## Young Investigator Award Session D

Sunday, November 5, 2017, 10:00 am - 3:00 pm Convention Center - Room 328/329 (Level 300)

The Young Investigator Award is presented to outstanding young researchers during the Annual Meeting. This award encourages developing young scientists to pursue careers in various aspects of tropical disease research. Support these young scientists by attending their presentations during this session.

Presentation Number	Title	Author Block
	Judge	Stephen Davies Department of Microbiology and Immunology, USUHS, Bethesda, MD, United States
	Judge	Miranda Oakley FDA, Silver Spring, MD, United States
	Judge	Prakash Srinivasan NIH, Rockville, MD, United States
117	Therapeutic potential of Interferon-α and Ribavirin as combination therapy against Dengue virus in different cell lines	<b>Camilly P. Pires de Mello</b> , George L. Drusano, Justin J. Pomeroy, Evelyn J. Franco, Jaime L. Rodriquez, Ashley N. Brown University of Florida, Orlando, FL, United States
370	Var code: a new molecular epidemiology tool for monitoring Plasmodium falciparum in a high transmission area of Ghana, West Africa	Shazia Ruybal-Pesántez <sup>1</sup> , Kathryn E. Tiedje <sup>1</sup> , Gerry Tonkin-Hill <sup>2</sup> , Shai Pilosof <sup>3</sup> , Abraham Oduro <sup>4</sup> , Kwadwo A. Koram <sup>5</sup> , Mercedes Pascual <sup>3</sup> , Karen P. Day <sup>1</sup> <sup>1</sup> Bio21 Institute/University of Melbourne, Melbourne, Australia, <sup>2</sup> Walter and Eliza Hall Institute, Melbourne, Australia, <sup>3</sup> University of Chicago, Chicago, IL, United States, <sup>4</sup> Navrongo Health Research Centre, Navrongo, Ghana, <sup>5</sup> Noguchi Memorial Institute for Medical Research, Legon, Ghana
377	Novel <i>Plasmodium vivax</i> Duffy Binding Protein vaccine candidate are associated strong and persistent naturally acquired IgG and binding-inhibitory antibodies response, in long- term exposure population	<b>Camilla V. Pires</b> <sup>1</sup> , Jéssica R. Alves <sup>1</sup> , Barbara A. Lima <sup>1</sup> , Flora S. Kano <sup>1</sup> , Francis B. Ntumngia <sup>2</sup> , John H. Adams <sup>2</sup> , Luzia H. Carvalho <sup>1</sup>

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684	Antibiotic resistance in dense, low-income neighborhoods: the role of sanitation in gene dispersion	David Berendes <sup>1</sup> , David Holcomb <sup>2</sup> , Jackie Knee <sup>1</sup> , Trent Sumner <sup>1</sup> , Rassul Nala <sup>3</sup> , Joe Brown <sup>1</sup> <sup>1</sup> Georgia Institute of Technology, Atlanta, GA, United States, <sup>2</sup> University of North Carolina, Chapel Hill, NC, United States, <sup>3</sup> Minesterio da Saude, Maputo, Mozambique
703	NOT1-G is a novel member of the CAF1/CCR4/NOT complex that is essential for host to vector malarial transmission	Kevin J. Hart, Michael P. Walker, Scott E. Lindner The Pennsylvania State University, University Park, PA, United States
738	Trafficking and Topology Identification of <i>Plasmodium</i> <i>falciparum</i> Maurer's Cleft two Transmembrane protein	<b>Raghavendra Yadavalli</b> <sup>1</sup> , John W. Peterson <sup>2</sup> , Judith A. Drazba <sup>2</sup> , Tobili Yvonne Sam-Yellowe <sup>1</sup> <sup>1</sup> Cleveland State University, Cleveland, OH, United States, <sup>2</sup> The Cleveland Clinic, Cleveland, OH, United States
940	Complexity of infection and parasite relatedness of Plasmodium falciparum parasite populations in patients administered artemether- lumefantrine (AL) in Kenya	Lorna J. Chebon <sup>1</sup> , Peninnah Muiruri <sup>2</sup> , Dennis Juma <sup>3</sup> , Hosea M. Akala <sup>3</sup> , Ben Andagalu <sup>3</sup> , Edwin Kamau <sup>4</sup> , Matthew Brown <sup>3</sup> <sup>1</sup> JKUAT/Institute of Tropical Medicine and Infectious Diseases (ITROMID)/Walter Reed Project, Kisumu, Kenya, <sup>2</sup> Africa Biosystems Limited, Nairobi-Kenya, Nairobi, Kenya, <sup>3</sup> KEMRI/USAMRD-K/Walter Reed Project, Kisumu, Kenya, <sup>4</sup> Walter Reed National Medical Military Center, Bethesda, MD, United States
983	Identification of approved drugs that have activity against <i>Plasmodium falciparum</i> using <i>in</i> <i>silico</i> and <i>in vitro</i> approaches	Reagan M. Mogire <sup>1</sup> , Hoseah M. Akala <sup>2</sup> , Dennis W. Juma <sup>2</sup> , Agnes C. Cheruiyot <sup>2</sup> , Rosaline W. Macharia <sup>3</sup> , Hans A. Elshemy <sup>4</sup> , Ben Andagalu <sup>2</sup> , Matthew L. Brown <sup>2</sup> , Steven G. Nyanjom <sup>5</sup> <sup>1</sup> Pan African University, Nairobi, Kenya, <sup>2</sup> United States Army Medical Research Directorate – Kenya (The Walter Reed Project), Kisumu, Kenya, <sup>3</sup> University of Nairobi Centre for Biotechnology and Bioinformatics, Kenya Medical Research Institute/U.S., Kenya, <sup>4</sup> Cairo University, Cairo, Egypt, <sup>5</sup> Jom Kenyatta University of Agriculture and Technology, Kenya Medical Research Institute/U.S., Kenya
1043	Quantifying <i>var</i> gene expression in uncomplicated malaria	<b>Emily M. Stucke</b> <sup>1</sup> , Antoine Dara <sup>1</sup> , James Matsumura <sup>2</sup> , Matthew Adams <sup>1</sup> , Kara A. Moser <sup>2</sup> , Drissa Coulibaly <sup>3</sup> , Modibo Daou <sup>3</sup> ,

