

TABLE OF CONTENTS

SPOTLIGHT

Articles of Significant Interest Selected from This Issue by the Editors	707
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STRUCTURE AND ASSEMBLY

Comprehensive Mutational Analysis Reveals p6 ^{Gag} Phosphorylation To Be Dispensable for HIV-1 Morphogenesis and Replication	Benjamin Radestock, Ivonne Morales, Sheikh Abdul Rahman, Sonja Radau, Bärbel Glass, René Peiman Zahedi, Barbara Müller, Hans-Georg Kräusslich	724–734
Structure of the St. Louis Encephalitis Virus Postfusion Envelope Trimer	Vincent C. Luca, Christopher A. Nelson, Daved H. Fremont	818–828
Comparative Proteomics Reveal Fundamental Structural and Functional Differences between the Two Progeny Phenotypes of a Baculovirus	Dianhai Hou, Leike Zhang, Fei Deng, Wei Fang, Ranran Wang, Xijia Liu, Lin Guo, Simon Rayner, Xinwen Chen, Hualin Wang, Zhihong Hu	829–839
Visualizing a Complete <i>Siphoviridae</i> Member by Single-Particle Electron Microscopy: the Structure of Lactococcal Phage TP901-1	Cecilia Bebeacua, Livia Lai, Christina Skovgaard Vegge, Lone Brøndsted, Marin van Heel, David Veesler, Christian Cambillau	1061–1068
Biogenesis of the Vaccinia Virus Membrane: Genetic and Ultrastructural Analysis of the Contributions of the A14 and A17 Proteins	Bethany Unger, Jason Mercer, Kathleen A. Boyle, Paula Traktman	1083–1097
Oligomeric Properties of Adeno-Associated Virus Rep68 Reflect Its Multifunctionality	Francisco Zarate-Perez, Jorge Mansilla-Soto, Martino Bardelli, John W. Burgner II, Maria Villamil-Jarauta, Demet Kekilli, Monserrat Samso, R. Michael Linden, Carlos R. Escalante	1232–1241

GENOME REPLICATION AND REGULATION OF VIRAL GENE EXPRESSION

Minimum Requirements for Bluetongue Virus Primary Replication <i>In Vivo</i>	Eiko Matsuo, Polly Roy	882–889
Viral Genome Methylation Differentially Affects the Ability of BZLF1 versus BRLF1 To Activate Epstein-Barr Virus Lytic Gene Expression and Viral Replication	Coral K. Wille, Dhananjay M. Nawandar, Amanda R. Panfil, Michelle M. Ko, Stacy R. Hagemeyer, Shannon C. Kenney	935–950
Independent Activation of Hepatitis B Virus Biosynthesis by Retinoids, Peroxisome Proliferators, and Bile Acids	Vanessa C. Reese, Claudia E. Oropeza, Alan McLachlan	991–997
Requirement of the N-Terminal Activation Domain of Herpes Simplex Virus ICP4 for Viral Gene Expression	Lauren M. Wagner, Avraham Bayer, Neal A. DeLuca	1010–1018
Characterization of the Nonstructural Proteins of the Bocavirus Minute Virus of Canines	Loretta Sukhu, Olufemi Fasina, Lisa Burger, Ayushi Rai, Jianming Qiu, David J. Pintel	1098–1104
Expression of Prototype Foamy Virus Pol as a Gag-Pol Fusion Protein Does Not Change the Timing of Reverse Transcription	Dana L. Jackson, Eun-Gyung Lee, Maxine L. Linial	1252–1254
A Hepatitis C Virus NS5A Phosphorylation Site That Regulates RNA Replication	K. L. LeMay, J. Treadaway, I. Angulo, T. L. Tellinghuisen	1255–1260

Continued on following page

GENETIC DIVERSITY AND EVOLUTION

Mapping Viral Functional Domains for Genetic Diversity in Plants	Justin S. Pita, Marilyn J. Roossinck	790–797
Whole-Genome Sequencing of the Akata and Mutu Epstein-Barr Virus Strains	Zhen Lin, Xia Wang, Michael J. Strong, Monica Concha, Melody Baddoo, Guorong Xu, Carl Baribault, Claire Fewell, William Hulme, Dale Hedges, Christopher M. Taylor, Erik K. Flemington	1172–1182
Systematic Identification of H274Y Compensatory Mutations in Influenza A Virus Neuraminidase by High-Throughput Screening	Nicholas C. Wu, Arthur P. Young, Sugandha Dandekar, Hemani Wijersuriya, Laith Q. Al-Mawsawi, Ting-Ting Wu, Ren Sun	1193–1199
Fixation of Emerging Interviral Recombinants in <i>Cucumber Mosaic Virus</i> Populations	Justin S. Pita, Marilyn J. Roossinck	1264–1269
Identification of Contamination in the American Type Culture Collection Stock of Human Adenovirus Type 8 by Whole-Genome Sequencing	Shotaro Yamane, Amanda Wei Ling Lee, Nozomu Hanaoka, Gabriel Gonzalez, Hisatoshi Kaneko, Susumu Ishida, Nobuyoshi Kitaichi, Shigeaki Ohno, Kanako O. Koyanagi, Koki Aoki, Tsuguto Fujimoto, Nobuyo Yawata, Hidemi Watanabe	1285–1286

