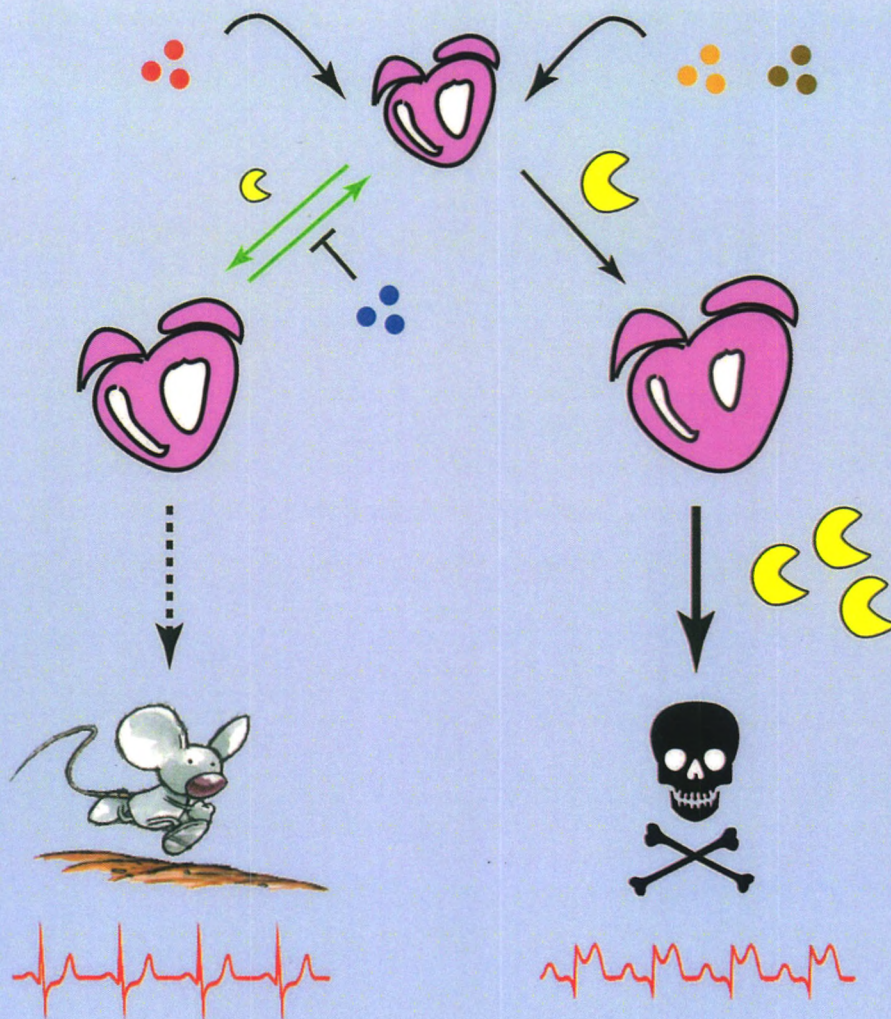


# Cell Research



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**Cardiotrophin 1 stimulates beneficial heart remodeling**  
**Roles of m<sup>6</sup>A writers in spermatogenesis**  
**5hmC signatures in cell-free DNA as cancer biomarkers**  
**A novel technology to identify protein-protein interactions**

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SPRINGER NATURE

Coordinating Editor for this issue  
Fangfang Hu

## RESEARCH HIGHLIGHTS

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### 1189 New path towards a better rice architecture

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## ORIGINAL ARTICLES

### 1195 Cardiostrophin 1 stimulates beneficial myogenic and vascular remodeling of the heart *Open*

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### 1216 Mettl3-/Mettl14-mediated mRNA N<sup>6</sup>-methyladenosine modulates murine spermatogenesis

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### 1231 5-Hydroxymethylcytosine signatures in cell-free DNA provide information about tumor types and stages *Open*

*Chun-Xiao Song, Senlin Yin, Li Ma, Amanda Wheeler, Yu Chen, Yan Zhang, Bin Liu, Junjie Xiong, Weihai Zhang, Jiankun Hu, Zongguang Zhou, Biao Dong, Zhiqi Tian, Stefanie S Jeffrey, Mei-Sze Chua, Samuel So, Weimin Li, Yuquan Wei, Jiajie Diao, Dan Xie, Stephen R Quake*

