canada.

259A
Tight coevolution of proliferating cell nuclear antigen (PCNA)-partner interaction networks in fungi leads to interspecies network incompatibility. Amir Aharoni, Lyad Zamir, Inga Sandler, Eitan Rubin. 1) Department of Life Sciences, Ben-Gurion University, Beer-Sheva, Israel; 2) National Institute for Biotechnology in the Negev, Ben-Gurion University, Beer-Sheva, Israel; 3) Department of Microbiology and Immunology, Ben-Gurion University, Beer-Sheva, Israel; 4) Department of Biological Regulation, Weizmann Institute of Science, Rehovot, Israel.

260B
Characterizing the mechanism of variation in genomic uracil content. Debra Sue Bryan, Kerri York, Jay Hesselberth. Biochemistry and Molecular Genetics, Univ Colorado School Medicine, Aurora, CO.

261C

Chromosome Dynamics: Transposition

262A
The human Meier-Gorlin Syndrome mutation in ORC4 reduces replication initiation and rDNA copy number in Saccharomyces cerevisiae. Joseph Carlo Sanchez, M. K. Raghurama, Bonny Brewer. Genome Sciences, University of Washington, Seattle, WA.
266B
A role for the budding yeast separase, Esp1, in Ty1 element transposition. Krystina Ho1,2, Lina Ma1, Stephanie Cheung3, Nancy Fang2, Barry Young4, Christopher Loewen1, Thibault Mayor3, Vivien Measday1,2. 1) Wine Research Centre, University of British Columbia, Vancouver, British Columbia, Canada; 2) Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, British Columbia, Canada; 3) Centre for High-Throughput Biology, University of British Columbia, Vancouver, British Columbia, Canada; 4) Department of Cellular and Physiological Sciences, University of British Columbia, Vancouver, British Columbia, Canada.

267C
Functional analysis of Ty1 Gag: trans-dominance and nucleic acid chaperone activity. Yuri Nishida1, Katarzyna Pachulska-Wieczorek2, Jessica Mitchell1, Katarzyna J. Purzycka2, David Garfinkel1. 1) Biochemistry & Molecular Biology, University of Georgia, Athens, GA; 2) Polish Academy of Sciences, Institute of Bioorganic Chemistry, Poznan, Poland.

268A
Regulation of sexual differentiation in Kluyveromyces lactis by endonuclease activity of the transposase-related gene KAT1. Naghmeh Rajaei1, Jonathan Hildreth, David Garfinkel1. Biochemistry and Molecular Biology, University of Georgia, Athens, GA.

269B
A Trans-dominant form of Ty1 Gag mediates Copy Number Control of the Ty1 Retrotransposon in Saccharomyces. Agniva Saha, Jessica Mitchell, Yuri Nishida, Jonathan Hildreth, David Garfinkel. Biochemistry and Molecular Biology, University of Georgia, Athens, GA.

270C
A Tetraploid Intermediate Precedes Aneuploid Formation in Yeasts Exposed to Fluconazole. Benjamin Harrison1, Maayan Bibi2, Rebecca Pulver2, Melanie Wellington2, Jordan Hashemi3, Guillermo Sapiro3, Judith G. Berman4. 1) Dept Mol Micro & Biotept Mol Micro & Biotechnol, Tel Aviv University, Ramat Aviv, Israel; 2) Department of Genetics, Cell Biology & Development, University of Minnesota, Minneapolis, MN; 3) Department of Pediatrics, University of Rochester Medical Center, Rochester NY; 4) Department of Electrical and Computer Engineering, Duke University, Durham, NC.

271A
DNA replication and kinetochore mutants exhibit increased DNA:RNA hybrid formation. A. Chan1, P. Hieter1,2. 1) University of British Columbia, Vancouver, BC, Canada; 2) Michael Smith Laboratories, University of British Columbia, Vancouver, BC, Canada.

272B

273C
Evidence that the extra dose of ACT1 causes slow growth in an aneuploid strain disomic for chromosome VI through a dosage imbalance with COF1. Alex Murphy, Keegan Gies, Kun Yang, Emma Kershinik, Kirk Anders. Biology Department, Gonzaga University, Spokane, WA.

Gene Expression: Chromatin

274A
Evolution of chromatin accessibility and gene expression levels during the heat shock response in Saccharomyces sensu stricto yeast. Caitlin Connelly, Joshua Akey. Genome Sciences, University of Washington, Seattle, WA.

275B
A High-Resolution View Of Chromatin Architecture And Transcriptional Repression At Native Telomeres in Saccharomyces cerevisiae. Aisha Ellahi, Deborah Thurtle, Jasper Rine. Dept of Molecular and Cell Biology, Univ California, Berkeley, Berkeley, CA.

276C

277A
Studies addressing a possible role for TORC1 in controlling chromatin structure and transcription elongation in S. cerevisiae. Jasmine Haller1, Mary Allison1, Meet Modi1, James Dornhoffer1, Sarah Marshall1, Taylor McElroy1, Marine Boucherle2, Anne Rufiange2, Malena Outhay1, Jennifer Harper1, Amine Nourani2, Andrea Duina1. 1) Biology Department, Hendrix College,
**Poster Session Listings**

Conway, AR; 2) Centre de Recherche en Cancérologie de l’Université Laval, L’Hotel-Dieu de Québec, Québec, Canada.

**278B**
**Loss of transcriptional silencing is not an obligate precursor of yeast senescence.** Gavin S. Schlissel, Jasper Rine. UC Berkeley, Berkeley, CA.

**279C**
**Keeping Quiet: Does heterochromatin stay silent during homologous recombination?** Katie Sieverman1, Jasper Rine1,2. 1) Department of Molecular and Cell Biology, University of California - Berkeley, Berkeley, CA; 2) California Institute for Quantitative Biosciences, University of California - Berkeley, Berkeley CA.

**Gene Expression: Epigenetic Mechanisms**

**280A**
**Promoting a balanced acetylation state bypasses the requirement for two essential NuA4 subunits in S. cerevisiae.** Ana Lilia Torres-Machorro1,2, Naomi E. Frank Searle1,2, Lorraine Pillus1,2. 1) Section of Molecular Biology, Division of Biological Sciences University of California, San Diego, La Jolla, California 92093; 2) UC San Diego Moores Cancer Center, La Jolla, California 92093; 3) Biomedical Science Graduate Program, University of California, San Diego, La Jolla, California 92093.

**281B**
**Ubiquitin-mediated regulation of Snf1/AMPK by Ubp8 and Ubp10 in budding yeast.** Hsiang-En Hsu1, Tzu-Ning Liu2, Yi-Chen Lo2, Cheng-Fu Kao1. 1) Institute of Cellular and Organismic Biology, Taipei, Taiwan; 2) Institute of Food Science and Technology, College of Bio-Resources and Agriculture, National Taiwan University, Taipei, Taiwan.

**282C**
**Accumulation of onco-metabolite 2-hydroxyglutarate impacts heterochromatin stability.** Ryan Janke, Jasper Rine. Department of Molecular and Cell Biology and California Institute for Quantitative Biosciences, University of California, Berkeley, CA 94720.

**283A**
**Synergistic repression of FLO11 and histone methylation by the Cyclin C/Cdk8 complex and histone demethylase Jhd2p.** Michael J. Law, Kerri Ciocciagione. Rowan University-GSBS, Stratford, NJ.

**284B**
**A cre-lox recombination-based assay for the study of yeast chronological aging in nutrient-rich media conditions.** David McCleary, Jasper Rine. UC Berkeley, Berkeley, CA.

**Gene Expression:**

**Nucleo/Cytoplasmic Transport**

**285C**
**De novo amino acid biosynthesis influences starvation-induced changes in tRNA distribution.** Rebecca L. Hurto1,2, Anita K. Hopper1,2. 1) Molecular Genetics, Ohio State Univ, Columbus, OH; 2) The Center for RNA Biology, OSU.

**286A**
**The prion-like domain of the RNA-binding protein Ssd1 regulates the nuclear barcoding of Ssd1 to define its cytoplasmic destiny.** Cornelia Kurischko, James R. Broach. Biochemistry and Molecular Biology, College of Medicine, Penn State University, Hershey, PA.

**Gene Expression: RNA processing**

**287B**
**Ribosome Subunit Biosynthesis Crosstalk During Repression of Ribosomal Protein Synthesis.** Brian K. Gregory, Lasse Lindahl. Biological Sciences, UMBC, Baltimore, MD.