VIRUS-CELL INTERACTIONS

Macropinocytosis-Like HIV-1 Internalization in Macrophages Is CCR5 Dependent and Leads to Efficient but Delayed Degradation in Endosomal Compartments	Lise-Andrée Gobeil, Robert Lodge, Michel J. Tremblay	735–745
AMP-Activated Protein Kinase Is Required for the Macropinocytic Internalization of Ebola Virus	Andrew S. Kondratowicz, Catherine L. Hunt, Robert A. Davey, Sara Cherry, Wendy J. Maury	746–755
A Second CRM1-Dependent Nuclear Export Signal in the Influenza A Virus NS2 Protein Contributes to the Nuclear Export of Viral Ribonucleoproteins	Shengping Huang, Jingjing Chen, Quanjiao Chen, Huadong Wang, Yanfeng Yao, Jianjun Chen, Ze Chen	767–778
The Viral Interferon Regulatory Factors of Kaposi's Sarcoma-Associated Herpesvirus Differ in Their Inhibition of Interferon Activation Mediated by Toll-Like Receptor 3	Sarah R. Jacobs, Sean M. Gregory, John A. West, Amy C. Wollish, Christopher L. Bennett, David J. Blackburn, Mark T. Heise, Blossom Damania	798–806
Rotavirus Viroplasm Proteins Interact with the Cellular SUMOylation System: Implications for Viroplasm-Like Structure Formation	Michela Campagna, Laura Marcos-Villar, Francesca Arnoldi, Carlos F. de la Cruz-Herrera, Pedro Gallego, José González-Santamaría, Dolores González, Fernando Lopitz-Otsoa, Manuel S. Rodriguez, Oscar R. Burrone, Carmen Rivas	807–817
Effect of <i>Wolbachia</i> on Replication of West Nile Virus in a Mosquito Cell Line and Adult Mosquitoes	Mazhar Hussain, Guangjin Lu, Sheshy Torres, Judith H. Edmonds, Brian H. Kay, Alexander A. Khromykh, Sassan Asgari	851–858
The Herpes Simplex Virus 1 Us11 Protein Inhibits Autophagy through Its Interaction with the Protein Kinase PKR	Marion Lussignol, Christophe Queval, Marie-Françoise Bernet-Camard, Jacqueline Cotte-Laffitte, Isabelle Beau, Patrice Codogno, Audrey Esclatine	859–871
The West Nile Virus Capsid Protein Blocks Apoptosis through a Phosphatidylinositol 3-Kinase-Dependent Mechanism	Matt D. Urbanowski, Tom C. Hobman	872–881

