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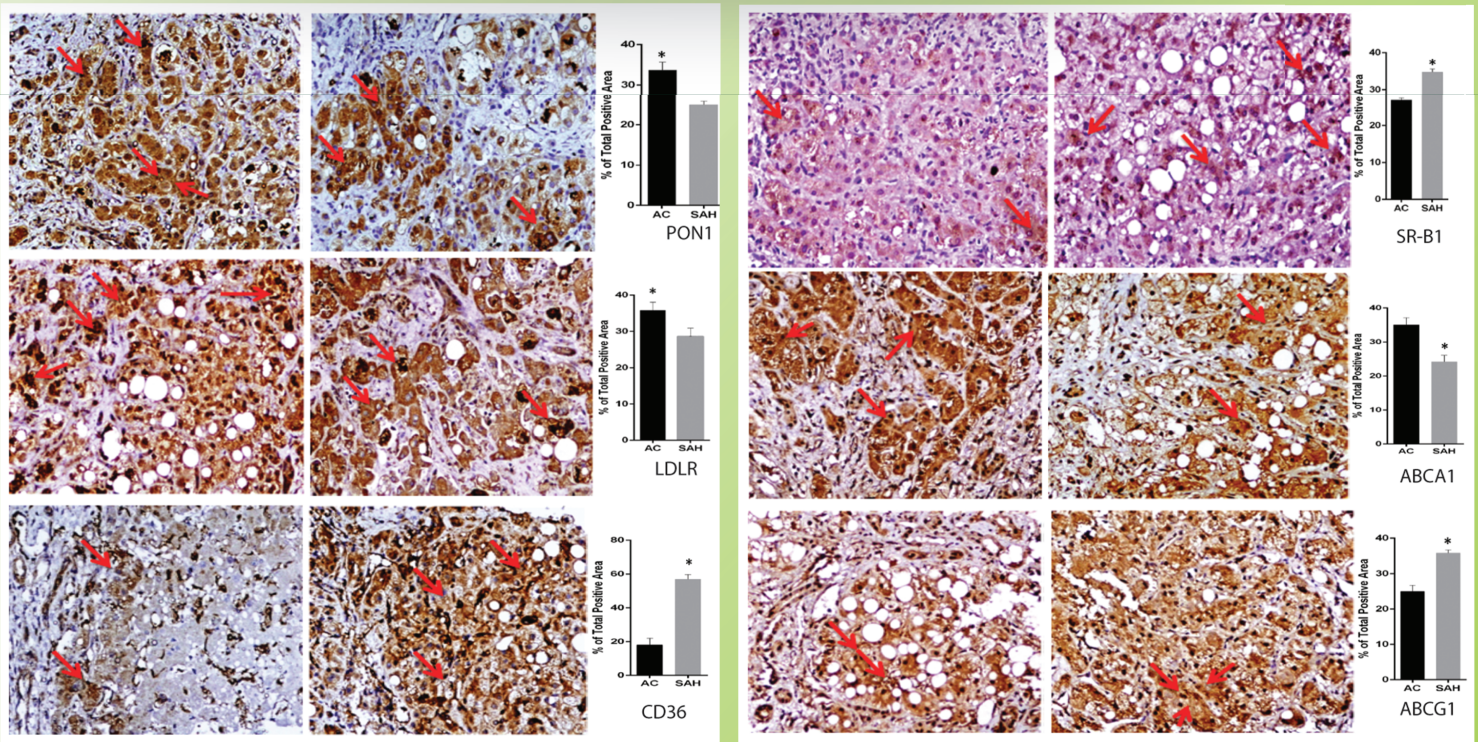

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IN THIS ISSUE OF

HEPATOLOGY COMMUNICATIONS

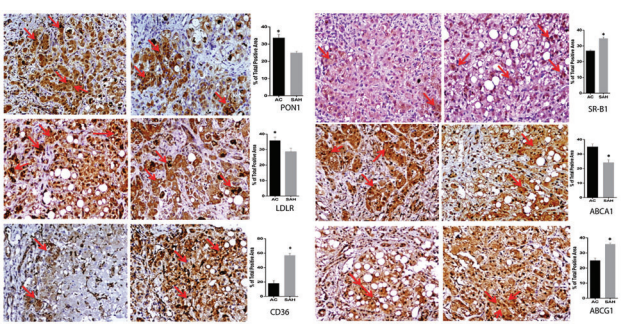
Volume 3 • Number 12 December 2019

Review

1563 Designing Clinical Trials in Pediatric Nonalcoholic Steatohepatitis: Tips for Patient Selection and Appropriate Endpoints
Naim Alkhouri, Rohit Kohli, and Ariel E. Feldstein