### 1243 5-Hydroxymethylcytosine signatures in circulating cell-free DNA as diagnostic biomarkers for human cancers *Open*

*Wenshuai Li, Xu Zhang, Xingyu Lu, Lei You, Yanqun Song, Zhongguang Luo, Jun Zhang, Ji Nie, Wanwei Zheng, Diannan Xu, Yaping Wang, Yuanqiang Dong, Shulin Yu, Jun Hong, Jianping Shi, Hankun Hao, Fen Luo,*

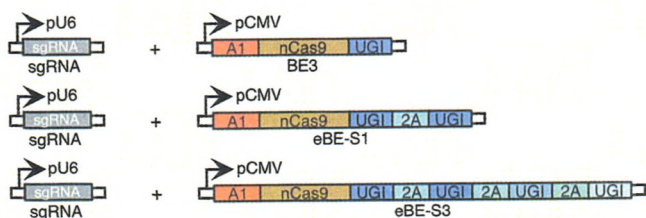


Cardiostrophin 1 stimulates beneficial heart remodeling. Models of left ventricle in hypertension. Some algorithms to include a 3D55 in various dimensions. A novel technology to identify protein-protein interactions.

**Cover:** Physiological cardiac remodeling induced by human cardiostrophin 1 (red circles) promotes reversible and beneficial remodeling (green arrows and thin dotted arrow; left side) by restraining caspase activity (smaller yellow circular sector) via casein kinase 2 (blue circles), whereas pathological cardiac remodeling induced by adrenergic agonists phenylephrine/isoproterenol (orange/brown circles) or by exposure to hypoxia/pulmonary arterial hypertension leads to unrestrained caspase activation (larger yellow circular sectors) and progression to cardiac dysfunction (thick black arrow; right side). See page 1195-1215 by Mohammad Abdul-Ghani *et al.* for details.



Gross morphology of representative testes from an adult control and age-matched *Mettl3*-vKO mutant. See page 1216-1230 by Zhen Lin *et al.* for details.



Schematic diagram illustrating the enhanced base editing system by co-expressing BE3 with free uracil DNA glycosylase inhibitor (UGI). See page 1289-1292 by Lijie Wang *et al.* for details.

Luchun Hua, Peng Wang, Xiaoping Qian, Fang Yuan, Lianhuan Wei, Ming Cui, Taiping Zhang, Quan Liao, Menghua Dai, Ziwen Liu, Ge Chen, Katherine Meckel, Sarbani Adhikari, Guifang Jia, Marc B Bissonnette, Xinxiang Zhang, Yupei Zhao, Wei Zhang, Chuan He, Jie Liu

**1258 Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq**

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**1275 Cryo-EM structures of the 80S ribosomes from human parasites *Trichomonas vaginalis* and *Toxoplasma gondii***

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**1289 Enhanced base editing by co-expression of free uracil DNA glycosylase inhibitor *Open***

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**1293 Altered neurogenesis and disrupted expression of synaptic proteins in prefrontal cortex of SHANK3-deficient non-human primate**

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**ADVANCE ONLINE PUBLICATION (published weekly on Tuesday and Friday)**

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**Intermittent fasting promotes adipose thermogenesis and metabolic homeostasis via VEGF-mediated alternative activation of macrophage *Open***

Kyoung-Han Kim, Yun Hye Kim, Joe Eun Son, Ju Hee Lee, Sarah Kim, Min Seon Choe, Joon Ho Moon, Jian Zhong, Kiya Fu, Florine Lenglin, Jeong-Ah Yoo, Philip J Bilan, Amira Klip, Andras Nagy, Jae-Ryong Kim, Jin Gyoony Park, Samer MI Hussein, Kyung-Oh Doh,

