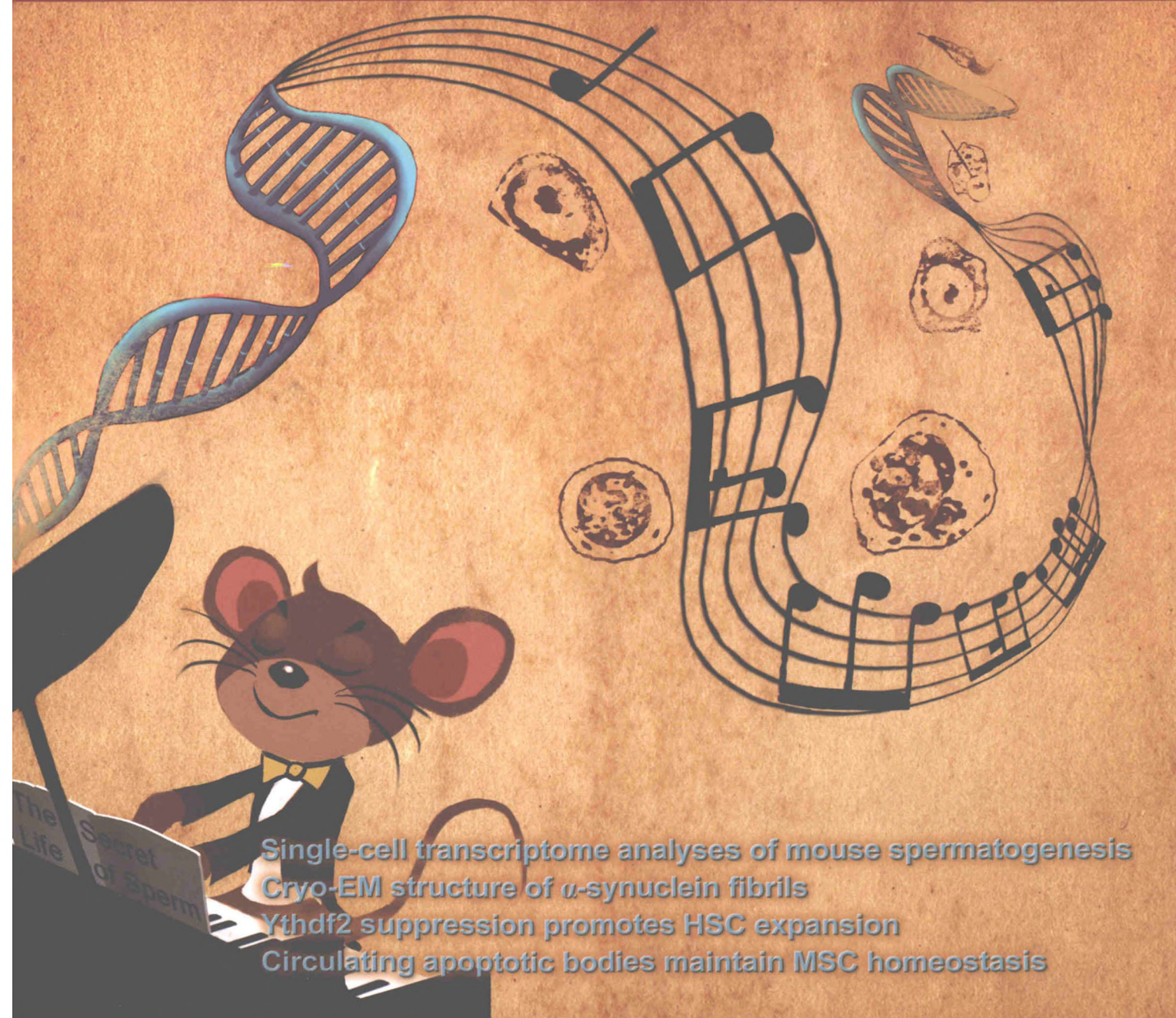




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Single-cell transcriptome analyses of mouse spermatogenesis
Cryo-EM structure of α -synuclein fibrils
Ythdf2 suppression promotes HSC expansion
Circulating apoptotic bodies maintain MSC homeostasis

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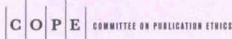
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SPRINGER NATURE

Coordinating Editor for this issue
Li Lu

RESEARCH HIGHLIGHTS

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877 p53 REEPs to sow ER-mitochondrial contacts

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918 Circulating apoptotic bodies maintain mesenchymal stem cell homeostasis and ameliorate osteopenia via transferring multiple cellular factors

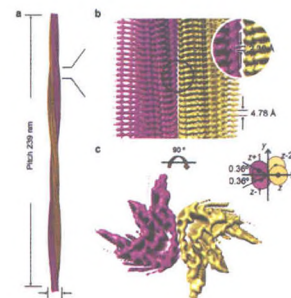
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934 Imbalance of the reciprocally inhibitory loop between the ubiquitin-specific protease USP43 and EGFR/PI3K/AKT drives breast carcinogenesis

