U.S. Department of Health and Human Services
National Institutes of Health
Division of Program Coordination, Planning, and Strategic Initiatives
Office of Research Infrastructure Programs
Division of Comparative Medicine

Validation of Animal Models and Tools for Biomedical Research Session I. Validation of Invertebrate Models for Preclinical Research

Tuesday, November 17, 2020
Virtual Meeting

Workshop Report

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Executive Summary

The first of 10 sessions of the Virtual Workshop on Validation of Animal Models and Tools for Biomedical Research was held on November 17, 2020. This workshop is intended as a venue to discuss the status and needs regarding the validation of animal models and tools used in biomedical research. The goal of the workshop is to brainstorm about reagents, tools, and resources across the National Institutes of Health (NIH) and to enable both basic research and translational approaches relevant to the validation of animal models and tools. The participants were asked to consider biological questions, the approaches needed to answer them, and the tools to facilitate those efforts. Invertebrate models (e.g., *Drosophila melanogaster*, *Caenorhabditis elegans*) have played a significant role in the understanding of biological processes. Session I focused on the development of tools and technologies to enable the use of invertebrate model organisms for basic biological discoveries. The ideas encompassed a wide range of biological questions (e.g., neuronal function, developmental biology, gene expression, cell biology). During discussion, the following needs were identified: (1) improving and developing technologies (e.g., nonmutagenic CRISPR, vetting of orthogonal recombinases for *C. elegans*, multiplex genome engineering strategies, injection robots, targeted gene mutagenesis, optimal split inteins, multi-coloring for molecular trafficking characterization); (2) improving workflows; (3) providing broader access to technologies and resources (e.g., imaging technologies); (4) developing, expanding, integrating, and supporting databases (e.g., FlyBase, Saccharomyces Genome Database, Mouse Genome Informatics, WormBase, Zebrafish Information Network) and stock centers (e.g., Bloomington Drosophila Stock Center); and (5) advancing a large-scale single-cell RNA sequencing program. Several participants discussed the need to support metabolomic, transcriptomic, and proteomic resources. Integration within and across databases (i.e., between molecular levels and organisms) is needed. Several participants expressed interest in strategies for molecular engineering, which has many potential uses (e.g., nanobodies, inteins, recombinases) for investigators. Participants also discussed the potential benefits and disadvantages of using nanobodies and nanotags in research; validation and technological development are important factors to consider.

Session Co-Chairs
Hugo Bellen, D.V.M., Ph.D., Baylor College of Medicine
Julie Simpson, Ph.D., University of California, Santa Barbara

Presenters
Gregory Jefferis, Ph.D., Medical Research Council (MRC) Laboratory of Molecular Biology
Erik Jorgensen, Ph.D., The University of Utah
Norbert Perrimon, Ph.D., Harvard Medical School
Gerald Rubin, Ph.D., Howard Hughes Medical Institute
Meng Wang, Ph.D., Baylor College of Medicine
Benjamin White, Ph.D., National Institute of Mental Health

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Sige Zou, Ph.D., Coordinator, Program Official, Office of Research Infrastructure Programs (ORIP)

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Xiaoli Zhao, Ph.D., National Institute of General Medical Sciences

Workshop Report

Opening Remarks
Franziska B. Grieder, D.V.M., Ph.D., Director, ORIP
Sige Zou, Ph.D., Coordinator, Program Official, ORIP

Drs. Franziska B. Grieder, Director, ORIP, and Sige Zou, Coordinator, Program Official, ORIP, welcomed the participants and expressed appreciation to the Organizing Committee and Session Chairs for their efforts in organizing the event. They explained that the meeting is the first in a series of 10 sessions. Drs. Grieder and Zou also acknowledged the support of several NIH Institutes: the National Heart, Lung, and Blood Institute (NHLBI); National Institute on Aging (NIA); National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK); National Institute of General Medical Sciences (NIGMS); and National Institute of Neurological Disorders and Stroke (NINDS). Dr. Grieder reminded the participants that validation of animal models and tools is a critical part of ORIP's trans-NIH efforts. She expressed appreciation for the participants' input.