Host mTORC1 Signaling Regulates Andes Virus Replication	Shannon McNulty, Mike Flint, Stuart T. Nichol, Christina F. Spiropoulou	912–922
Engagement of the ATR-Dependent DNA Damage Response at the Human Papillomavirus 18 Replication Centers during the Initial Amplification	Tormi Reinson, Mart Toots, Meelis Kadaja, Regina Pipitch, Mihkel Allik, Ene Ustav, Mart Ustav	951–964
The Adenoviral Oncogene E1A-13S Interacts with a Specific Isoform of the Tumor Suppressor PML To Enhance Viral Transcription	Julia Berscheminski, Peter Groitl, Thomas Dobner, Peter Wimmer, Sabrina Schreiner	965–977
The Replication Defect of ICP0-Null Mutant Herpes Simplex Virus 1 Can Be Largely Complemented by the Combined Activities of Human Cytomegalovirus Proteins IE1 and pp71	Roger D. Everett, Adam J. Bell, Yongxu Lu, Anne Orr	978–990
Influenza Virus Induces Apoptosis via BAD-Mediated Mitochondrial Dysregulation	Anh T. Tran, John P. Cortens, Qiujiang Du, John A. Wilkins, Kevin M. Coombs	1049–1060
Nucleolar Trafficking of the Mouse Mammary Tumor Virus Gag Protein Induced by Interaction with Ribosomal Protein L9	Andrea R. Beyer, Darrin V. Bann, Breanna Rice, Ingrid S. Pultz, Melissa Kane, Stephen P. Goff, Tatyana V. Golovkina, Leslie J. Parent	1069–1082
Gangliosides Have a Functional Role during Rotavirus Cell Entry	Miguel Angel Martínez, Susana López, Carlos F. Arias, Pavel Isa	1115–1122
Increasing Expression of MicroRNA 181 Inhibits Porcine Reproductive and Respiratory Syndrome Virus Replication and Has Implications for Controlling Virus Infection	Xue-kun Guo, Qiong Zhang, Li Gao, Ning Li, Xin-xin Chen, Wen-hai Feng	1159–1171
A Bovine Herpesvirus 1 Protein Expressed in Latently Infected Neurons (ORF2) Promotes Neurite Sprouting in the Presence of Activated Notch1 or Notch3	Devis Sinani, Leticia Frizzo da Silva, Clinton Jones	1183–1192
Cyclin T1 and CDK9 T-Loop Phosphorylation Are Downregulated during Establishment of HIV-1 Latency in Primary Resting Memory CD4⁺ T Cells	Sona Budhiraja, Marylinda Famiglietti, Alberto Bosque, Vicente Planelles, Andrew P. Rice	1211–1220
Critical Roles of Glucocorticoid-Induced Leucine Zipper in Infectious Bursal Disease Virus (IBDV)-Induced Suppression of Type I Interferon Expression and Enhancement of IBDV Growth in Host Cells via Interaction with VP4	Zhonghua Li, Yongqiang Wang, Xiang Li, Xiaoqi Li, Hong Cao, Shijun J. Zheng	1221–1231
SNX17 Facilitates Infection with Diverse Papillomavirus Types	Martina Bergant, Lawrence Banks	1270–1273
Inefficient Vaginal Transmission of Tenofovir-Resistant HIV-1	Morgan Chateau, Michael D. Swanson, J. Victor Garcia	1274–1277
Unstable Polymerase-Nucleoprotein Interaction Is Not Responsible for Avian Influenza Virus Polymerase Restriction in Human Cells	Anna V. Cauldwell, Olivier Moncorgé, Wendy S. Barclay	1278–1284
CELLULAR RESPONSE TO INFECTION		
Stress Granule Formation Induced by Measles Virus Is Protein Kinase PKR Dependent and Impaired by RNA Adenosine Deaminase ADAR1	Kristina M. Okonski, Charles E. Samuel	756–766
TRANSFORMATION AND ONCOGENESIS		
Human T Cell Leukemia Virus Type 2 Tax-Mediated NF-κB Activation Involves a Mechanism Independent of Tax Conjugation to Ubiquitin and SUMO	Chloé Journo, Amandine Bonnet, Arnaud Favre-Bonvin, Jocelyn Turpin, Jennifer Venera, Emilie Côté, Sébastien Alain Chevalier, Youmna Kfoury, Ali Bazarbachi, Claudine Pique, Renaud Mahieux	1123–1136
Human Papillomavirus E7 Induces Rereplication in Response to DNA Damage	Xueli Fan, Yingwang Liu, Susan A. Heilman, Jason J. Chen	1200–1210

GENE DELIVERY

Highly Attenuated Recombinant Vesicular Stomatitis Virus VSV-12' GFP Displays Immunogenic and Oncolytic Activity

Anthony N. van den Pol, John N. Davis 1019–1034

VACCINES AND ANTIVIRAL AGENTS

HIV-1 Resistance to Maraviroc Conferred by a CD4 Binding Site Mutation in the Envelope Glycoprotein gp120

Annette N. Ratcliff, Wuxian Shi, Eric J. Arts 923–934

Straightforward Selection of Broadly Neutralizing Single-Domain Antibodies Targeting the Conserved CD4 and Coreceptor Binding Sites of HIV-1 gp120

Julie Matz, Pascal Kessler, Jérôme Bouchet, Olivier Combes, Oscar Henrique Pereira Ramos, Francis Barin, Daniel Baty, Loïc Martin, Serge Benichou, Patrick Chames 1137–1149

Seasonal Trivalent Inactivated Influenza Vaccine Does Not Protect against Newly Emerging Variants of Influenza A (H3N2v) Virus in Ferrets

Katherine V. Houser, Jacqueline M. Katz, Terrence M. Tumpey 1261–1263

PATHOGENESIS AND IMMUNITY

Cumulative Impact of Host and Viral Factors on HIV-1 Viral-Load Control during Early Infection

Ling Yue, Heather A. Prentice, Paul Farmer, Wei Song, Dongning He, Shabir Lakhi, Paul Goepfert, Jill Gilmour, Susan Allen, Jianming Tang, Richard A. Kaslow, Eric Hunter 708–715

Cellular LITAF Interacts with Frog Virus 3 75L Protein and Alters Its Subcellular Localization