**288C**
**Mitochondria outer membrane proteins are required for the proper function and localization of tRNA splicing endonucleases in Saccharomyces cerevisiae.** Yao Wan1,2, Jingyan Wu1,2, Anita Hopper1,2. 1) Molecular Genetics, The Ohio State University, Columbus, OH; 2) Center for RNA Biology, The Ohio State University, Columbus, OH.

**Gene Expression: RNA turnover**

**289A**
**Determination of in vivo RNA kinetics using RATE-seq.** David Gresham, Benjamin Neymotin, Rodoniki Athanasiadou. Center for Genomics and Systems Biology, Department of Biology, New York University, New York, NY.
**Poster Session Listings**

**290B**
Global analysis of 5'-hydroxyl RNA surveillance and turnover.
Sally Peach, Kerri York, Jay Hesselberth.
University of Colorado School of Medicine, Department of Biochemistry and Molecular Genetics, Program in Molecular Biology, Aurora, CO.

**291C**
Genome-wide study of the interdependence between the cellular growth rate and mRNA turnover.
1) Departamento de Bioquímica y Biología Molecular, Universitat de Valencia, Spain; 2) Departamento de Genetica, Universitat de Valencia, Spain; 3) Departamento de Estadistica e Investigacion Operativa, Universitat de Valencia, Spain; 4) Instituto de Ciencias de la Vida y del Vino. Logrono, Spain; 5) Department of Chemistry and Molecular Biology, University of Gothenburg, Gothenburg, Sweden.

**292A**
Systematic Identification and Analysis of pre-mRNA Splicing Regulators in *Saccharomyces cerevisiae*. H. Wang, T. Chang, M. Hwang.
1) Academia Sinica, Taipei, Taiwan; 2) Genome and Systems Biology Degree Program, NTU, Taipei, Taiwan.

**293B**
In search of PP2A/Cdc55 targets involved in stress induced transcription.
Jessica Ferrari, Wolfgang Reiter, David Hollenstein, Gustav Ammerer.
Dept Biochem & Cell Biology, University of Vienna, Vienna, Austria.

**294C**
Regulation of stress induced gene expression in yeast.
Vasudha Bharatula, Nils Elving, Razvan Chereji, Stephan Bjorklund, Alexandre Morozov, James Broach.
1) Department of Biochemistry and Molecular Biology, Penn State College of Medicine, Hershey, PA 17033, USA; 2) Department of Medical Biochemistry and Biophysics, Umeå University, Umeå 901 87, Sweden; 3) Department of Physics and Astronomy, Rutgers University, Piscataway, NJ 08854, USA; 4) BioMaPS Institute for Quantitative Biology, Rutgers University, Piscataway, NJ 08854, USA.

**295A**
Natural yeast promoter variants harbour different levels of transcriptional-mediated noise.
Jian Liu, Mariñe Vuillemin, Hélène Martin-Yken, Frédéric Bigey, Sylvie Dequin, Jean-Marie François, Jean-Pascal Capp.
1) LISBP, INSA/Univ. of Toulouse, Toulouse, France; 2) INRA, UMR 1083, Montpellier, France.

**296B**
Role of Chromosomal Looping in the Transcriptional Regulation of Molecular Chaperone Genes in *Saccharomyces cerevisiae*. Surabhi Chowdhary, David Gross.
Biochemistry and Molecular Biology, Louisiana State University Health Sciences Center, Shreveport, LA.

**297C**
Transciptional Profiling of Budding Yeast Biofilm Suppressors.
Gareth Cromie, Zhihao Tan, Eric Jeffery, Michelle Hays, Cecilia Garmendia, Aimée Dudley.
1) Dudley Group, Pacific Northwest Diabetes Research Inst, Seattle, WA; 2) Molecular and Cellular Biology Program, University of Washington, Seattle, WA USA; 3) Institut de Génétique et de Biologie Moléculaire et Cellulaire, Strasbourg, France.

**298A**
Unanticipated complexity at the *GAT1* locus.
I. Georis, R. Rai, J. J. Tate, T. G. Cooper, E. Dubois.
1) Institut de Recherches Microbiologiques J.-M. Wiame, Brussels, Belgium; 2) Dept. Microbiology, Immunology and Biochemistry, University of Tennessee Health Science Center, Memphis, TN, USA.

**299B**
Selective interaction of RNA-binding proteins with transcript isoforms shapes the post-transcriptional life of mRNA.
Ishaan Gupta, Bernd Klaus, Sandra Cluader-Münster, Aino Jäverlin, Raeka Aiyar, Vicente Pelechano, Lars Steinmetz.
1) European Molecular Biology Laboratory (EMBL), Genome Biology Unit, Meyerhofstrasse 1, 69117 Heidelberg, Germany; 2) European Molecular Biology Laboratory (EMBL), Centre for Statistical Data Analysis, Meyerhofstrasse 1, 69117 Heidelberg, Germany; 3) Stanford University School of Medicine, Department of Genetics, Stanford, CA 94305, USA; 4) Stanford Genome Technology Center, 855 California Ave, Palo Alto, CA 94305, USA.

**300C**
1) Dept Molecular Genetics, Ohio State Univ, Columbus, OH; 2) Dept of Chemistry and Biochemistry, Ohio State Univ, Columbus OH.

**301A**
Controlling isoprenoid production using a microaerobic-responsive switch in yeast.
Hanxiao Jiang, Robert Dahl, Adam Meadows.
Amyris Inc., 5885 Hollis St. Suite 100, Emeryville, CA 94608.

**302B**
Changes in RNA Polymerase II catalytic activity influence transcription start site utilization on a global scale.
1) Department of
303C
CK2-dependent Regulation of Ifh1 Transcription Factor Involved in the Expression of Ribosomal Protein Genes. Myung Sup Kim, Ji-Sook Hahn. School of Chemical and Biological Engineering, Seoul National University.

304A
Effect of Modulating the Level of the Seventh Largest Subunit of RNA Polymerase II in Schizosaccharomyces pombe. Deepak Kumar, Nimisha Sharma. University School of Biotechnology, G.G.S Indraprastha University, Sec.16C, Dwarka, New Delhi, India-110078.

305B
DNA Replication Checkpoint Regulation of Cell-Cycle Transcription Dynamics. Adam R. Leman1, Kevin A. McGoff2, Xin Guo3, John Harer2, Steven B. Haase2. 1) Biology, Duke University, Durham, NC; 2) Mathematics, Duke University, Durham, NC; 3) Statistical Sciences, Duke University, Durham, NC.

306C
The thiamine signal transduction pathway in Candida glabrata. Sarah Grace Leone, Nicholas Attanasio, Michael Peel, Christine Iosue, Dennis Wykoff. Biology, Villanova University, Villanova, PA.

307A
Transcriptional Regulation of HAP4 by the Mediator Complex and Adenine Levels in Saccharomyces cerevisiae. Chad Bush, Denise Capps, Mengying Chiang, Tammy Pracheil, Zhengchang Liu. Dept. of Biological Sciences, University of New Orleans, 200 Lakeshore Drive, New Orleans, LA 70148.

308B

309C
Phenotypic landscape of the conserved and essential RNA Polymerase II trigger loop: a high-throughput structure-function analysis. Chenxi Qiu, Olivia Erinne, Ping Cui, Kenny Lam, Sarabeesheh Babu, Huiyan Jin, Alvin Tang, Nandhini Mutukrishnan, Craig Kaplan. Biochemistry&Biophysics, Texas A&M University, College Station, TX.

310A
Analysis of ncDNA transcription for roles in regulating gene expression. Elizabeth A. Raupach1, Joseph Martens2. 1) Biological Sciences, University of Pittsburgh, Pittsburgh, PA; 2) Biology, Hamilton College, Clinton, NY.

311B

312C
Functional analysis of stress regulated non-coding RNAs in budding yeast. Amanda N. Scholes, Tara N. Stuecker, Jeffery A. Lewis. Biological Sciences, University of Arkansas, Fayetteville, AR.

313A
FACS-based genetic screen in S. cerevisiae identifies genes involved in the alpha-factor response. Anna Sliva1,2, Zheng Kuang1,2, Jef Boeke1,2. 1) High Throughput Biology Center, Johns Hopkins University School of Medicine, Baltimore, MD 21205; 2) New York University Langone Medical Center, New York, NY 10016.

314B
Adaptive evolution of transcription and translation in pathogenic yeast. Xuepeng Sun1,2, Zhe Wang1, Zhenglong Gu1. 1) Division of nutritional sciences, Ithaca, NY; 2) College of Agriculture and Biotechnology.

