

Highlights of This Issue 499

MINIREVIEW

- 501** Dysregulated GPCR Signaling and Therapeutic Options in Uveal Melanoma
Vivian Chua, Dominic Lapadula, Clinita Randolph, Jeffrey L. Benovic, Philip B. Wedegaertner, and Andrew E. Aplin


CELL CYCLE AND SENESCENCE

- 507** Mutant IDH1 Disrupts the Mouse Subventricular Zone and Alters Brain Tumor Progression
Christopher J. Pirozzi, Austin B. Carpenter, Matthew S. Waitkus, Catherine Y. Wang, Huishan Zhu, Landon J. Hansen, Lee H. Chen, Paula K. Greer, Jie Feng, Yu Wang, Cheryl B. Bock, Ping Fan, Ivan Spasojevic, Roger E. McLendon, Darell D. Bigner, Yiping He, and Hai Yan

CELL DEATH AND SURVIVAL

- 521** Exploiting AR-Regulated Drug Transport to Induce Sensitivity to the Survivin Inhibitor YM155
Michael D. Nyquist, Alexandra Corella, John Burns, Ilsa Coleman, Shuai Gao, Robin Tharakan, Luke Riggan, Changmeng Cai, Eva Corey, Peter S. Nelson, and Elahe A. Mostaghel

CHROMATIN, EPIGENETICS, AND RNA REGULATION

- 532** Prognostic Relevance of Tumor Purity and Interaction with MGMT Methylation in Glioblastoma
 Eva Schulze Heuling, Felix Knab, Josefine Radke, Eskil Eskilsson, Emmanuel Martinez-Ledesma, Arend Koch, Marcus Czabanka, Christoph Dieterich, Roel G. Verhaak, Christoph Harms, and Philipp Euskirchen

GENOMICS

- 541** Distinctive Histogenesis and Immunological Microenvironment Based on Transcriptional Profiles of Follicular Dendritic Cell Sarcomas
Maria Antonella Laginestra, Claudio Tripodo, Claudio Agostinelli, Giovanna Motta, Sylvia Hartmann, Claudia Döring, Maura Rossi, Federica Melle, Maria Rosaria Sapienza, Valentina Tabanelli, Alessandro Pileri, Fabio Fuligni, Anna Gazzola, Claudia Mannu, Carlo Alberto Sagramoso, Silvia Lonardi, Luisa Lorenzi, Francesco Bacci, Elena Sabattini, Anita Borges, Ingrid Simonitsch-Klupp, Jose Cabecadas, Elias Campo, Juan Rosai, Martin-Leo Hansmann, Fabio Facchetti, and Stefano Aldo Pileri
- 553** Genome-Wide Analysis Identifies MEN1 and MAX Mutations and a Neuroendocrine-Like Molecular Heterogeneity in Quadruple WT GIST
Maria A. Pantaleo, Milena Urbini, Valentina Indio, Gloria Ravagnini, Margherita Nannini, Matilde De Luca, Giuseppe Tarantino, Sabrina Angelini, Alessandro Gronchi, Bruno Vincenzi, Giovanni Grignani, Chiara Colombo, Elena Fumagalli, Lidia Gatto, Maristella Saponara, Manuela Ianni, Paola Paterini, Donatella Santini, M. Giulia Pirini, Claudio Ceccarelli, Annalisa Altimari, Elisa Gruppioni, Salvatore L. Renne, Paola Collini, Silvia Stacchiotti, Giovanni Brandi, Paolo G. Casali, Antonio D. Pinna, Annalisa Astolfi, and Guido Biasco
- 563** Comprehensive Transcriptome and Mutational Profiling of Endemic Burkitt Lymphoma Reveals EBV Type-Specific Differences
Yasin Kaymaz, Cliff I. Oduor, Hongbo Yu, Juliana A. Otieno, John Michael Ong'echa, Ann M. Moormann, and Jeffrey A. Bailey

METABOLISM

- 577** Novel Assay to Detect RNA Polymerase I Activity *In Vivo*
Gunes Guner, Paul Sirajuddin, Qizhi Zheng, Baoyan Bai, Alexandra Brodie, Hester Liu, Taija af Hällström, Ibrahim Kulac, Marikki Laiho, and Angelo M. De Marzo

Table of Contents

ONCOGENES AND TUMOR SUPPRESSORS

- 585** Tumor-induced Stromal STAT1 Accelerates Breast Cancer via Dereulating Tissue Homeostasis
Victoria R. Zellmer, Patricia M. Schnepf, Sarah L. Fracci, Xuejuan Tan, Erin N. Howe, and Siyuan Zhang

SIGNAL TRANSDUCTION

- 598** Combined TRAF6 Targeting and Proteasome Blockade Has Anti-myeloma and Anti-Bone Resorptive Effects
Haiming Chen, Mingjie Li, Eric Sanchez, Cathy S. Wang, Tiffany Lee, Camilia M. Soof, Christian E. Casas, Jasmin Cao, Colin Xie, Kyle A. Udd, Kevin DeCorso, George Y. Tang, Tanya M. Spektor, and James R. Berenson

- 610** Constitutive Phosphorylation of STAT3 by the CK2–BLNK–CD5 Complex
Uri Rozovski, David M. Harris, Ping Li, Zhiming Liu, Preetesh Jain, Ivo Veletic, Alessandra Ferrajoli, Jan Burger, Susan O'Brien, Prithviraj Bose, Philip Thompson, Nitin Jain, William Wierda, Michael J. Keating, and Zeev Estrov

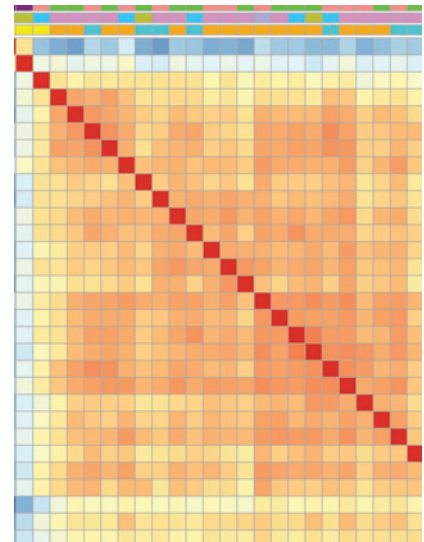
- 619** A Transcriptional Program for Detecting TGF β -Induced EMT in Cancer
Momeneh Foroutan, Joseph Cursons, Soroor Hediye-Zadeh, Erik W. Thompson, and Melissa J. Davis

 AC icon indicates Author Choice

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ABOUT THE COVER

In this issue, Kaymaz and colleagues (beginning on page 563) investigate transcriptome expression and mutational profiles of patient-derived endemic Burkitt lymphoma (BL) tumors using RNA sequencing. The cover image shows the unsupervised hierarchical clustering heatmap of BL tumors based on their expression profiles of the most variant genes. While 2 sporadic BLs separate out from 28 endemic BLs, eBL tumor expression profiles demonstrate greater correlation within eBLs compared with sBLs. Transcriptome-wide gene expression correlations between eBLs did not reveal significant groupings suggesting that eBL tumors are relatively homogenous with no major underlying molecular phenotypes. Based on further analysis, the study reveals subtler differences in terms of gene expression as well as the pattern of somatic mutations that correlates EBV presence and EBV type in the tumor B cells.



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