Chi-chung Hui and Hoon-Ki Sung

doi:10.1038/cr.2017.126

**Suppression of MAPK11 or HIPK3 reduces mutant Huntingtin levels in Huntington's disease models *Open***

Meng Yu, Yuhua Fu, Yijiang Liang, Haikun Song, Yao Yao, Peng Wu, Yuwei Yao, Yuyin Pan, Xue Wen, Lixiang Ma, Saiyin Hexige, Yu Ding, Shouqing Luo and Boxun Lu

doi:10.1038/cr.2017.113

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**A high-quality genome assembly of quinoa provides insights into the molecular basis of salt bladder-based salinity tolerance and the exceptional nutritional value *Open***

Changsong Zou, Aojun Chen, Lihong Xiao, Heike M Muller, Peter Ache, Georg Haberer, Meiling Zhang, Wei Jia, Ping Deng, Ru Huang, Daniel Lang, Feng Li, Dongliang Zhan, Xiangyun Wu, Hui Zhang, Jennifer Bohm, Renyi Liu, Sergey Shabala, Rainer Hedrich,

Jian-Kang Zhu and Heng Zhang

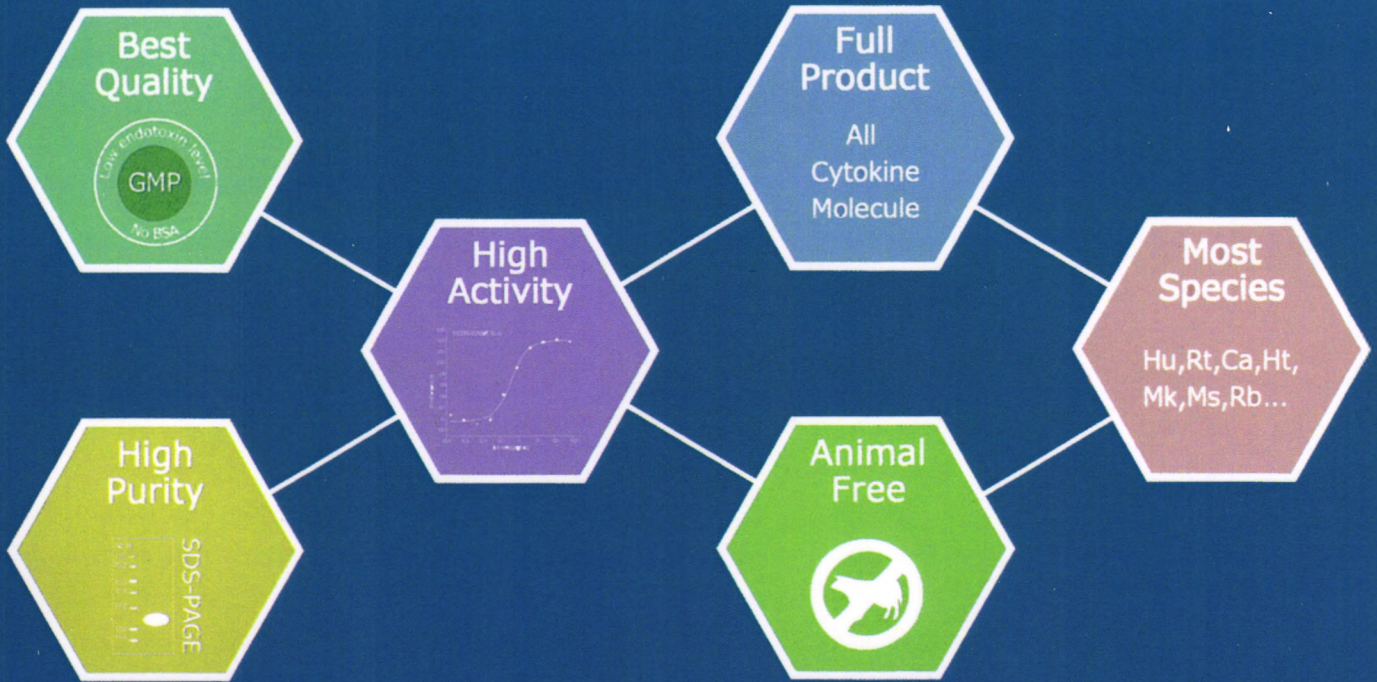
doi:10.1038/cr.2017.124



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