315C

316A
S. cerevisiae rRNA Synthesis by RNA Polymerase (Pol) II in Response to Nitrogen Deprivation. Arjuna Rao Vallabhaneni, Merita Kabashi, Kushal Bhatt, Heather Conrad-Webb. Biology, Texas Woman's University, Denton, TX.

317B

318C
319A

320B
Accumulation of a threonine biosynthetic intermediate attenuates general amino acid control by inducing degradation of promoter-bound Gcn4. FNU Yashpal, Hongfang Qiu, Alan G. Hinnebusch. Laboratory of Gene Regulation and Development, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, Maryland 20892.

**Gene Expression: Translation**

321C
Codon Context and Translation Efficiency in Yeast. Caitlin E. Gamble1, Christina Brule2, Stanley Fields1,3, Elizabeth Grayhack2. 1) Genome Sciences, University of Washington, Seattle, WA; 2) University of Rochester School of Medicine and Dentistry, Rochester, NY; 3) Howard Hughes Medical Institute.

322A
Functional analysis of CaMCA1 and EDC3 in oxidative stress response and apoptotic cell death in *Candida albicans*. Jeong-Hoon Jeong, Jong-hwan Jung, Jinmi Kim. Department of Microbiology and Molecular biology, Chungnam National University, Daejeon, South Korea.

323B
Roles of decapping activators in mRNA translation and P-body formation during mating. Daeehee Jung, Yuseon Lee, Jinmi Kim. Department of Microbiology and Molecular Biology, Chungnam National University, Daejeon, South Korea.

324C

**Gene Expression: Other**

325A
Improving heterologous cytochrome P450 function in *S. cerevisiae*. Anita Emmerstorfer1, Miriam Wimmer1, Tamara Wriessnegger2, Erich Leitner2, Monika Müller3, Iwona Kaluzna2, Martin Schurmann2, Daniel Mink1, Guenther Zellnig3, Harald Pichler1,2, 3) ACIB GmbH, Petersgasse 14, 8010 Graz, Austria; 2) Institute of Analytical Chemistry and Food Chemistry, Graz University of Technology, Steyrergasse 9, 8010 Graz, Austria; 3) DSM Innovative Synthesis B.V., Urmroenderbaan 22, 6167 RD Geleen, The Netherlands; 4) Institute of Plant Sciences, University of Graz, Schubertstrasse 51, 8010 Graz, Austria; 5) Institute of Molecular Biotechnology, Graz University of Technology, Petersgasse 14/2, 8010 Graz, Austria.

326B
Mutants defective in stress granule formation exhibit a deregulated stress response. Elena Garre1, Xiaoxue Yang2, Yi Shen3, Xinxin Hao1, Daniel Krumlinde1, Marija Cvijovic1,2, Christina Arens1, Thomas Nystrom1, Beidong Liu1,2, Per Sunnerhagen1. 1) Department of Chemistry and Molecular Biology, University of Gothenburg, Göteborg, Sweden; 2) School of Life Science and Engineering, Harbin Institute of Technology, Harbin, China; 3) Department of Mathematical Sciences, Chalmers University of Technology, Göteborg, Sweden; 4) Department of Mathematical Sciences, University of Gothenburg, Göteborg, Sweden.

327C
Securing autoselection in yeast ACNase killer toxin systems by mRNA fragmentation. Alene Kast, Friedhelm Meinhardt. Institute of Molecular Microbiology and Biotechnology, University of Münster, Corrensstr. 3, 48149 Münster, Germany.

328A
Gene copy number and colony morphology in wild yeast strains. Derek Wilkinson1, Vratislav Stovicek2, Libuse Vachova2, Zdena Palkova1. 1) Department of Genetics and Microbiology, Faculty of Science, Charles University in Prague, Vinicna 5, 128 44 Prague 2, Czech Republic; 2) Institute of Microbiology of the ASCR, v.v.i., Videska 1083, 142 20 Prague 4, Czech Republic; 3) The Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kogle Alle 6, 2970 Horsholm, Denmark.

329B
Chaperonins enabled functional expression of bacterial xylose isomerases in yeast. Jianjun Yang1, Min Qi1, Kristen Kelly1, Sarah Rush2, Luan Tao2, Rick Ye1, Paul Viitanen2, William Hitz2. 1) Biotechnology, DuPont Central Research and Development, Experimental Station, Wilmington, DE; 2) DuPont Industrial Biosciences, Experimental Station, Wilmington, DE.

330C
Dissecting the mechanism of gene-dosage response in naturally aneuploid, wild isolates of *Saccharomyces cerevisiae*. Mun Hong Yong1, James Hose1, Audrey Gasch1,2. 1) Laboratory of Genetics, University of Wisconsin-Madison, Madison, WI; 2) Genome Center of...
Global Analysis: Evolution/Comparative Genomics

331A
Rerouting resources from cell size to population growth drives evolution of cancer drug resistance in yeast. E. Alonso-Perez1, N. Srinivas1, M. Kakavandi1, K. Ludwig1, I. Jonassen2, SW Omholt3, P. Sunnerhagen1, J. Warringer1. 1) Department of Chemistry & Molecular Biology, University of Gothenburg, Gothenburg, Sweden; 2) Uni Computing, Uni Research AS, Bergen, Norway; 3) Center for Integrative Genetics (CIGENE), Norwegian University of Life Sciences (UMB), Ås, Norway.

332B
Inferring Genetic Networks through Evolutionary Signatures. Zelia Ferreira1, Jennifer Walker1, Allyson O'Donnell2, Nathan Clark1. 1) Computational and Systems Biology, University of Pittsburgh, PA; 2) Department of Cell Biology, University of Pittsburgh, PA.

333C
The mating pathway as a model for the genetic analysis of complex traits. Michael W. Dorrity1,2, Josh T. Cuperus3, Christine Queitsch2, Stanley Fields2,3. 1) Department of Biology, University of Washington, Seattle, WA; 2) Department of Genome Sciences, University of Washington, Seattle, WA; 3) Howard Hughes Medical Institute, University of Washington, Seattle, WA.

334A
Functional Evolution of SIR1 In Saccharomyces cerevisiae And Related Budding Yeasts. Aisha Ellahi, Jasper Rine. Dept MCB, Univ California, Berkeley, Berkeley, CA.

335B
Microevolution of a human fungal pathogen in a mouse model of systemic infection. Juliana Ene1, Matthew Hirakawa1, Emily Mallick2, Christina Cuomo2, Richard Bennett1. 1) Molecular Microbiology and Immunology, Brown University, Providence, RI; 2) Broad Institute, Cambridge, MA.

336C

337A
Emergence of Novel Ecological Interactions in an Evolving Cooperative Community. Robin Green1,2, Chichun Chen1, Jose Pineda1, Wenying Shou1. 1) Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Molecular and Cellular Biology Program, University of Washington, Seattle, WA.

338B
Tracking the genetic factors of Saccharomyces cerevisiae strains under the selective pressures of the beer brewing process. Noah A. Hanson, Celia Payen, Maitreya Dunham. Genome Sciences, University of Washington, Seattle, WA.

339C
Ploidy-regulated variation in biofilm-related phenotypes in natural isolates of Saccharomyces cerevisiae. Elyse A. Hope, Maitreya J. Dunham. Department of Genome Sciences, University of Washington, Seattle, WA.

340A
A two loci genetic incompatibility leads to offspring respiratory deficiency within the Saccharomyces cerevisiae species. Jing Hou, Anne Freidrich, Joseph Schacherer. Laboratoire de génétique moléculaire, génomique et microbiologie, Université de Strasbourg/CNRS UMR7156, Strasbourg, France.

341B
Site-directed changes to CgPMU1 convert it into a broad range acid phosphatase like CgPMU2 in Candida glabrata. Christine L. Issue, Kelly A. Orlando, Sarah G. Leone, Danielle L. Davies, Dennis D. Wykoff. Biol Dept, Villanova Univ, Villanova, PA.

342C
Why do some yeast species have duplicate copies of GALactose network genes? Meihua Christina Kuang1,2, Chris Hittinger1,2. 1) Laboratory of Genetics, University of Wisconsin-Madison, Madison, WI; 2) Graduate Program in Cellular and Molecular Biology, University of Wisconsin-Madison, WI.

343A
Single-cell analysis reveals natural variability in a potential bet-hedging trait. Colin S. Maxwell, Paul Magwene. Department of Biology, Duke University, Durham, NC.