Goals of the Invertebrate Workshop
Julie Simpson, Ph.D., University of California, Santa Barbara

Dr. Julie Simpson, Co-Chair, stated that the workshop will address reagents, tools, and resources, as well as basic research and translational approaches that could be developed within the next 10 years. She asked participants to consider biological questions, the approaches needed to answer those questions, and tools to facilitate those efforts. Invertebrate models (e.g., *D. melanogaster*, *C. elegans*) have played an important role in understanding biological processes. She noted that that her group's work on neurons and motor sequences requires numerous tools. She expressed, for example, her desire to develop synthetic enhancers (which require knowledge of transcription factor binding sites and transcription factor expression patterns) and a tools index (to search for relevant publications). This session will focus on the development of tools and technologies to validate and enable the use of invertebrate model organisms for basic biological discovery. The ideas will encompass a wide range of biological questions (e.g., neuronal function, developmental biology, gene expression, cell biology). Three areas of focus are genomics, phenomics, and informatics. Dr. Simpson emphasized the impact that new tools and techniques have made; she thanked the tool builders for their work and the NIH for its support. Dr. Hugo Bellen, Co-Chair, introduced the speakers.

High-Throughput Gene Tagging in *C. elegans*
Erik Jorgensen, Ph.D., The University of Utah

Dr. Erik Jorgensen spoke on his group's efforts to generate high-throughput CRISPR-tagging in *C. elegans*. Knowledge of genes and proteins is crucial to understanding cell function; relevant tools (e.g., recombinases, tags) are required. Current technologies for gene tagging include single-copy transgenes at landing pads and endogenous gene tagging by CRISPR. Synthesis-dependent strand annealing, however, is prone to error. Flp-mediated recombinase-mediated cassette exchange provides an alternative approach. Current strategies for endogenous gene tagging use both Cre (for excision of selection) and Flp (for regulated protein tagging) recombinases. Optimizing tags for each gene, however, is not feasible. Multiplex CRISPR tagging currently is in development to address this issue; a single injection enables tagging of dozens of genes via Goldengate assembly. In *C. elegans*, injected DNA is concatemerized into an extrachromosomal assembly, with hundreds of copies of injected plasmid maintained as semistable minichromosomes. A host promoter expresses guide RNA, which is oriented to cut and open a gene of interest. The address from the guide RNA gene is amplified and sequenced. Currently, all the individual steps except the opener cut have been validated. Recombinase-mediated

inserts help to address the issue of double-strand breaking associated with CRISPR. Flp can be used to generate tag incorporation by germline expression of serine integrase. Efficient worm-compatible recombinases are necessary to apply the approach to all genes. Dr. Jorgensen concluded by summarizing current needs: nonmutagenic CRISPR, vetting of orthogonal recombinases for *C. elegans*, multiplex genome engineering strategies, injection robots, downstream workflows (e.g., for automated cell expression identification, automated localization in signature cells, protein colocalization by super-resolution, protein proximity in time and place, binding proteins in time and place), and targeted gene mutagenesis.

Stock Centers and High-Resolution Light and Electron Microscopy Imaging Tools
Gerald Rubin, Ph.D., Howard Hughes Medical Institute

Dr. Gerald Rubin presented on the distribution of tools and technology and the importance of stock centers. He noted that these two topics are closely intertwined. Stock centers (e.g., the Bloomington Drosophila Stock Center) play a crucial role in the efficient distribution of organisms for tool building. Imaging development generally does not represent a rate-limiting factor in research. Many cutting-edge high-resolution microscopy techniques have been developed in the past few years, but these technologies should be distributed more widely to investigators. Additionally, non-perturbing paths for imaging of individual molecules are needed. Basic light microscopes are widely accessible to investigators, but advanced microscopes offer unique capabilities that are not available broadly. Isotropic multi-view light-sheet microscopy enables the production of live movies, allowing investigators to visualize biological features (e.g., neuronal morphology and neuronal activity in embryos). Additionally, expansion microscopy, combined with lattice light-sheet microscopy, enables high-resolution expansion. Further, focused ion beam–scanning electron microscopy enables large-volume three-dimensional imaging and processing. Dr. Rubin emphasized that many of these technologies are well-established but remain inaccessible to many investigators. He explained that most biological laboratories lack the capacity to maintain these types of instruments. The high equipment cost and specialized skillsets (e.g., physicists) required to construct and operate the instruments make these imaging technologies inaccessible to 99% of research laboratories. The Advanced Imaging Center at Howard Hughes Medical Institute provides access to these technologies, but long-distance travel is impractical for many investigators. Dr. Rubin proposed that centers at large institutions across the United States provide these crucial services more broadly; he suggested that ORIP consider supporting efforts in this area. He also noted that these concerns span many biological models, including invertebrates. He suggested making the developed cutting-edge technology more available to researchers rather than developing new methods.