	infections using whole genome sequence data	Ahmadou Dembele <sup>3</sup> , Issa Diarra <sup>3</sup> , Abdoulaye K. Kone <sup>3</sup> , Bourema Kouriba <sup>3</sup> , Matthew B. Laurens <sup>1</sup> , Amadou Niangaly <sup>3</sup> , Karim Traore <sup>3</sup> , Youssouf Tolo <sup>3</sup> , Mahamadou A. Thera <sup>3</sup> , Abdoulaye A. Djimde <sup>3</sup> , Ogobara K. Doumbo <sup>3</sup> , Christopher V. Plowe <sup>1</sup> , Joana C. Silva <sup>2</sup> , Mark A. Travassos <sup>1</sup> <sup>1</sup> Division of Malaria Research, Institute for Global Health, University of Maryland School of Medicine, Baltimore, MD, United States, <sup>2</sup> Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD, United States, <sup>3</sup> Malaria Research and Training Center, University of Science, Techniques and Technologies, Bamako, Mali
1225	Anti-leishmanial Activities of Synthetic Endoperoxides, N-89 and N-251	Kofi D. Kwofie <sup>1</sup> , Sato Kai <sup>2</sup> , Akina Hino <sup>1</sup> , Sanjoba Chizu <sup>2</sup> , Shimogawara Rieko <sup>1</sup> , Irene Ayi <sup>3</sup> , Daniel Boakye <sup>3</sup> , Hye-Sook Kim <sup>4</sup> , Mitsuko Ohashi <sup>1</sup> , Yoshitsugu Matsumoto <sup>2</sup> , Nobuo Ohta <sup>1</sup> <sup>1</sup> Tokyo Medical and Dental University, Tokyo, Japan, <sup>2</sup> The University of Tokyo, Tokyo, Japan, <sup>3</sup> Noguchi Memorial Institute for Medical Research, Accra, Ghana, <sup>4</sup> Okayama University, Okayama, Japan
1297	A malaria genetic cross generated in a humanized mouse indicate multi-gene control of resistances to artemisinin and piperaquine	<ul> <li>Sage Z. Davis<sup>1</sup>, Lisa Checkley<sup>1</sup>, Richard S. Pinapati<sup>1</sup>, Ashley Vaughan<sup>2</sup>, Matthew Fishbaugher<sup>2</sup>, Nelly Camargo<sup>2</sup>, Marina McDew-White<sup>3</sup>, Shalini Nair<sup>3</sup>, François H. Nosten<sup>4</sup>, Stefan Kappe<sup>2</sup>, Ian Cheeseman<sup>3</sup>, Timothy JC Anderson<sup>3</sup>, Michael T. Ferdig<sup>1</sup></li> <li><sup>1</sup>Eck Institute for Global Health, Department of Biological Sciences, University of Notre Dame, South Bend, IN, United States, <sup>2</sup>Center for Infectious Disease Research, Seattle, WA, United States, <sup>3</sup>Texas Biomedical Research Institute, San Antonio, TX, United States, <sup>4</sup>Shoklo Malaria Research Unit, Mahidol- Oxford Tropical Medicine Research Unit, Mahidol, Mahidol, Thailand</li> </ul>
1300	Transcriptional response of <i>P.</i> <i>vivax</i> parasites to chloroquine in vivo	Adam Kim <sup>1</sup> , Jean Popovici <sup>2</sup> , Didier Menard <sup>2</sup> , David Serre <sup>1</sup> <sup>1</sup> University of Maryland, Baltimore, MD,