344B
Combining natural sequence variation with high throughput mutational data to reveal protein interaction sites. Daniel Melamed1,2, David Young2, Christina Miller1,2, Stanley Fields1,2,3. 1) Howard Hughes Medical Institute; 2) Department of Genome Sciences, University of Washington; 3) Department of Medicine, University of Washington.
Poster Session Listings

345C
Transport differences in two recently high affinity HXT paralogous. A. Mena1,2, E. Barrio3, F. N. Arroyo-López3. 1) University of Valencia Calle Doctor Moliner, 50, 46100 Burjasot, Valencia; 2) IATA-CSIC Institute of Agrochemistry and Food Technology Carrer Catedrátic Agustín Escardino Benlloch, 7, 46980 Paterna, Valencia; 3) CSIC Instituto de la Grasa, Department of Food Biotechnology Av Padre García Tejero, 4, 41012 Sevilla.

346A
Novelty by necessity: Loss of sulfate transport in yeast repeatedly selects for mutations in an uncharacterized transporter YIL166C in sulfate-limited environments. Aaron W. Miller, Ivan Liachko, Anna B. Sunshine, Maitreya J. Dunham. Genome Sciences, University of Washington, Seattle, WA.

347B
The Genetic Architecture of Invasive Growth in a Clinical Isolate of S. cerevisiae. Helen A. Murphy1,2, Debra Murray3, Jason Smyth4, Cliff W. Zeyl4, Paul M. Magwene5. 1) Biology, William and Mary, Williamsburg, VA; 2) Biology, Duke University, Durham, NC; 3) Biology, Wake Forest University, NC.

348C
Mitochondrial-Nuclear Epistasis and Coevolution in Natural Isolates of Saccharomyces cerevisiae. Swati Paliwal, Anthony C. Fiumera, Heather L. Fiumera. Biological Sciences, Binghamton University, State University of New York, Binghamton, NY 13902.

349A
Investigating reticulate evolution in the Saccharomyces genus and repeating it for the bioethanol industry. David Peris Navarro1,2, Kayla Sylvester3, Maria Sardi4, William Alexander5, Diego Libkind1, Paula Gonçalves6, Josè Sampaio1, Lucas Parreiras3, Trey Sato4, Chris Hittinger5,6. 1) Department of Genetics, Genome Center of Wisconsin, University of Wisconsin-Madison, WI; 2) Wisconsin Energy Institute, DOE Great Lakes Bioenergy Research Center, University of Wisconsin-Madison, WI; 3) Laboratorio de Microbiologia Aplicada y Biotecnologia, Instituto de Investigaciones en Biodiversidad y Medio-ambiente, INIBIOMA (CONICET-UNComahue), Bariloche, Argentina; 4) Centro de Recursos Microbiológicos, Departamento de Ciências da Vida, Faculdade de Ciências e Tecnologia, Universidad Nova de Lisboa, Caparica, Portugal.

350B
‘Natural and experimental evolutionary dynamics of Saccharomyces killer yeast’. Magdalena Pieczynska1,2, Ryszard Korona3, J. Arjan G. M. de Visser4. 1) Laboratory of Genetics, Plant Sciences Group, Wageningen, Netherlands; 2) Institute of Environmental Sciences, Jagiellonian University, Gronostajowa 7, Kraków, Poland.

351C
Natural variation in mutational robustness among strains of Saccharomyces cerevisiae. Marcin Płechn1, J. Arjan G. M. de Visser2, Ryszard Korona3. 1) Institute of Environmental Sciences, Department of Biology, Jagiellonian University, Kraków, Poland; 2) Genetics Lab, Plant Sciences Group, University of Wageningen, The Netherlands.

352A
Genetic variation acting on protein translation and degradation rates is common in Saccharomyces cerevisiae. Daniel Pollard, Homa Rahnemoun, Scott Rifkin. Biological Sciences, UCSD, La Jolla, CA.

353B
Genome-wide patterns of genetic variation reveal chromosome-scale heterogeneous evolution in a protoploid yeast. Anne Friedrich1, Paul Jung1, Cyrielle Reisser2, Gilles Fischer3, Joseph Schacherer1. 1) Department of Genetics and Genomics, University of Strasbourg, Strasbourg, France; 2) Sorbonne Universités, UPMC Univ Paris 06, UMR 7238, Biologie Computationnelle et Quantitative, Paris, France; 3) CNRS, UMR7238, Biologie Computationnelle et Quantitative, Paris, France.

354C
Genome sequence and evolution of Saccharomyces carlsbergensis, the world’s first pure culture lager yeast. Andrea Walther, Ana Hesselbart, Jurgen W. Wendland. Yeast Genetics, Carlsberg Laboratory, Copenhagen V, Denmark.

355A
Evolutionary Exploration of Yeast Hap4p Regulatory Networks. Ruoyu Zhang, Xiaoxian Guo, Zhenglong Gu. Division of Nutritional Science, Cornell University, Ithaca, NY.

Global Analysis: Genomics

356B
The yeast phenome: mapping the functional organization of a eukaryotic cell through an integrative study of genome-wide phenotypic surveys. Anastasia Baryshnikova1, Monica Sanchez2, Maitreya Dunham2. 1) Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ; 2) Department of Genome Sciences, University of Washington, Seattle, WA.

357C
Multiplexed genome engineering in Saccharomyces cerevisiae. Josh Cuperus1,2, Russel Lo1,2, Stanley Fields1,2. 1) Department of Genome Sciences, University of Washington, Seattle, WA 98195, USA; 2) Howard Hughes
Poster Session Listings

Medical Institute, University of Washington, Seattle, Washington 98195, USA.

358A
WITHDRAWN

359B
Multiple global approaches for deciphering the molecular basis of low temperature adaptation in wine yeast. Estefani Garcia-Rios1, Maria Lopez-Malo1,2, Jose Manuel Guillamon1. 1) Departamento de Biotecnologia de los alimentos, Instituto de Agroquimica y Tecnologia de los Alimentos (CSIC), Avda. Agustin Escardino, 7, E-46980-Paterna, Valencia, Spain; 2) Biotecnologia Enológica, Departament de Bioquimica i Biotecnologia, Facultat de Enologia, Universitat Rovira i Virgili. Marcelli Domingo s/n, 43007, Tarragona, Spain.

360C
Expression adaptation and gene-dosage response in naturally aneuploid strains of wild S. cerevisiae. James Hose1, Chris Yong1, Zhishi Wang2, Michael A. Newton2, Audrey P. Gasch1. 1) Laboratory of Genetics & Genome Ctr, U. Wisconsin-Madison, Madison, WI; 2) Departments of Statistics & Biostatistics & Medical Informatics, U. Wisconsin-Madison, Madison, WI.

361A
MKT1 interacts with nitrogen metabolism and mitochondrial signaling pathways to modulate sporulation efficiency variation. Saumya Gupta1, Aparna Radhakrishnan1, Julien Gagneur2, Himanshu Sinha1. 1) Department of Biological Sciences, Tata Institute of Fundamental Research, Mumbai 400005, India; 2) Gene Center Munich, Department of Biochemistry, Ludwig Maximilians University, 81377 Munich, Germany.

362B
Identification of novel pathways involved in ploidy maintenance in Saccharomyces cerevisiae. P. S. Hung1,2, T. L. Sing1, S. Ohnuki1, B. San-Luis2, J. P. Paw2, M. Costanzo2, C. Nislow2, C. Boone2,4, Y. Ohya1, G. W. Brown1,2. 1) Department of Biochemistry, University of Toronto, Toronto, Ontario, Canada; 2) Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario, Canada; 3) Department of Integrated Biosciences, University of Tokyo, Tokyo, Japan; 4) Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 5) Department of Pharmaceutical Sciences, University of British Columbia, Vancouver, British Columbia, Canada.

363C
Cost-effective Genotyping and Karyotyping Using Double Digest-RAD Sequencing in S. cerevisiae. C. albicans and C. glabrata. E. Jeffery1, G. Cromie2, A. Forche2, J. Usher3, K. Haynes3, J. Berman4, A. M. Dudley3. 1) Pacific Northwest Diabetes Research Inst, Seattle, WA. USA; 2) Bowdoin College, Department of Biology, Brunswick, ME. USA; 3) University of Exeter, College of Life and Environmental Sciences, Exeter, UK; 4) Tel-Aviv University, Department of Molecular Microbiology and Biotechnology, Tel-Aviv, Israel.