Original Articles

1571 A Pilot Genome-Wide Analysis Study Identifies Loci Associated With Response to Obeticholic Acid in Patients With NASH
Samer Gawrieh, Xiuqing Guo, Jingyi Tan, Marie Lauzon, Kent D. Taylor, Rohit Loomba, Oscar W. Cummings, Sreekumar Pillai, Pallav Bhatnagar, Kris V. Kowdley, Katherine Yates, Laura A. Wilson, Yii-Der Ida Chen, Jerome I. Rotter, and Naga Chalasani, NASH Clinical Research Network



Cover Figure: Quantitative proteomic analysis identifies significantly down-regulated lipid transporter proteins in SAH. IHC showing expression of PON1, LDL, CD36, SRA1, ABCA1, and ABCG1 in SAH (n = 5) and AC (n = 5). For all IHC analyses, relative quantization of positively stained cells are expressed as mean number of positive cells/10 high-power field (40×) and *P < 0.05.

1585 Fat Accumulation, Liver Fibrosis, and Metabolic Abnormalities in Chinese Patients With Moderate/Severe Versus Mild Hepatic Steatosis
Wei Zhang, Rui Huang, Yi Wang, Huiying Rao, Lai Wei, Grace L. Su, and Anna S. Lok

1598 Dysregulated Lipid Transport Proteins Correlate With Pathogenesis and Outcome in Severe Alcoholic Hepatitis
Jaswinder Singh Maras, Sukanta Das, Adil Bhat, Ashish Kumar Vyas, Gaurav Yadav, Sudrishti Chaudhary, Sukriti Sukriti, Abhishak C. Gupta, Chagan Bihari, Rakhi Mahiwall, and Shiv Kumar Sarin

1626 Nontranscriptional Activity of Interferon Regulatory Factor 3 Protects Mice From High-Fat Diet-Induced Liver Injury
Carlos Sanz-Garcia, Megan R. McMullen, Saurabh Chattopadhyay, Sanjoy Roychowdhury, Ganes Sen, and Laura E. Nagy

1642 Activation of WNT/Beta-Catenin Signaling and Regulation of the Farnesoid X Receptor/Beta-Catenin Complex After Murine Bile Duct Ligation
Rong Zhang, Toshimasa Nakao, Jing Luo, Yuhua Xue, Pamela Cornuet, Michael Oertel, Karis Kosar, Sucha Singh, and Kari Nejak-Bowen

1656 Liver-Targeted Angiotensin Converting Enzyme 2 Therapy Inhibits Chronic Biliary Fibrosis in Multiple Drug-Resistant Gene 2-Knockout Mice
Indu G. Rajapaksha, Lakmie S. Gunarathne, Khashayar Asadi, Sharon C. Cunningham, Alexandra Sharland, Ian E. Alexander, Peter W. Angus, and Chandana B. Herath

1674 Up-regulation of miR-let7a-5p Leads to Decreased Expression of ABCC2 in Obstructive Cholestasis
Natarajan Balasubramaniyan, Michael W. Devereaux, David J. Orlicky, Ronald J. Sokol, and Frederick J. Suchy

1687 MicroRNA-10a Impairs Liver Metabolism in Hepatitis C Virus-Related Cirrhosis Through Deregulation of the Circadian Clock Gene Brain and Muscle Aryl Hydrocarbon Receptor Nuclear Translocator-Like 1
Rika Horii, Masao Honda, Takayoshi Shirasaki, Tetsuro Shimakami, Ryogo Shimizu, Souma Yamanaka, Kazuhisa Murai, Kazunori Kawaguchi, Kuniaki Arai, Tatsuya Yamashita, Yoshio Sakai, Taro Yamashita, Hikari Okada, Mikiko Nakamura, Eishiro Mizukoshi, and Shuichi Kaneko

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1704 Insulin Resistance and Genetic Risk Predict Liver-Related Outcomes and Death in Nonalcoholic Fatty Liver Disease
Christopher J. Danford, Z. Gordon Jiang, Veikko Salomaa, Martti Färkkilä, Antti Jula, Satu Männistö, Annamari Lundqvist, Liisa Valsta, Markus Perola, and Fredrik Åberg