		United States, <sup>2</sup> Institut Pasteur in Cambodia,
		Phnom Penh, Cambodia
1320	Comparison of PCR-methods for Onchocerca volvulus detection in skin biopsies from the Tshopo Province, DRC	Jessica Prince-Guerra <sup>1</sup> , Vitaliano A. Cama <sup>2</sup> , Nana Wilson <sup>2</sup> , Josias Likwela <sup>3</sup> , Nestor Ndakala <sup>4</sup> , J. Muzinga Muzinga <sup>4</sup> , Nicholas Ayebazibwe <sup>5</sup> , Yassa Ndjakani <sup>6</sup> , Naomi Awaca <sup>3</sup> , D. Mumba <sup>7</sup> , Antoinete Tshefu <sup>8</sup> , Paul Cantey <sup>2</sup> <sup>1</sup> ASM/CDC Fellowship Program, Atlanta, GA, United States, <sup>2</sup> CDC, Atlanta, GA, United States, <sup>3</sup> Programme National de la Lutte contre l'Onchocercose, Kinshasa, Congo, Democratic Republic of the, <sup>4</sup> FELTP, Kinshasa, Congo, Democratic Republic of the, <sup>5</sup> AFENET, Kampala, Uganda, <sup>6</sup> CDC-DRC, Kinshasa, Congo, Democratic Republic of the, <sup>7</sup> Institut National de Recherche Biomedicale, Kinshasa, Congo, Democratic Republic of the, <sup>8</sup> Ecole de Sante Publique, Kinshasa, Congo, Democratic Republic of the
1343	Using single-cell transcriptomics to elucidate sexual commitment and differentiation in <i>Plasmodium falciparum</i>	Katelyn A. Walzer, Liane Y. Emerson, Danielle Kubicki, David L. Corcoran, Jen-Tsan Ashley Chi Duke University, Durham, NC, United States
1646	Optimizing approaches to generate whole-genome sequence from non-leukocyte depleted <i>Plasmodium falciparum</i> clinical samples	Zalak Shah <sup>1</sup> , Matthew Adams <sup>1</sup> , Kara Moser <sup>2</sup> , Miriam K. Laufer <sup>1</sup> , Joana C. Silva <sup>2</sup> , Shannon Takala Harrison <sup>1</sup> <sup>1</sup> Division of Malaria Research, Institute for Global Health, University of Maryland School of Medicine, Baltimore, MD, United States, <sup>2</sup> Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD, United States
1649	Whole genome sequence capture to generate high quality genomic data for <i>Plasmodium</i> <i>vivax</i> from clinical isolates	Sonia Agrawal <sup>1</sup> , Fang Huang <sup>1</sup> , Biraj Shrestha <sup>1</sup> , Matthew Adams <sup>1</sup> , Sandra Ott <sup>2</sup> , Lisa Sadzewicz <sup>2</sup> , Hui Liu <sup>3</sup> , David Serre <sup>1</sup> , Shannon Takala-Harrison <sup>1</sup> , Christopher V. Plowe <sup>4</sup> , Myaing M. Nyunt <sup>1</sup> , Joana C. Silva <sup>2</sup> <sup>1</sup> Division of Malaria Research, Institute for Global Health, University of Maryland School of Medicine, Baltimore, MD, United States, <sup>2</sup> Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD,

		United States, <sup>3</sup> Yunnan Institute of Parasitic Diseases, Pu'er, China, <sup>4</sup> Institute for Global Health, University of Maryland School of Medicine, Baltimore, MD, United States
1659	Gene co-expression network analysis of malaria parasite transcription refines potential gene interaction underlying artemisinin resistance	Katrina A. Button-Simons, Sage Z. Davis, Michael T. Ferdig Eck Institute for Global Health, Department of Biological Sciences, University of Notre Dame, Notre Dame, IN, United States
1663	Accurate assembly of regions of complex diversity in P. falciparum from shotgun genome sequencing and assessment of strain specific immunitytowards optimal formulation of polyvalent vaccines	Nicholas J. Hathaway <sup>1</sup> , James Kazura <sup>2</sup> , Ann M. Moormann <sup>1</sup> , John Vulule <sup>3</sup> , Jonathan J. Juliano <sup>1</sup> , Jeffrey A. Bailey <sup>1</sup> <sup>1</sup> University Of Massachusetts Medical School, Worcester, MA, United States, <sup>2</sup> Case Western Reserve University, Cleveland, OH, United States, <sup>3</sup> Kenya Medical Research Institute, Busia, Kenya
1880	Evidence of RNA editing in Babesia microti	<b>Olukemi O. Ifeonu</b> , Ankit Dwivedi, Joana C. Silva University of Maryland School of Medicine, Baltimore, MD, United States