364A
A higher-throughput accurate method for unraveling the genetic basis of Chronological Life Span in yeast. Paul P. Jung1, Nils Christian1, Daniel Kay1, Aimée M. Dudley2, Alexander Skupin3, Carole L. Linster1. 1) University of Luxembourg, Luxembourg Centre for Systems Biomedicine, Esch-sur-Alzette, Luxembourg; 2) Pacific Northwest Diabetes Research Institute, Seattle.

365B
Evidence that mutation accumulation does not cause aging in Saccharomyces cerevisiae. Alaattin Kay, Alexei V. Lobanov, Vadim N. Gladyshev. Medicine, Harvard University, Boston, MA.

366C
Pooled Segregant Sequencing Reveals Genetic Determinants of Yeast Pseudohyphal Growth. Qingxuan Song1, Cole Johnson1, Thomas Wilson1, Anuj Kumar1. 1) Dept. of Mol., Cell., and Dev. Biology, University of Michigan, Ann Arbor, MI; 2) Dept. of Pathology, University of Michigan Medical School, Ann Arbor, MI.

367A
Genetic Incompatibilities in Hybrid Yeast. Samuel M. Lancaster, Miiaetrey J. Dunham. Genome Sciences, University of Washington, Seattle, WA.

368A
An Evaluation of High-Throughput Approaches to QTL Mapping in Saccharomyces cerevisiae. Stefan Wilkening1, Gen Lin1, Emilie Fritsch1, Manu Tekkedil1, Simon Anders1, Raul Kuehn2, Michelle Nguyen2, Raeka Aiyar1, Michael Proctor1, Nikita Sakhaneko1, David Galas1, Julien Gagneur1, Adam Deutschbauer2, Lars Steinmetz1. 1) European Molecular Biology Laboratory, Genome Biology Unit, 69117 Heidelberg, Germany; 2) Stanford Genome Technology Center, Palo Alto, California 94304; 3) Pacific Northwest Diabetes Research Institute, Seattle, Washington 98122; 4) Luxembourg Centre for Systems Biomedicine, University of Luxembourg, L-4362, Esch-sur-Alzette, Luxembourg; 5) Physical Biosciences Division, Lawrence Berkeley National Laboratory, Berkeley, California 94720.

369C
An Assessment of Terminal Phenotypes in S. cerevisiae Using Synthetic Genetic Array and High-Content Screening. Dara Lo1, Jason Moffatt1, Brenda Andrews1, Charles Boone1. 1) Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 2) Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario, Canada.
Poster Session Listings

370A
Beyond Beer and Wine: Isolating Wild Yeast from Unroasted Cacao and Coffee Beans. Catherine Ludlow1, Cecilia Garmanda Torres2, Amy Sirj, Michelle Hays3, Colby Field4, Gareth Cromie5, Eric W. Jeffery5, Aimee M. Dudley5, 1) Pacific Northwest Diabetes Research Institute, Seattle, Washington, USA; 2) Departamento de Biotecnología, Universidad de las Américas, Quito, Ecuador; 3) Department of Molecular Biology, NCCR Program “Frontiers in Genetics”, and Institute of Genetics and Genomics in Geneva, 30 quai Ernest Ansermet, CH-1211 Geneva 4, Switzerland; 4) DKFZ-ZMBH Alliance, University of Heidelberg, Im Neuenheimer Feld 282, 69120 Heidelberg, Germany; 5) Dipartimento di Biologia, University of Rome ‘Tor Vergata’, Via della Ricerca Scientifica 1, 00133 Rome, Italy.

371B
Exploring the endocytic pathway by combining high-throughput genetics and high-content microscopy. Mojca Mattiazzi Usaj1, Matej Usaj1, Marinka Zitnik2, Blaz Zupan2, Brenda Andrews1, Charles Boone1. 1) The Donnelly Centre, University of Toronto, Toronto, Ontario, Canada; 2) Faculty of Computer and Information Science, University of Ljubljana, Ljubljana, Slovenia.

372C
Navigating the chemical space of large compound libraries using high-throughput chemical genomics. Jeff Piotrowski1, Sheena Li2, Raamesh Deshpande2, Scott Simpkins2, Justin Nelson2, Jacqueline Barber2, Hiroyuki Osada3, Minoru Yoshida4, Chad Myers5, Charlie Boone1. 1) Great Lakes Bioenergy Research Centre University of Wisconsin - Madison, USA 53726; 2) Center for Sustainable Resource Science, RIKEN, 2-1 Hirosawa, Wako, Saitama, Japan 351-0198; 3) Department of Computer Science and Engineering, University of Minnesota, Minneapolis, MN 55455, USA; 4) 4. Banting and Best Department of Medical Research and Department of Molecular Genetics, Donnelly Centre, University of Toronto, 160 College St., Toronto, ON, Canada M5S 3E1.

373A

374B
Transcriptional variations among Saccharomyces cerevisiae strains harboring different alleles of a transcription factor Yrr1. Xiaqiong Rong-Mullins3, Wei Zheng5, Hogune Im2, Erin Mitsunaga2, Michael Snyder2, Jennifer Gallagher3, 1) Biology, West Virginia University, Morgantown, WV; 2) Genetics, Stanford University, Stanford, CA.

375C
Comparative analysis of stress responses in diverse wild yeast strains. Nikolay S. Rovinsky1, Dana J. Wohlbach1, Jeff Lewis1,2, Maria I. Sardi1,2, Wendy S. Schackwitz2, Joel A. Martin3, Shweta Deshpande1, Chris Daum4, Troy K. Sato2, Audrey P. Gasch1,2. 1) Genetics, University of Wisconsin-Madison, Madison, WI; 2) Great Lakes Bioenergy Research Center; Madison, Wisconsin 53706; 3) US Department of Energy Joint Genome Institute; Walnut Creek, California 94598.

376A
Chromatin organization in quiescent yeast. Mark T. Rutledge1, Jon-Matthew Belton1, Mariano Russo2, Job Dekker1, James R. Broach1. 1) Dept. of Molecular Biology, Princeton University, Princeton, NJ; 2) Dept. of Biochemistry and Molecular Biology, Pennsylvania State University College of Medicine, Hershey, PA; 3) Program in Systems Biology, Dept. of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, Worcester, MA.

377B
Genomic approaches to understanding Saccharomyces cerevisiae tolerance to lignocellulosic-hydrolysate toxins. Maria I. Sardi1, Dana J. Wohlbach, Audrey P. Gasch. University of Wisconsin-Madison, Madison, WI.

378C
A phenomic assessment of sub-cellular morphology in S. cerevisiae using Synthetic Genetic Array analysis and high-content screening. Erin B. Styles1, Lee Zambaro1, Karen Fourn1, Oren Kraus1,2, Dogus Altintas3, Marco Graf3, Daniele Novarino5, Tina Sing1, Grant W. Brown1, Marco Muzi-Falconi1, Brian Luke2, David Shore2, Brendan Frey2, Zhaolei Zhang1, Charles Boone1, Brenda J. Andrews1. 1) Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON, Canada; 2) Electrical and Computer Engineering, University of Toronto, Toronto, ON, Canada; 3) Department of Molecular Biology, NCCR Program “Frontiers in Genetics”, and Institute of Genetics and Genomics in Geneva, 30 quai Ernest Ansermet, CH-1211 Geneva 4, Switzerland; 4) DKFZ-ZMBH Alliance, University of Heidelberg, Im Neuenheimer Feld 282, 69120 Heidelberg, Germany; 5) Dipartimento di Bioscienze Universita’ degli Studi di Milano, Milano, Italy.

379A
Genetic basis for Saccharomyces cerevisiae biofilm in liquid medium. Kaj S. Andersen1, Laura G. R. Sorensen1, Rasmus Bojsen2,3, Martin W. Nielsen2,3, Michael Lisby1, Anders Folkesson2,3, Birgitte Regenberg1. 1) Department of Biology, University of Copenhagen, Copenhagen, Denmark; 2) Department of Systems Biology, Technical University of Denmark, Copenhagen, Denmark; 3) National Veterinary Institute, Technical University of Denmark, Copenhagen, Denmark.
380B
An all-in-one yeast library - creating a new toolbox for studying the proteome. Uri Weill, Ido Yofe, Maya Schuldiner. Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel.

381C

382A
Mapping resistance to targeted cancer therapeutics using a deep mutational scanning approach in Saccharomyces cerevisiae. Ethan Ahler, Douglas Fowler. Department of Genome Sciences, University of Washington, Seattle, WA.

