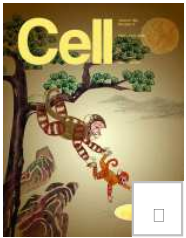


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On the cover: Molecular mechanisms of ovarian aging and female age-related fertility are topics of intense interest. In this issue, Wang et al. ... [Show more](#)

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Preview

The Magnifying GLASS: Longitudinal Analysis of Adult Diffuse Gliomas

Ashwin Narayanan, Sevin Turcan

Diffuse gliomas inevitably progress, but our understanding of the molecular events

associated with recurrence is limited. Recent work from the Glioma Longitudinal
 GLASS) consortium (Barthel et al., 2019) reports temporal DNA sequencing on s

cohort of primary and recurrent glioma pairs, establishing the evolutionary molecular characteristics of adult diffuse gliomas.

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Articles

[Modulation of RNA Condensation by the DEAD-Box Protein eIF4A](#)

Devin Tauber, Gabriel Tauber, Anthony Khong, Briana Van Treeck, Jerry Pelletier, Roy Parker

RNA-RNA interactions promote formation of RNP condensates, which can be counteracted by DEAD-box proteins to curb excessive granule formation.

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[DIX Domain Polymerization Drives Assembly of Plant Cell Polarity Complexes](#)

Maritza van Dop, Marc Fiedler, Sumanth Mutte, Jeroen de Keijzer, Lisa Olijslager, Catherine Albrecht, Che-Yang Liao, Marcel E. Janson, Mariann Bienz, Dolf Weijers

The identities of cell polarity determinants are not conserved between animals and plants; however, characterization of a DIX-domain containing protein in land plants reveals that the physical principles of polar complex assembly are preserved across eukaryotes.

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[Co-incidence of Damage and Microbial Patterns Controls Localized Immune Responses in Roots](#)

Feng Zhou, Aurélie Emonet, Valérie Dénervaud Tendon, Peter Marhavy, Dousheng Wu, Thomas Lahaye, Niko Geldner

Roots require both microbial molecular patterns and plant tissue damage in order to mount localized antibacterial immune responses, revealing an effective way to respond appropriately to pathogens while sparing commensals.

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[Host-Specific Evolutionary and Transmission Dynamics Shape the Functional Diversification of *Staphylococcus epidermidis* in Human Skin](#)

Wei Zhou, Michelle Spoto, Rachel Hardy, Changhui Guan, Elizabeth Fleming, Peter J. Larson, Joseph S. Brown, Julia Oh

Matched isolate sequencing and shotgun metagenomics reconstruct *Staphylococcus epidermidis* spatiotemporal strain diversity, demonstrating how strain admixture can affect virulence, evolution, and metabolism within the human skin microbiome.

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Restriction of HIV-1 Escape by a Highly Broad and Potent Neutralizing Antibody

Philipp Schommers, Henning Gruell, Morgan E. Abernathy, My-Kim Tran, Adam S. Dings, Harry B. Gristick, Christopher O. Barnes, Till Schoofs, Maike Schlotz, Kanika Vanshylla, Christoph Kreer, Daniela Weiland, Udo Holtick, Christof Scheid, Markus M. Valter, Marit J. van Gils, Rogier W. Sanders, Jörg J. Vehreschild, Oliver A. Cornely, Clara Lehmann, Gerd Fätkenheuer, Michael S. Seaman, Jesse D. Bloom, Pamela J. Bjorkman, Florian Klein

Broadly neutralizing antibodies targeting the HIV-1 envelope protein are a promising option for prevention and treatment of HIV-1 infection. However, development of viral resistance can limit clinical efficacy. Schommers et al. identify a highly broad and potent antibody that targets the CD4 binding site of HIV-1. Compared with other potent CD4 binding site antibodies, it restricts the development of viral escape and effectively suppresses HIV-1 *in vivo*.

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Cryo-EM Reveals Integrin-Mediated TGF- β Activation without Release from Latent TGF- β

Melody G. Campbell, Anthony Cormier, Saburo Ito, Robert I. Seed, Andrew J. Bondesson, Jianlong Lou, James D. Marks, Jody L. Baron, Yifan Cheng, Stephen L. Nishimura

Analysis of intermediate conformations of the interaction between $\alpha\beta 8$ integrin and latent TGF- β suggests an activation mechanism that does not require release and diffusion of mature TGF- β , which has implications for current approaches to targeting TGF- β signaling therapeutically.

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Astrocytic *trans*-Differentiation Completes a Multicellular Paracrine Feedback Loop Required for Medulloblastoma Tumor Growth

Maojin Yao, P. Britten Ventura, Ying Jiang, Fausto J. Rodriguez, Lixin Wang, Justin S.A. Perry, Yibo Yang, Kelsey Wahl, Rowena B. Crittenden, Mariko L. Bennett, Lin Qi, Cong-Cong Gong, Xiao-Nan Li, Ben A. Barres, Timothy P. Bender, Kodi S. Ravichandran, Kevin A. Janes, Charles G. Eberhart, Hui Zong

Tumors shape a microenvironmental network by acting as a source of tumor-associated astrocytes that provide paracrine stimulation to microglia to secrete IGF1, which is critical for tumor progression in SHH-activated mouse medulloblastoma models.

