

Research

- The aberrant epigenome of *DNMT3B*-mutated ICFI patient iPSCs is amenable to correction, with the exception of a subset of regions with H3K4me3- and/or CTCF-based epigenetic memory 169
Varsha Poondi Krishnan, Barbara Morone, Shir Toubiana, Monika Krzak, Salvatore Fioriniello, Floriana Della Ragione, Maria Strazzullo, Claudia Angelini, Sara Selig, and Maria R. Matarazzo
- Genome-wide evaluation of the effect of short tandem repeat variation on local DNA methylation 184
Alejandro Martin-Trujillo, Paras Garg, Nihir Patel, Bharati Jadhav, and Andrew J. Sharp
- Regulation of endogenous retrovirus-derived regulatory elements by *GATA2/3* and *MSX2* in human trophoblast stem cells 197
Cui Du, Jing Jiang, Yuzhuo Li, Miao Yu, Jian Jin, Shuai Chen, Hairui Fan, Todd S. Macfarlan, Bin Cao, and Ming-an Sun

Methods

- Atlas-scale single-cell chromatin accessibility using nanowell-based combinatorial indexing 208^{OA}
Brendan L. O'Connell, Ruth V. Nichols, Dmitry Pokholok, Jerushah Thomas, Sonia N. Acharya, Andrew Nishida, Casey A. Thornton, Marissa Co, Andrew J. Fields, Frank J. Steemers, and Andrew C. Adey
- Matching queried single-cell open-chromatin profiles to large pools of single-cell transcriptomes and epigenomes for reference supported analysis 218
Shreya Mishra, Neetesh Pandey, Smriti Chawla, Madhu Sharma, Omkar Chandra, Indra Prakash Jha, Debarka SenGupta, Kedar Nath Natarajan, and Vibhor Kumar
- Complex hierarchical structures in single-cell genomics data unveiled by deep hyperbolic manifold learning 232
Tian Tian, Cheng Zhong, Xiang Lin, Zhi Wei, and Hakon Hakonarson
- Characterization of network hierarchy reflects cell state specificity in genome organization 247
Jingyao Wang, Yue Xue, Yueying He, Hui Quan, Jun Zhang, and Yi Qin Gao

Resources

- The Planemo toolkit for developing, deploying, and executing scientific data analyses in Galaxy and beyond 261^{OA}
Simon Bray, John Chilton, Matthias Bernt, Nicola Soranzo, Marius van den Beek, Bérénice Batut, Helena Rasche, Martin Čech, Peter J.A. Cock, Björn Grüning, and Anton Nekrutenko

(continued)

A temporal in vivo catalog of chromatin accessibility and expression profiles in pineoblastoma reveals a prevalent role for repressor elements **269**

Salam Idriss, Mohammad Hallal, Abdullah El-Kurdi, Hasan Zalzali, Inaam El-Rassi, Erik A. Ehli, Christel M. Davis, Philip E.D. Chung, Deena M.A. Gendoo, Eldad Zacksenhaus, Raya Saab, and Pierre Khoueiry

A chromosome-scale epigenetic map of the *Hydra* genome reveals conserved regulators of cell state **283**

Jack F. Cazet, Stefan Siebert, Hannah Morris Little, Philip Bertemes, Abby S. Primack, Peter Ladurner, Matthias Achraimer, Mark T. Fredriksen, R. Travis Moreland, Sumeeta Singh, Suiyuan Zhang, Tyra G. Wolfsberg, Christine E. Schnitzler, Andreas D. Baxevanis, Oleg Simakov, Bert Hobmayer, and Celina E. Juliano

Open Access paper



Cover Freshwater cnidarian polyp *Hydra vulgaris* with developing asexual bud. In this issue, a chromosome-level epigenetic map of *Hydra vulgaris* reveals insights into evolution of genomes and gene regulation. (Cover photo by Stefan Siebert. [For details, see Cazet et al., pp. 283–298.])