383B
Synthetic dosage lethality of CTF4 and the identification of orthologs amplified in breast cancer. Eric Bryant1, John Dittmar2, Robert J. D. Reid2, Rodney Rothstein2. 1) Biological Sciences, Columbia University, New York, NY 10027; 2) Genetics and Development, Columbia University Medical Center, New York, NY 10032.

384C
Identification of biological roles for yeast Rbd2, a member of a subfamily of rhomboid proteins implicated in human disease. Christa L. Cortesio1, Eric B. Lewellyn1, Nathaniel I. Krefman1, Catherine C. Wong2, John R. Yates 3rd2, David G. Drubin1. 1) Molecular and Cell Biology, University of California-Berkeley, Berkeley, CA; 2) Department of Chemical Physiology, The Scripps Research Institute, La Jolla, CA.

385A

386B

387C
Yeast - it simply has a lot to say about human disease. Selina S. Dwight, Kalpana Karra, J. Michael Cherry. SGD Project. Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305.

388A
Deep mutational scanning of amyloid β to illuminate mechanisms of protein aggregation and chaperone interactions. Vanessa E. Gray, Jason J. Stephany, Douglas M. Fowler. Genome Sciences, School of Medicine at the University of Washington, Seattle, WA, USA.

389B
Solving protein structure with large-scale mutagenesis. Katherine A. Sitko, Douglas M. Fowler, Margaret L. Griset. Genome Sciences, School of Medicine at the University of Washington, Seattle, WA.

390C

391A
Anticancer ruthenium complex KP1019 induces the heat shock response in yeast. Laura Stultz1, Alexandra Hunsecker2, Evan Grovenstein2, James Mobley3, Pamela Hanson2. 1) Chemistry Department, Birmingham-Southern College, Birmingham, AL; 2) Biology Department, Birmingham-Southern College, Birmingham, AL; 3) Mass Spectrometry/Proteomics Facility, University of Alabama at Birmingham, AL.

392B

393C
S. cerevisiae as a Platform for High Throughput Screening and Variant Analysis of the Sphingosine-1-Phosphate Receptor Family. Jacob Hornick1, Son Nguyen4, Pam Benegal1, Shen-Shu Sung2, James Broach'. 1) Department of Biochemistry and Molecular Biology, Pennsylvania State University College of Medicine, Hershey, PA; 2) Department of Pharmacology, Pennsylvania State University College of Medicine, Hershey, PA; 3) Department of Molecular Biology, Princeton University, Princeton, NJ; 4) Union College, Schenectady, NY.
**Poster Session Listings**

394A  
Ribosomal Perturbation as a Strategy for Improving Protein Biogenesis in Cystic Fibrosis. Mert Icyuz1, Kathryn E. Oliver2, Eric J. Sorscher2, John L. Hartman IV3.  
1) Genetics, University of Alabama at Birmingham, BIRMINGHAM, AL; 2) Gregory Fleming James Cystic Fibrosis Research Center, University of Alabama at Birmingham, BIRMINGHAM, AL.

395B  
Arg-Trp-Arg based peptidomimetics with antifungal activity. Camilla E. Larsen1, Camilla J. Larsen2, Henrik Franzyk2, Birgitte Regenberg1.  
1) Department of Biology, University of Copenhagen, Copenhagen, Denmark; 2) Department of Drug Design and Pharmacology, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark.

396C  
Expression, modification and characterization of fungal natural products in Saccharomyces cerevisiae. C. Harvey, J. Li, M. Hillenmeyer, R. Davis. Stanford Genome Technology Center, Stanford University, Stanford, CA.

397A  
Chemical genomic profiling in S. cerevisiae and S. pombe to functionally annotate large compound collections. Sheena C. Li, Jeff Piotrowski, Raamesh Deshpande, Scott Simpkins, Justin Nelson, Jacqueline Barber, Minoru Yoshida, Chad L. Myers, Charles Boone.  
1) RIKEN CSRS, Wako, Saitama, Japan; 2) University of Wisconsin-Madison; 3) University of Minnesota; 4) University of Toronto, Canada.

398B  
1) Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 2) Terrance Donnelly Center for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario, Canada; 3) Banting and Best Department of Medical Research, University of Toronto, Toronto, Ontario, Canada.

399C  
Shared pHenotypes: Using a yeast genetic screen as a way to identify mammalian genes required for cellular survival during intracellular acidification. Jennifer A. McQueen, John Shin, Susan Li, Pamela Austin, Calvin Roskelley, Christopher Loewen.  
Cellular and Physiological Sciences, Univ British Columbia, Vancouver, BR., BC, Canada.

400A  
The Effects of Omega-3-Fatty Acids on Intracellular inositol levels in Saccharomyces Cerevisiae. Marlene N. Murray, Bomi Kim, Jee Yeon Lee. Biology, Andrews University, Berrien Springs, MI.

401B  
Making Genetic Suppressors for Yeast Genes Whose Orthologs are Involved in Human Retinitis Pigmentosa. Zahra NaghdiGheslaghi, Jolanda van Leeuwen, Brenda Andrews, Charles Boone. Donnelly Centre, University of Toronto, Toronto, ON, Canada.

402C  
Department of Biochemistry and Molecular Biology, Rutgers University - R W Johnson Medical School, Piscataway, NJ.

403A  
1) Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 2) Terrance Donnelly Center for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario, Canada; 3) Banting and Best Department of Medical Research, University of Toronto, Toronto, Ontario, Canada.

404B  
A connection between chromosome condensation/cohesion pathways and the toxic effects of the Huntington disease protein in a yeast model. Biranchi N. Patra, Scott Breslow, Jocelyn Wensel, Animesh Ray. School of Applied Life Sciences, Keck Graduate Institute, Claremont, CA.

405C  
1) School of Applied Sciences- Biosciences, RMIT University, Melbourne-Bundoora, VIC, Australia; 2) Materials Science and Engineering, CSIRO Preventative Health Flagship, 343 Royal Parade, Parkville, Victoria 3052, Australia; 3) School of Applied Sciences, Applied Chemistry, RMIT University, Melbourne, Victoria 3000, Australia.

406A  
A yeast synthetic genetic interaction screen predicts the importance of Plk1 for the viability of cancer cells over-expressing CKS1b. Robert J. D. Reid, Xing Du, Ivan Sunjevaric, Vinayak Rayannavar, John Dittmar, Matt Maurer, Rodney Rothstein.  
1) Genetics & Development, Columbia University Medical Center, New York, NY; 2) Dept of Medicine, Columbia University Medical Center, New York, NY.

407B  
1) Organic Chemistry, Institute of Chemistry, UNESP, Araraquara, Sao Paulo, Brazil; 2)
Poster Session Listings

Biological Sciences, School of Pharmaceutical Sciences, UNESP, Araraquara, SP, Brazil.

408C

409A
Developing assays for pathogenic human variation via systematic testing of yeast/human complementation. Song Sun1,2,3,4,5, Fan Yang1,2,3,4, Michael Costanzo1,2, Rose Oughtred6, Jodi Hirschman8, Chandra Thesefeld7, Analyn Yu1,2,3,4, Tanya Tyagi1,2,3,4, Brenda Andrews1,2, Nidhi Sahni7,8, Song Yi7,8, David Hill7,8, Marc Vidal7,8, Charlie Boone1,2, Kara Dolinski6, Frederick Roth1,2,3,4,7. 1) Donnelly Centre, University of Toronto, Toronto, Ontario, Canada; 2) Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; 3) Department of Computer Science, University of Toronto, Toronto, Ontario, Canada; 4) Lunenfeld-Tanenbaum Research Institute, Mt. Sinai Hospital, Toronto, Ontario, Canada; 5) Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; 6) Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, New Jersey, USA; 7) Center for Cancer Systems Biology (CCSB), Dana-Farber Cancer Institute, Boston, MA, USA; 8) Department of Genetics, Harvard Medical School, Boston, MA, USA.

410B

Global Analysis: Informatics/Computational Biology

411C

412A
TreeView 3.0: Visualization and Analysis of Two-Dimensional Genomic Data. Christopher Kel, Anastasia Baryshnikova. Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ.

413B
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414C
Tyre: An in Silico Simulator of Population Dynamics. Jill N. Wright1, Jessica Stilwell1, Christopher Zahner1, Hui Hua1, Brandt L. Schneider1. 1) Cell Biology and Biochemistry, Texas Tech University Health Sciences Center, Lubbock, TX; 2) Texas Tech University, Howard Hughes Medical Institute, Lubbock, TX.