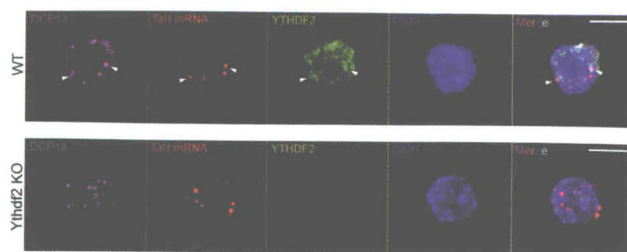
Lin He, Xinhua Liu, Jianguo Yang, Wanjin Li, Shumeng Liu, Xujun Liu, Ziran Yang, Jie Ren, Yue Wang, Lin Shan, Chengjian Guan, Fei Pei, Liandi Lei, Yu Zhang, Xia Yi, Xiaohan Yang, Jing Liang, Rong Liu, Luyang Sun, Yongfeng Shang



Cover: *The Secret Life of Sperm* comprises of 20 musical notes that flow and entwine to tell the charming and enigmatic story of spermatogenesis. Excerpted from *One Thousand and One Nights* by Rimsky-Korsakov, the 20 musical notes in the illustration represent the 20 stages of development in mouse spermatogenic cells. To unravel the mystery of spermatogenesis in mice, see page 879-896 by Yao Chen et al. for details.



A fibril reconstruction density map of the full-length α -Synuclein at the resolution of 3.07 Å by cryo-electron microscopy (cryo-EM). See page 897-903 by Yaowang Li et al. for details.



Fluorescence in situ hybridization of *Tal1* mRNA (red) and fluorescence immunostaining of DCP1a (P-body marker) (magenta), YTHDF2 (green) in wt and *Ythdf2* KO HSPCs. See page 904-917 by Zhenrui Li et al. for details.

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952 Mettl3–Mettl14 methyltransferase complex regulates the quiescence of adult hematopoietic stem cells

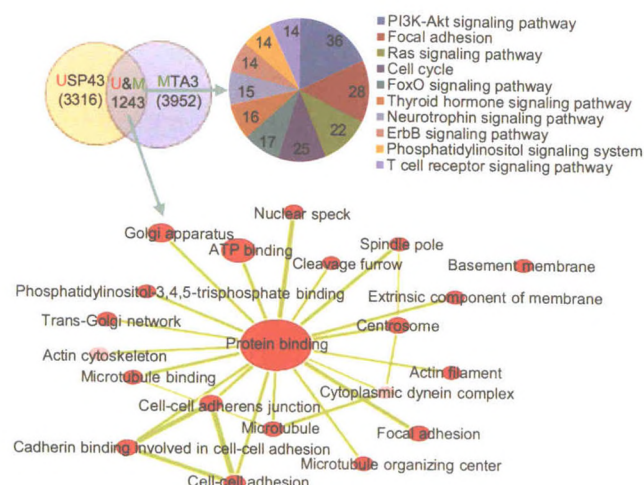
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955 m⁶A RNA modification controls autophagy through upregulating ULK1 protein abundance

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958 Cryo-EM structure of the human $\alpha 5\beta 3$ GABA_A receptor

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Venn diagrams of overlapping target genes of USP43 and MTA3 in MCF-7 cells (upper left). The 1243 overlapping target genes of USP43/MTA3 were clustered into KEGG pathways (upper right) or functional groups (lower). See page 934-951 by Lin He et al. for details.

ADVANCE ONLINE PUBLICATION

The RNA-binding protein ROD1/PTBP3 cotranscriptionally defines AID-loading sites to mediate antibody class switch in mammalian genomes **Open**

Juan Chen, Zhaokui Cai, Meizhu Bai, Xiaohua Yu, Chao Zhang, Changchang Cao, Xihao Hu, Lei Wang, Ruibao Su, Di Wang, Lei Wang, Yingpeng Yao, Rong Ye, Baidong Hou, Yang Yu, Shuyang Yu, Jinsong Li and Yuanchao Xue

doi:10.1038/s41422-018-0076-9

STAT3 associates with vacuolar H⁺-ATPase and regulates cytosolic and lysosomal pH **Open**

Bin Liu, Johan Palmfeldt, Lin Lin, Alexandria Colaço, Knut K. B. Clemmensen, Jinrong Huang, Fengping Xu, Xin Liu, Kenji Maeda, Yonglun Luo and Marja Jäättelä

doi:10.1038/s41422-018-0080-0

Structure of the intact 14-subunit human cytochrome c oxidase

Shuai Zong, Meng Wu, Jinke Gu, Tianya Liu, Runyu Guo and Maojun Yang

doi:10.1038/s41422-018-0071-1

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