The Potential Benefits of G Protein-Coupled Receptor Biosensors, Scarless Split Inteins, and Methods for Manipulating Dense-Core Vesicle Release
Benjamin White, Ph.D., National Institute of Mental Health

Dr. Benjamin White reviewed challenges his group has faced that might be resolved by development of new tools. He discussed the application of three tools that might be generally useful to researchers working in a variety of organisms on a variety of questions: split inteins (e.g., for refined cellular targeting), G protein-coupled receptor (GPCR) biosensors (e.g., for monitoring the time and location of hormone and neuromodulator action), and methods for manipulating dense-core vesicle release (e.g., suppressing and activating endocrine, neuroendocrine, and neuromodulator processes). Split proteins have been applied to multiple domains (e.g., bacterial transformation, yeast two-hybrid systems, identification of synaptic partners, combinatorial genetic targeting of cell types). Split inteins allow the two fragments of a split protein to be targeted using distinct enhancers to small groups of cells, where they then can self-splice back into a full-length protein. The self-splicing efficiency, however, often is dependent on the sequence flanking the split inteins. Two solutions to this issue are (1) developing an expanded library of split inteins with differing flanking sequence profiles and (2) creating optimal split

inteins with reduced flanking dependence. Development support in this area would provide a useful toolkit for investigators. Dr. White explained that GPCR biosensors are critical for monitoring hormone and neuromodulator signaling because these processes are challenging to monitor in small invertebrate organisms and in the brains of vertebrate organisms. He also explained that many drugs target GPCRs. These receptors are ubiquitous signaling molecules in metazoans and have been critical to understanding cellular processes. Recent insights into GPCR signaling have led to breakthroughs in developing genetically encoded biosensors for hormones and neuromodulators. However, only a few GPCR biosensors have been produced to date. Creating a complete set of genetically encoded GPCR biosensors—that span the full range of hormones and neuromodulators found in animals and can be targeted to specific cell types—would be a very useful resource. Areas in which this technology might be further optimized include expanding the range of fluorescent reporters (i.e., colors) used and improving cellular trafficking of the biosensors to the membrane. Dr. White also noted that he is unaware of current methods for manipulating dense-core vesicle release, but work in this area would provide value for investigators. He concluded by inviting participants to provide feedback on available tools relevant to his research questions.

Metabolic Imaging and Profiling in Model Organisms
Meng Wang, Ph.D., Baylor College of Medicine

Dr. Meng Wang spoke on metabolic imaging and profiling in *C. elegans*. Her group studies the interface between longevity and metabolism, with specific interest in identifying signaling metabolites that contribute to lipid metabolism homeostasis and longevity. Of particular interest are metabolites that mediate signaling communication across networks (e.g., cellular, organismal, ecological). An understanding of the genomic–phenomic links within these metabolites is crucial. Many organism-level phenotypes (e.g., morphology, behavior, lifespan) can be characterized via microscopy. Cellular- and molecular-level phenotypes, however, require studying RNA transcripts, protein expression, and metabolites. Dr. Wang introduced the concepts of (1) optical transparency, which allows spatial and temporal visualization of cellular phenotypes in the context of the live organism; (2) genetic tractability, which investigates new regulatory genes in a systematic manner; and (3) metabolic conservation, which contributes to the understanding of metabolic mechanisms that are applicable to other organisms. Her goals are to (1) identify metabolites of interest using mass spectrometry (MS) or nuclear magnetic resonance–based metabolomic profiling; (2) visualize the metabolites *in vivo* using imaging MS, fluorescence sensors, and chemical imaging; and (3) characterize their regulatory roles using functional genomics. Metabolomic profiling technology currently is limited because most metabolites cannot be annotated with chemical specificity using available techniques. Additionally, the current technologies for chemical imaging are limited either by spatial resolution or deconvolution ability. The three goals have unique challenges, including chemical annotation, imaging deconvolution, and increasing throughput.