415A

Global Analysis: Networks

416B
Profiling the RNA maturation landscape in yeast. Alexander Ratushny1,2, Marlene Oeffinger1, Wei-Ming Chen1, Karen Wer4, Peter Fridy3, Richard Rogers1, Ramsey Saleem1,2, Garrett Poshusta1, Michael Rout1, John Atchison1,2. 1) Systems Biology, Institute for Systems Biology, Seattle, WA, USA; 2) Seattle Biomedical Research Institute, Seattle, WA, USA; 3) Rockefeller University, New York, NY, USA; 4) Institut de recherches cliniques de Montréal, Montréal, Québec, Canada.

417C
Cin5, Gln3, Hmo1, and Zap1 Contribute to the Gene Regulatory Network Controlling the Cold Shock Response in Saccharomyces cerevisiae. Kam D. Dahlquist1, Ben G. Fitzpatrick1, Cybele Arsan1, Wesley T. Citti1, Kevin C. Entzinger1, Andrew F. Herman1, Lauren N. Kubeck1, Stephanie D. Kuebbs2, Heather King1, Elizabeth M. Liu1, Matthew Mejia1, Kenny R. Rodriguez1, Nicholas A. Rohacz2, Olivia S. Sakhon1, Katrina Sherbina2, Alondra J. Vega2. 1) Biol, Loyola Marymount Univ, Los Angeles, CA; 2) Math, Loyola Marymount Univ, Los Angeles, CA.

418A
Dissecting the Regulation of the Yeast Pleiotropic Drug Response. Colin Harvey, Ulrich Schlecht, Sundari Suresh, Robert St. Onge, Ronald Davis, Maureen Hillenmeyer. Stanford Genome Technology Center, Stanford University, Palo Alto, CA.

419B
Transferability of protein-protein interactions and protein function between closely related species. Hsueh-lui Ho1, Maxime Huvet1, Michael Stumpf2, Ken Haynes1. 1) Biosciences, 3rd floor Geoffrey Pope Building, Exeter University, Exeter, Devon, EX4 4QD United Kingdom; 2) Theoretical System Biology, Imperial College London, London, United Kingdom.
420C
Measuring changes in genetic interactions over environments using iSeq. Mia Jaffe1, Gavin Sherlock1, Sasha F. Levy2. 1) Dept of Genetics, Stanford University, Stanford, CA; 2) Laufer Center for Physical and Quantitative Biology, Stony Brook University, Stony Brook, NY.

421A
Extensive inbound and feedback signal integration by Protein Kinase A. Christian Landry1, Marie Filteau1, Guillaume Diss1, Francisco Torres-Quiroz2, Alexandre Dube1, Isabelle Gagnon-Arsenault1, Andree-Eve Chretien1, Ugo Dionne2, Anne-Lise Steunou1, Andrea Schraffl3, Jacques Coté4, Nicolas Bisson2, Eduard Stefan1. 1) Département de Biologie, PROTEO and Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, Québec, G1V 0A6, Canada; 2) Département de Biologie Moléculaire, Biochimie Médicale et Pathologie, et Centre de Recherche sur le Cancer, Université Laval, Québec, Québec, G1V 0A6, Canada; 3) University of Innsbruck, Institute of Biochemistry and Center for Molecular Biosciences Innsbruck (CMBI), A-6020 Innsbruck, Austria.

422B
Genome-scale analyses of Saccharomyces cerevisiae strains evolved for bio-ethanol production under aerobic and anaerobic growth conditions. Kevin S. Myers1,2, Nicholas M. Riley3,4, Trey K. Sato5, Joshua J. Coon4,5, Audrey P. Gasch3,4,5, Audrey P. Gasch1,2. 1) Laboratory of Genetics, UW-Madison, Madison, WI; 2) Great Lakes Bioenergy Research Center, UW-Madison, Madison, WI; 3) Department of Chemistry, UW-Madison, Madison, WI; 4) Genome Center, UW-Madison, Madison, WI; 5) Department of Biomolecular Chemistry, UW-Madison, Madison, WI.

423C
A gene network model of cellular aging and its applications. Hong Qin. Biology, Spelman College, Atlanta, GA.

424A
Genetic pathways involved in response to the phenol-based compounds bisphenol-A (BPA), butylated hydroxyanisole (BHA), and butylated hydroxytoluene (BHT) in Saccharomyces cerevisiae. Shrava L. Raju1, Julia Levy2, Elizabeth Martin3, Mia Pecora1, Gretchen Edwards-Gilbert1,2,3. 1) Scripps College, Claremont, CA; 2) Pitzer College, Claremont, CA; 3) Claremont McKenna College, Claremont, CA.

425B
Widespread changes in the yeast protein interaction network in response to diverse environmental cues. U. Schlecht1, J. Smith1, A. Celaj2, S. Suresh1, M. Miranda1, R. W. Davis1, F. Roth1, R. P. StOnge1. 1) Biochemistry, Stanford University, Palo Alto, CA; 2) Donnelly Centre, University of Toronto, Toronto, Ontario.

426C
TheCellMap.org: storing and visualizing genetic interactions in S. cerevisiae. Matej Usaj1, Michael Costanzo1, Chad L. Myers2, Brenda Andrews1, Charles Boone1, Anastasia Baryshnikova1. 1) Donnelly CCBR, University of Toronto, Toronto, Ontario, Canada; 2) Department of Computer Science and Engineering, University of Minnesota, Minneapolis, MN, USA; 3) Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ, USA.

427A
Unraveling protein network evolution through whole-proteome cross-species interactome mapping. Haiyuan Yu. Biological Statistics and Computational Biology, Cornell University, Ithaca, NY.

Global Analysis: Other Yeasts

428B
Functional Characterisation of Candida glabrata Open Reading Frames with no Orthologue in Saccharomyces cerevisiae. Lauren C. Ames1, Jane Usher1, Ilias Kounatidis2, Petros Ligoxygakis1, Ken Haynes1. 1) Biosciences, University of Exeter, United Kingdom; 2) Department of Biochemistry, University of Oxford, UK.

429C
Comparative genomics and transcriptomics of the industrial yeast species Dekkera (Brettanomyces) bruxellensis. Anthony Borneman1, Lucy Joseph2, Toni Cordente1, Robyn Kievel1, Ryan Zeppel1, Warren Albertin1, Isabelle Masneuf-Pomarede1, Christ Curtin1. 1) Australian Wine Research Institute, Urrbrae, SA 5064, South Australia, Australia; 2) Department of Viticulture and Enology, University of California, Davis, 595 Hilgard Lane, Davis, CA 95616; 3) Univ. de Bordeaux, ISVV, EA 4577, Unité de recherche Œnologie, F-33140 Villenave 13 d'Ornon, France.

430A
Assembling the Schizosaccharomyces kambucha genome and the dynamic transposon landscape of fission yeasts. Michael Eickbush1, Sarah Zanders1, Gerry Smith1, Harmit Malik1. 1) Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Howard Hughes Medical Research Institution, Chevy Chase, MD.

431B
Evolutionary genomics of ecological speciation in Saccharomyces paradoxus. Jean-Baptiste Leducq, Lou Niely-Thibaut, Guillaume Charron, Christian Landry. Département de Biologie, Université Laval, Quebec, QC, Canada.
432C
Comparative Genomics of Yeast Genome Conformation and Functional Annotation by Multiplexed Hi-C. Ivan Liachko, Joshua Burton, Jay Shendure, Maitreya Dunham. Genome Sciences, University of Washington, Seattle, WA.

433A

434B

Global Analysis: Proteomics

435C
Evaluating Common Humoral Responses Against Fungal Infections With Yeast Protein Microarrays. Paulo Coelho1,2, Hogune Im3, Karl Clemons1,2, Michael Snyder1, David Stevens1. 1) Dept of Medicine, Stanford University, Palo Alto, CA; 2) Calif. Inst. Med. Res., San Jose, CA; 3) Dept of Genetics, Stanford University, Palo Alto, CA.

436A
The caveolin-binding motif of the pathogen-related yeast protein Pry1, a member of the CAP protein superfamily, is required for in vivo export of cholesteryl acetate. Rabih Darwiche1, Vineet Choudhary2, David Gfeller2, Olivier Michielin2, Vincent Zoet2, Roger Schneiter1. 1) Division of Biochemistry, Department of Biology, University of Fribourg, 1700 Fribourg, Switzerland; 2) Molecular Modeling, Swiss Institute of Bioinformatics, Quartier Sorge, Batiment Genopole, 1015 Lausanne, Switzerland.