Heather E. Eaton, Andressa Ferreira Lacerda, Guillaume Desrochers, Julie Metcalf, Annie Angers, Craig R. Brunetti 716–723

Antiviral Therapy Can Reverse the Development of Immune Senescence in Elderly Mice with Latent Cytomegalovirus Infection

Mark Beswick, Annette Pachnio, Sarah N. Lauder, Clive Sweet, Paul A. Moss 779–789

Crystal Structure of the Cowpox Virus-Encoded NKG2D Ligand OMCP

Eric Lazear, Lance W. Peterson, Chris A. Nelson, Daved H. Fremont 840–850

Mucosal Tissue Tropism and Dissemination of HIV-1 Subtype B Acute Envelope-Expressing Chimeric Virus

Deborah F. L. King, Asna A. Siddiqui, Viviana Buffa, Lucia Fischetti, Yong Gao, Daniel Stieh, Paul F. McKay, Paul Rogers, Christina Ochsensbauer, John C. Kappes, Eric J. Arts, Robin J. Shattock 890–899

Humoral Immunity to Smallpox Vaccines and Monkeypox Virus Challenge: Proteomic Assessment and Clinical Correlations

M. B. Townsend, M. S. Keckler, N. Patel, D. H. Davies, P. Felgner, I. K. Damon, K. L. Karem 900–911

hsp70 and a Novel Axis of Type I Interferon-Dependent Antiviral Immunity in the Measles Virus-Infected Brain

Mi Young Kim, Yaoling Shu, Thomas Carsillo, Jianying Zhang, Lianbo Yu, Cornelia Peterson, Sonia Longhi, Sarah Girod, Stefan Niewiesk, Michael Oglesbee 998–1009

Repeated Exposure to Trace Amounts of Woodchuck Hepadnavirus Induces Molecularly Evident Infection and Virus-Specific T Cell Response in the Absence of Serological Infection Markers and Hepatitis

Shashi A. Gujar, Patricia M. Mulrooney-Cousins, Tomasz I. Michalak 1035–1048

Lethal Canine Distemper Virus Outbreak in Cynomolgus Monkeys in Japan in 2008	Kouji Sakai, Noriyo Nagata, Yasushi Ami, Fumio Seki, Yuriko Suzuki, Naoko Iwata-Yoshikawa, Tadaki Suzuki, Shuetsu Fukushi, Tetsuya Mizutani, Tomoki Yoshikawa, Noriyuki Otsuki, Ichiro Kurane, Katsuhiko Komase, Ryoji Yamaguchi, Hideki Hasegawa, Masayuki Saijo, Makoto Takeda, Shigeru Morikawa	1105–1114
Myxovirus Resistance Gene A (MxA) Expression Suppresses Influenza A Virus Replication in Alpha Interferon-Treated Primate Cells	Shannon R. Matzinger, Timothy D. Carroll, Joseph C. Dutra, Zhong-Min Ma, Christopher J. Miller	1150–1158
Critical Role of MDA5 in the Interferon Response Induced by Human Metapneumovirus Infection in Dendritic Cells and <i>In Vivo</i>	M. Del Rocío Baños-Lara, Arpita Ghosh, Antonieta Guerrero-Plata	1242–1251
ERRATA		
Incorporation of Host Complement Regulatory Proteins into Newcastle Disease Virus Enhances Complement Evasion	Moanaro Biswas, John B. Johnson, Sandeep R. P. Kumar, Griffith D. Parks, Subbiah Elankumaran	1287
Intrinsic Temperature Sensitivity of Influenza C Virus Hemagglutinin-Esterase-Fusion Protein	Emi Takashita, Yasushi Muraki, Kanetsu Sugawara, Hironobu Asao, Hidekazu Nishimura, Koji Suzuki, Takashi Tsuji, Seiji Hongo, Yoshiro Ohara, Yoshihiro Kawaoka, Makoto Ozawa, Yoko Matsuzaki	1288

Cover photograph (Copyright © 2013, American Society for Microbiology. All Rights Reserved.): Artistic rendering of a human leukocyte antigen (HLA) class I protein similarity matrix resembles a kaleidoscopic quilt. Pairwise genetic distances between HLA subtypes occurring at >0.05% phenotypic frequency in an HIV-1 subtype B-infected cohort were calculated using PHYLIP and visualized using a blue to red color gradient. HLA-A, B, and C alleles are organized in alphabetic and numeric order with the A locus in the corners and C at the center. The probability that two HLA subtypes belonging to the same allele group will select distinct immune escape mutations in HIV-1 increases proportionally with the genetic distance between them. Image by Jonathan M. Carlson, Zabrana L. Brumme, and Anna R. Adams. (See related article in December 2012, vol. 86, no. 24, p. 13202.)