Protein Tagging, Nanobodies, Proximity Labeling Methods, and User-Friendly Bioinformatic Tools for Data Mining
Norbert Perrimon, Ph.D., Harvard Medical School

Dr. Norbert Perrimon presented on tools and resources for proteomics (e.g., nanobodies, epitope tagging, proximity labeling) and database resources. Proteins are important for understanding gene expression, localization, modification, and interaction. The correlation between mRNA expression and protein abundance is poor; thus, both components should be considered. Resources for detecting proteins include antibodies and green fluorescent protein (GFP) tags. FlyBase provides both capabilities, but each approach has benefits (e.g., unmodified native protein, wide variety of colors, live cells) and disadvantages (e.g., cost, specificity, interference, limited colors). Single-chain nanobodies are highly specific, high-affinity, and sustainable reagents; they can be used in studies of visualization, degradation,

relocalization, extracellular trapping, and enzymatic activities. Screening can be achieved though alpaca immunized libraries, phage display libraries, and yeast display libraries. Dr. Perrimon highlighted several small epitope tags that were recently characterized and are of particular interest for this approach. These nanobodies can be fused to degradation systems for studies of the process. Proximity labeling methods allow interrogation of the spatial proteome. These labels allow greater specificity, studies of purified organelles, and detection of transient weak interactions. Dr. Perrimon described the process of ascorbate peroxidase (APEX) targeting to the mitochondrial proteome. More recently, TurboID, an engineered biotin ligase, has been used in studies of interactions within the *Drosophila* organ secretome.

Dr. Perrimon also spoke on the need for continued funding for databases (e.g., FlyBase, Saccharomyces Genome Database, Mouse Genome Informatics, WormBase, Zebrafish Information Network). Long-term funding for these databases represents a challenge. He highlighted two current needs within the databases: integration of knowledge across organisms and integration of different databases that handle similar data. The Drosophila RNAi Screening Center Integrative Ortholog Prediction Tool, Model organism Aggregated Resources for Rare Variant ExpLoration (MARRVEL), and Gene2Function have pursued efforts in this area. He concluded by posing three recommendations for ORIP: invest in proteomics-based resources, invest in model organism databases, and invest in integration databases.

An Integrated Molecular and Connectomics Atlas of Brain Cell Types in *Drosophila*
Gregory Jefferis, Ph.D., MRC Laboratory of Molecular Biology

Dr. Gregory Jefferis discussed the need for an integrated molecular and connectomics atlas for neurodevelopment in *Drosophila*. He presented a three-dimensional rendition of the *Drosophila* brain, visualizing different cell types through visual tracing. New connectomics data sets recently have become available to investigators; more data sets are in development. The integration of neuroanatomy with molecular and development information poses a challenge for investigators; the Brain Research through Advancing Innovative Neurotechnologies® (BRAIN) Initiative is pursuing this topic in other models. Dr. Jefferis presented a three-dimensional image with colors depicting predictive cell image or predicted neurotransmitters and described the goal of creating a full central nervous system cell type atlas. He stated that the research community is interested in creating similar models for genes of interest; objectives include matching neurons between data sets (e.g., through molecular annotation and synaptic transmitter prediction) and integrating transcriptomes (e.g., by characterizing cell types and lineages). He suggested that ORIP support a large-scale single-cell RNA sequencing program, analytical and search tools for data integration, refinement and application for a molecular barcoding approach, and ongoing split-GAL4 generation and maintenance for different cell types. He concluded by posing the concept of reverse engineering the connectome from molecular cell types.

Group Discussion
Hugo Bellen, D.V.M., Ph.D., Baylor College of Medicine
Julie Simpson, Ph.D., University of California, Santa Barbara

Dr. Simpson reviewed comments submitted through the Zoom chat and encouraged participants to contribute additional comments through the chat and Google Doc for discussion. She explained that these notes will be used for the development of a 2- to 3-page summary describing the outcomes of the workshop.

Dr. Paul Sternberg asked Dr. Rubin what would be needed to support an accessible imaging center. Dr. Rubin stated that additional funding (~$200,000 for construction per instrument, ~$5 million per year for other costs) is needed. Most biological laboratories contain commercial instrumentation; non-commercial instruments require specialized personnel for construction and maintenance. Accessible

centers often have limited capacity to host outside investigators and restrict the time available to complete their experiments. Regional centers, similar to the cryogenic electron microscopy centers, would be ideal.