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All-Optical Electrophysiology Reveals the Role of Lateral Inhibition in Sensory Processing in Cortical Layer 1

Linlin Z. Fan, Simon Kheifets, Urs L. Böhm, Hao Wu, Kiryl D. Piatkevich, Michael E. Xie, Vicente Parot, Yooree Ha, Kathryn E. Evans, Edward S. Boyden, Anne E. Takesian, Adam E. Cohen

By simultaneously combining genetically targeted voltage imaging with optogenetic modulation of neuronal activity, Fan et al. demonstrate that all-optical electrophysiology in awake animals can be a powerful tool for revealing hidden principles of neural circuit function.

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Cerebellar Neurodynamics Predict Decision Timing and Outcome on the Single-Trial Level

Qian Lin, Jason Manley, Magdalena Helmreich, Friederike Schlumm, Jennifer M. Li, Drew N. Robson, Florian Engert, Alexander Schier, Tobias Nöbauer, Alipasha Vaziri

A specific motor decision and its timing can be predicted using information from the cerebellum >10 s before movement, during a cognitive task in larval zebrafish. Decision outcomes and timing can be predicted at the single-trial level, using neuroactivity information from whole-brain Ca²⁺ imaging, at single-cell resolution.

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Constant Sub-second Cycling between Representations of Possible Futures in the Hippocampus

Kenneth Kay, Jason E. Chung, Marielena Sosa, Jonathan S. Schor, Mattias P. Karlsson, Margaret C. Larkin, Daniel F. Liu, Loren M. Frank

Imagination, planning, and decision-making require the ability to generate representations of hypothetical experience. Kay et. al. find that neurons in the rat hippocampus can represent alternative hypothetical scenarios both regularly and quickly (every ~125 ms). Further, the underlying activity has a temporal structure that is equivalent across different representational correlates (location and direction), implying a common process.

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Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism

F. Kyle Satterstrom, Jack A. Kosmicki, Jiebiao Wang, Michael S. Breen, Silvia De Rubeis, Joon-Yong An, Minshi Peng, Ryan Collins, Jakob Grove, Lambertus Klei, Christine Stevens, Jennifer Reichert, Maureen S. Mulhern, Mykyta Artomov, Sherif Gerges, Brooke Sheppard, Xinyi Xu, Aparna Bhaduri, Utku Norman, Harrison Brand, Grace Schwartz, Rachel Nguyen, Elizabeth E. Guerrero, Caroline Dias, Autism Sequencing Consortium, iPSYCH-Broad Consortium, Catalina Betancur, Edwin H. Cook, Louise Gallagher, Michael Gill, James S. Sutcliffe, Audrey Thurm, Michael E. Zwick, Anders D. Børglum, Matthew W. State, A. Ercument Cicek, Michael E. Talkowski, David J. Cutler, Bernie Devlin, Stephan J. Sanders, Kathryn Roeder, Mark J.

Daly, Joseph D. Buxbaum

Large-scale sequencing of patients with autism allows identification of over 100 putative ASD-associated genes, the majority of which are neuronally expressed, and investigation of distinct genetic influences on ASD compared with other neurodevelopmental disorders.

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Resource

[Single-Cell Transcriptomic Atlas of Primate Ovarian Aging](#)

Si Wang, Yuxuan Zheng, Jingyi Li, Yang Yu, Weiqi Zhang, Moshi Song, Zunpeng Liu, Zheyang Min, Huifang Hu, Ying Jing, Xiaojuan He, Liang Sun, Lifang Ma, Concepcion Rodriguez Esteban, Piu Chan, Jie Qiao, Qi Zhou, Juan Carlos Izpisua Belmonte, Jing Qu, Fuchou Tang, Guang-Hui Liu

Single-cell transcriptomic analysis in ovaries of young and old cynomolgus monkeys identifies aging-associated and cell-type-specific dysregulation of antioxidative pathways.

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Correction

[Reconstructing Denisovan Anatomy Using DNA Methylation Maps](#)

David Gokhman, Nadav Mishol, Marc de Manuel, David de Juan, Jonathan Shuqrun, Eran Meshorer, Tomas Marques-Bonet, Yoel Rak, Liran Carmel

(Cell 179, 180–192.e1–e10; September 19, 2019)

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Snapshot

[SnapShot: Lysosomal Storage Diseases](#)

José A. Martina, Nina Raben, Rosa Puertollano

Lysosomal storage diseases (LSDs) represent a group of monogenic inherited metabolic disorders characterized by the progressive accumulation of undegraded substrates inside lysosomes, resulting in aberrant lysosomal activity and homeostasis. This

SnapShot summarizes the intracellular localization and function of proteins implicated in LSDs. Common aspects of LSD pathogenesis and the major current therapeutic approaches are noted. To view this SnapShot, open or download the PDF.

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