437B
Phosphoproteome analysis of the DNA damage response during S phase in Saccharomyces cerevisiae. Dongqing Huang, Brian Piening, Corey Weinert, Amanda Paulovich. Clinical Division, Fred Hutchinson Cancer Research Center, Seattle, WA.

438C
Functional profiling of the ubiquitin-proteasome system of protein degradation. Anton Khmelinskii1, Bernd Fischer2, Joseph D. Barry2, Matthias Meurer1, Daniel Kirrmaier1, Michael Costanzo3, Charles Boone3, Wolfgang Huber2, Michael Knop1. 1) Center for Molecular Biology of the University of Heidelberg (ZMBH), DFKZ-ZMBH Alliance, Heidelberg, Germany; 2) European Molecular Biology Laboratory (EMBL), Genome Biology Unit, Heidelberg, Germany; 3) Banting and Best Department of Medical Research and Department of Molecular Genetics, The Donnelly Centre, University of Toronto, Toronto, Ontario, Canada.

439A
Stable-seq: High-throughput Analysis of in vivo Protein Stability. Ikjin Kim1, Christina Miller1,2, Stanley Fields1,2, 1) Department of Genome Sciences, University of Washington, Seattle, WA, USA; 2) Howard Hughes Medical Institute, University of Washington, Seattle, WA, USA; 3) Department of Medicine, University of Washington, Seattle, WA, USA.

440B
Proteomic analysis and metabolic exploration of Yarrowia lipolytica under different culture conditions. J. Shi, W. Chen. Nanyang Technological University, Singapore.

441C
Identifying global changes in protein acetylation following heat shock. Rebecca E. Sides, Jeffrey A. Lewis. Biological Sciences, University of Arkansas, Fayetteville, AR.

442A
Identification of long-lived proteins in cells undergoing repeated asymmetric divisions. NH Thayer1,2,3, C. Leverich1,2, E. Marsh1, M. Fitzgilbert1, ZW Nelson1, KA Henderson1, J. Hsu1, DE Gottschling1. 1) Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Molecular and Cellular Biology Program, University of Washington, Seattle, WA; 3) These authors contributed equally to this work.

443B
A systematic investigation of small metabolite interactions with regulatory proteins in yeast. G. X. Yang, X. Li, M. Bruno, M. Snyder. Department of Genetics, Stanford University, Stanford, CA.

Global Analysis: Technology

444C
Measuring stress response in Saccharomyces cerevisiae using Isotopic Ratio Outlier Analysis (IROA) for metabolome-wide quantitation. Felice A. de Jong, Chris Beecher. IROA Technologies LLC, Ann Arbor MI.
### Poster Session Listings

**445A**


**446B**


**447C**

Biosensors engineered from conditionally stabilized ligand-binding domains. Benjamin Jester, Christine Tinberg, Justin Feng, Dan Mandell, George Church, David Baker, Stanley Fields. 1) Howard Hughes Medical Institute, University of Washington, Seattle, WA; 2) Department of Genome Sciences, University of Washington, Seattle, WA; 3) Department of Biochemistry, University of Washington, Seattle, WA; 4) Division of Medical Sciences, Harvard Medical School, Boston, MA; 5) Department of Genetics, Harvard Medical School, Boston, MA; 6) Department of Medicine, University of Washington, Seattle, WA.

**448A**

Acetylation of carotenoids in Yarrowia lipolytica improves cell viability and titers. Lisa Laprade, Maria Mayorga, Chris Farrell, Peter Houston, Dan Grenfell-Lee, Joshua Trueheart. DSM Microbia, Lexington, MA.

**449B**

Phenomic Analysis of TOR Signaling and dNTP Metabolism. Sean M. Santos, Chandler Stisher, Darryl Outlaw, Jingyu Guo, John L. Hartman IV. Department of Genetics, University of Alabama at Birmingham, Birmingham, AL.

**450C**

An automated system for time-lapse imaging of microbial biofilms. Adrian Scott, Aimée M. Dudley. Pacific Northwest Diabetes Research Institute, Seattle, WA.

**451A**

Development of ODELAY, a scalable, automated, multiparameter growth rate analysis platform, and application to a yeast model of Parkinson’s disease. David J. Dilworth, Alexander V. Ratushny, Thurston E. Herricks, Jennifer J. Smith, Song Li, John D. Aitchison. 1) Institute for Systems Biology, Seattle, WA; 2) Seattle Biomedical Research Institute, Seattle, WA.

**452B**

Genome Wide Manipulation of Transcription in Saccharomyces cerevisiae using CRISPR-Cas9 Transcription Factors. Justin D. Smith, Ulrich Schlecht, Sundari Suresh, Ron W. Davis, Leopold Parts, Robert P. St. Onge. 1) Department of Genetics, Stanford University School of Medicine, Stanford, CA; 2) Stanford Genome Technology Center, Stanford University, Palo Alto, CA; 3) Genome Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

### Global Analysis: Other

**453C**

Seeking a metabolic understanding of chronological aging. Haley Albright, Crystal Maharrey, Daniel Smith, John L. Hartman IV. Department of Genetics, University of Alabama at Birmingham, Birmingham, AL.

**454A**


**455B**

Instant killing of yeast for protein studies during continuous culture. Sara S. Dick, Khyla Rose Alorro, Sean McNabney. Biology, Valparaiso University, Valparaiso, IN.

**456C**


**457A**

Reverse Two Hybrid, a systematic approach for identifying genes and pathways that regulate a specific protein-protein interaction. Ifat Lev, Marina Volpe, Shay Bev Aroya. Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan, Israel.

**458B**


**459C**

Staying current and modern: Overhauling an actively-used model organism database website. Kelley M. Paskov, Stacia R. Engel, Gail Binkley, J. Michael Cherry. Department of Genetics, Stanford University, Stanford, CA.
460A
Underlying the phenotypic contribution of a single quantitative trait locus in yeast are effects of seven genes and their epistatic interactions. R. Shapira, T. Benbenishty, L. David. ANIMAL SCIENCES, FACULTY OF AGRICULTURE, FOOD AND ENVIRONMENTAL QUALITY SCIENCES, THE HEBREW UNIVERSITY OF JERUSALEM, ISRAEL, REHOVOT, ISRAEL.

461B
Stability and Patterning in Microbial Communities: Lessons from Engineered Yeast Populations and Mathematical Modeling. Wenying Shou1, Babak Momeni1, Kristine Brileya2, Matthew Fields2. 1) Fred Hutchinson Cancer Research Center, Seattle, WA; 2) Montana State University, Bozeman, MT.

462C
Regulation of biofilm development through the simultaneous activation and repression of functionally distinct extracellular proteins. Zhihao Tan1,2, Michelle Hays1, Cecilia Garmendia-Torres3, Gareth A. Cromie2, Amy Sirr2, Eric W. Jeffery2, Patrick May4, Aimée M. Dudley1,2. 1) Molecular and Cellular Biology Program, University of Washington, Seattle, WA; 2) Pacific Northwest Diabetes Research Institute, Seattle; 3) Institut de Génétique et de Biologie Moléculaire et Cellulaire, Illkirch, France; 4) Luxembourg Center for Systems Biomedicine, University of Luxembourg, Luxembourg.

Academic Teaching

463A
Interdisciplinary research on anticancer ruthenium complexes links undergraduate courses and improves student learning and confidence. Pamela Hanson1, Laura Stultz2. 1) Biology Department, Birmingham-Southern College, Birmingham, AL; 2) Chemistry Department, Birmingham-Southern College, Birmingham, AL.

464B
The 15-week PhD: research methods training for MS Biotechnology students through laboratory investigations of yeast cell physiology. Robert M. Seiser. Biological, Chemical and Physical Sciences, Roosevelt Univ, Schaumburg, IL.

465C
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Speaker and Author Index

This index includes names in alphabetical order of all invited authors, and co-authors published in this book.

The number following a name refers to the abstract’s program number. An asterisk denotes a presenting author.

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### Speaker and Author Index

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This is an index of genes mentioned in the abstracts. The current Yeast Database approved gene symbol is given in each case; non-current symbol synonyms or full names used in the abstracts are not indexed.

The index was prepared computationally based solely on the YBgn & gene symbol information provided by authors during abstract submission. GSA is not responsible for any incorrect indexing where genes stated to feature in an abstract do not actually appear. Numbers following each term refer to abstract program numbers: 1–69 are platform presentations and 70–465 are poster presentations.

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