Dr. Simpson asked about the possibility of maintaining centers for instrumentation design and engineering hubs, similar to the imaging centers. Dr. Rubin responded that the process would be handled best by small commercial shops; other mechanisms likely would be challenging.

Dr. Simpson observed that several questions had addressed strategies for molecular engineering; she noted the many potential uses (e.g., nanobodies, inteins, recombinases) of this technique for investigators. She suggested considering the best platforms to share this information. Dr. Oguz Kanca immediately set up a Slack channel to address this need.

Dr. Bellen noted that several participants highlighted the importance of stock centers and databases. He remarked that the research community must emphasize the value of these resources to ensure continued NIH support. Dr. Keith Cheng suggested posing an economic argument for the resources.

Dr. Sternberg commented that the need for more resources in this area (e.g., an integrated transcriptomic regulatory network, metabolomics networks) is evident. He added that these issues span many different organisms. Dr. Jefferis noted that for investigators, integrating data across approaches is challenging and costly. Outside resources (e.g., Neuron Breach) are valuable for addressing these topics.

Drs. Cheng and Jorgensen suggested developing a singular molecular anatomy atlas to represent different organisms. Dr. Jefferis commented that transcriptomic profiling would provide valuable insight into this system. Dr. Bellen also noted current work on combining gene expression patterns in cells of interest.

Dr. Jorgensen stated that characterization of organelles would require advanced technological approaches (e.g., array tomography). Dr. Wang spoke on her group's work to characterize molecular characteristics of organelles. Dr. Jorgensen responded that first, the organelle localization must be identified.

Dr. Simpson stated that many participants expressed interest in antibody generation and labeling. Dr. Perrimon responded that appropriate nanobodies must be generated first; novel technologies will provide enhanced capabilities in this area. Dr. Loren Looger stated that these resources are critical; methods for production should be distributed to investigators. Dr. Perrimon responded that investment in the technology will be crucial.

Dr. Perrimon remarked that validation of nanobodies can be challenging. Dr. Kai Zinn agreed, noting that specificity is difficult and time consuming. Dr. Bellen suggested validation using GFP tags in certain applications.

Dr. Daniel Dickinson asked whether databases have considered integrating nanobody information. Dr. Rubin commented that many investigators often do not consistently share nanobodies through databases; more efforts should be made in this area. Dr. Bellen agreed that he has observed a shortage of available nanobodies.

In response to a question from Dr. Brian Oliver, Dr. Simpson noted that nanobodies are encodable and might be an ideal option for protein engineering. Dr. Oliver replied that nanotags might be more successful at scale. Dr. Perrimon commented that this approach would create new challenges for validation. Dr. Kanca mentioned that nanobodies provide the advantage of molecular evolution to increase affinity. Dr. Oliver responded that nanotags might help address some of the identified issues. Dr. Fillip Port added that further development of nanotags might help address issues of scalability.

Dr. Simpson asked whether CRISPR reagents and databases require further discussion. Dr. Bellen explained that introns are important for the approach. He added that his group's funding currently is limited to genes with human homologs.

Dr. Frank Schroeder noted that, currently, a comprehensive database for the metabolomics in *C. elegans* or *Drosophila* has not been developed, which represents a major deficit for investigators. Establishment of appropriate infrastructure is crucial. Drs. Bellen and Wang agreed, stating the importance of data integration, standardization, and annotation. Dr. Cheng asked whether computational workflows have been applied. Dr. Schroeder remarked that a standardized approach has not yet been developed.

Dr. Bellen agreed that data mining in metabolomic studies is challenging; NIH support in this area is needed. Dr. Oliver added that economics and policy should be considered as part of the issue.

Additional Comments

In the Zoom chat, Dr. Oliver suggested a curated nanobodies toolbox with references. Dr. Kanca suggested a two-step CRISPR-mediated homologous recombination system: (1) integrate standardized gRNA and homology arms and (2) use the standardized homology arm to integrate the tag *in vivo*. Dr. Matt Rich responded that his laboratory is using a similar approach. Dr. Looger commented that finding appropriate protein regions should not be difficult. Dr. Kanca suggested temperature-sensitive split inteins to enhance temporal regulation. Dr. Yvette Fisher asked for clarification on the scarless reconstitution using the split inteins design.

Dr. Liqun Luo voiced support for continued funding of databases for model organisms. Drs. Sternberg and Jorgenson commented that databases allow investigators to compare data across different model organisms. Drs. Sternberg and Stephanie Mohr shared useful genomic resources: alliancegenome.org and gene2function.org. Dr. Luo also commented on the importance of integrating transcriptomic and connectomic data. Dr. Looger asked how the production, characterization, and distribution of antibodies can be shared among investigators. Dr. Rich commented on the importance of publishing negative results and suggested investigators seek out micropublications. Dr. Sternberg highlighted micropublication.org. Drs. Amelie Gubitz and Kevin Cook clarified that three NIH Institutes and Centers, including NIGMS, NICHD, and NINDS, are co-funding the Bloomington Drosophila Stock Center with ORIP.

Dr. Jefferis commented that cell types present a major issue for validation and voiced support for combining different types of data in analyses. Dr. Cheng stated that every disease is associated with micron-scale changes in specific cell types; these data should be computationally accessible.

Summary and Suggestions

Worms and flies will continue to play seminal roles in the discovery of new players in human biology and diseases, the elucidation of complex conserved pathways, and the discovery of therapeutic drugs. The participants discussed and provided the following areas that require new or continued support from ORIP and the NIH:

- Stock centers
- Model organism databases
- Molecular tagging of all genes in worms and flies using CRISPR
- Systematic links between genome science and phenomics (i.e., from genes to transcripts to proteins to metabolites)

- Technology to produce split proteins based on intein technology

- Library of GPCR fluorescent proteins for use in all model organisms

- Nanobody libraries for visualizing proteins and their functional analysis

- Interrogation of the proteome in its native environment based on proximity labeling to provide tools for mapping protein interactomes and subcellular proteomes in their native environments

- Combination of single-cell transcriptome profiling, electron microscopy atlases, and light-level imaging of genetically targeted neurons

- Centralized databases to mine data from other databases

- Four to six central microscopy facilities for isotropic spatial resolution, whole-brain imaging with molecular contrast and nanoscale resolution, and scanning electron microscopy for large-volume 3D imaging

Appendix A: Meeting Agenda

Session I. Validation of Invertebrate Models for Preclinical Research
2:00–4:00 p.m. EST
November 17, 2020

Chairs
Hugo Bellen, D.V.M., Ph.D., Baylor College of Medicine
Julie Simpson, Ph.D., University of California, Santa Barbara

2:00–2:05 p.m.	**Opening Remarks**

Franziska B. Grieder, D.V.M., Ph.D., Director, Office of Research Infrastructure
    Programs (ORIP)
Sige Zou, Ph.D., Coordinator, Program Official, ORIP

2:05–3:30 p.m.	**Presentations**

Julie Simpson, Ph.D., University of California, Santa Barbara
Goals of the Invertebrate Workshop

Erik Jorgensen, Ph.D., The University of Utah
High-Throughput Gene Tagging in C. elegans

Gerald Rubin, Ph.D., Howard Hughes Medical Institute
*Stock Centers and High-Resolution Light and Electron Microscopy Imaging
Tools*

Benjamin White, Ph.D., National Institute of Mental Health
*The Potential Benefits of G Protein-Coupled Receptor Biosensors, Scarless Split
Inteins, and Methods for Manipulating Dense-Core Vesicle Release*

Meng Wang, Ph.D., Baylor College of Medicine
Metabolic Imaging and Profiling in Model Organisms

Norbert Perrimon, Ph.D., Harvard Medical School
*Protein Tagging, Nanobodies, Proximity Labeling Methods, and User-Friendly
Bioinformatic Tools for Data Mining*

Gregory Jefferis, Ph.D., MRC Laboratory of Molecular Biology
An Integrated Molecular and Connectomics Atlas of Brain Cell Types in
Drosophila

3:30–4:00 p.m.	**Group Discussion**

Appendix B: Discussants List

Session I. Validation of Invertebrate Models for Preclinical Research
2:00–4:00 p.m. EST
November 17, 2020

Kristine Abraham, Ph.D., National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK)
Stein Aerts, Ph.D., Vlaams Instituut voor Biotechnologie–Katholieke Universiteit Leuven
Lola Ajayi, Office of Research Infrastructure Programs (ORIP)
James Anderson, M.D., Ph.D., Division of Program Coordination, Planning, and Strategic Initiatives
Alan Attie, Ph.D., University of California, San Diego
Hugo Bellen, Ph.D., Baylor College of Medicine
Andrea Brand, Ph.D., Gurdon Institute, University of Cambridge
Shreaya Chakroborty, Ph.D., National Institute on Aging (NIA)
Michael Chang, Ph.D., ORIP
Marc Charette, Ph.D., National Heart, Lung, and Blood Institute (NHLBI)
Keith Cheng, M.D., Ph.D., Penn State College of Medicine
Miguel Contreras, Ph.D., ORIP
Kevin Cook, Ph.D., Indiana University
Daniel Dickinson, Ph.D., University of Texas at Austin
Monica Dus, Ph.D., University of Michigan
Yvette Fisher, Ph.D., Harvard Medical School
Bruce Fuchs, Ph.D., ORIP
Marco Gallio, Ph.D., Northwestern University
Franziska B. Grieder, D.V.M., Ph.D., ORIP
Amelie Gubitz, Ph.D., National Institute of Neurological Disorders and Stroke (NINDS)
Oliver Hobert, Ph.D., Columbia University
Gregory Jefferis, Ph.D., Medical Research Council Laboratory of Molecular Biology
Erik Jorgensen, Ph.D., The University of Utah
Oguz Kanca, Ph.D., Baylor College of Medicine
Thomas Kaufman, Ph.D., Indiana University
Erica Larschan, Ph.D., Brown University
Andrew Leifer, Ph.D., Princeton University
Howard Lipshitz, Ph.D., University of Toronto
Carlos Lois, Ph.D., California Institute of Technology
Loren Looger, Ph.D., Howard Hughes Medical Institute
Liqun Luo, Ph.D., Stanford University
Cathleen Lutz, Ph.D., The Jackson Laboratory
Geoffrey Meissner, Ph.D., Howard Hughes Medical Institute
Peter Meister, Ph.D., University of Bern, Switzerland
D.P. Mohapatra, Ph.D., NINDS
Stephanie Mohr, Ph.D., Harvard Medical School
Stephanie Murphy, V.M.D., Ph.D., ORIP
Stuart Newfeld, Ph.D., Arizona State University
Michael Nonet, Ph.D., Washington University School of Medicine in St. Louis
Kate O'Connor-Giles, Ph.D., Brown University
Brian Oliver, Ph.D., National Institute of Diabetes and Digestive and Kidney Diseases
Annette Parks, Ph.D., Indiana University
Norbert Perrimon, Ph.D., Harvard Medical School/Howard Hughes Medical Institute
Fillip Port, Ph.D., German Cancer Research Center

Chris Potter, Ph.D., Johns Hopkins Hospital
Thomas Ravenscroft, Baylor College of Medicine
Olena Riabinina, Ph.D., Durham University
Matt Rich, Ph.D., Rutgers University
Rebecca Roof, Ph.D., NINDS
Gerald Rubin, Ph.D., Howard Hughes Medical Institute
Tim Schedl, Ph.D., Washington University School of Medicine
Frank Schroeder, Ph.D., Cornell University
Oren Schuldiner, Ph.D., Weizmann Institute of Science
Lisa Schwartz Longacre, Ph.D., NHLBI
Shai Shaham, Ph.D., The Rockefeller University
Julie Simpson, Ph.D., University of California, Santa Barbara
Paul Sternberg, Ph.D., California Institute of Technology
Steve Stowers, Ph.D., Montana State University
William Talbot, Ph.D., Stanford University
Burak Tepe, Ph.D., Baylor College of Medicine
Desiree von Kollmar, ORIP
Meng Wang, Ph.D., Baylor College of Medicine/Howard Hughes Medical Institute
Benjamin White, Ph.D., National Institute of Mental Health
Cale Whitworth, Ph.D., Indiana University
Xiaoli Zhao, Ph.D., National Institute of General Medical Sciences
Sam Zheng, Ph.D., Indiana University
Kai Zinn, Ph.D., California Institute of Technology
Jonathon Zirin, Ph.D., Harvard Medical School
Sige Zou, Ph.D., ORIP