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REVIEWS

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GENETICS



STRENGTH IN NUMBERS

Eusocial insects as model systems for behavioural epigenetics

From shy to seen for cytosine

Technological advances in profiling modified nucleotides



Incorporating sequencing technologies into genetic screens p662

CONTENTS

October 2014
volume 15 no. 10

REVIEWS

647 Advances in the profiling of DNA modifications: cytosine methylation and beyond

Nongluk Plongthongkum, Dinh H. Diep and Kun Zhang

Recent developments and refinements to DNA methylation assays have led to the availability of several methods to detect and quantify cytosine modifications. This Review discusses the principles behind the newly developed techniques, compares the strengths and weaknesses of the different methods, and provides guidelines for selecting the most appropriate methods for particular experimental contexts.

662 Using next-generation sequencing to isolate mutant genes from forward genetic screens

Korbinian Schneeberger

Forward genetic screens have a long history of uncovering the genetic mutations underlying phenotypes of interest. This Review describes how next-generation sequencing technology can be integrated into forward genetic screens not only to enhance their efficiency but also to allow them to be carried out using expanded repertoires of species, populations and experimental strategies.

677 Eusocial insects as emerging models for behavioural epigenetics

Hua Yan, Daniel F. Simola, Roberto Bonasio, Jürgen Liebig, Shelley L. Berger and Danny Reinberg

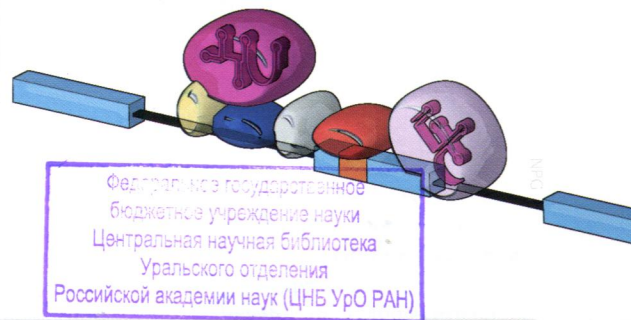
This Review provides insights into the use of eusocial insect species as models to study the role of epigenetic processes in regulating behaviour.

689 Context-dependent control of alternative splicing by RNA-binding proteins

FEATURED ARTICLE

Xiang-Dong Fu and Manuel Ares Jr

RNA-binding proteins (RBPs) influence alternative splicing in a highly context-sensitive and combinatorial manner, and it is therefore difficult to predict their actions on the basis of genomic sequence. However, recent progress in understanding alternative splicing, particularly using global approaches, has revealed new sets of rules for deciphering these patterns. This Review outlines the function of RBPs at different levels and describes the emerging rules of alternative splicing.



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The contribution of genetic variants to disease depends on the ruler
John S. Witte, Peter M. Visscher and Naomi R. Wray

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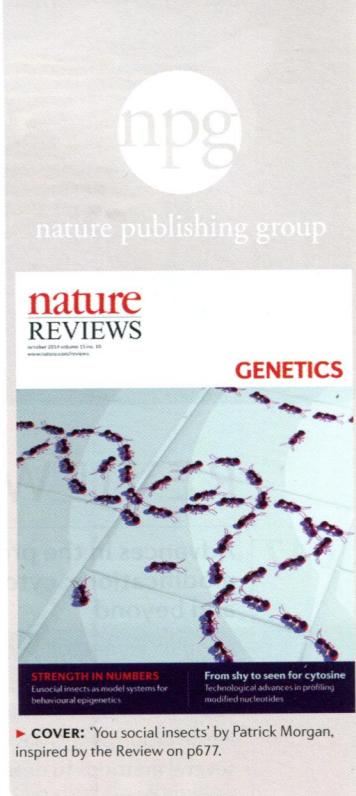
RESEARCH HIGHLIGHTS

- 641 Selections from the recent scientific literature
- 702 Identification and consequences of miRNA–target interactions — beyond repression of gene expression (Corrigendum)
Jean Hausser and Mihaela Zavolan



SERIES ON APPLICATIONS OF NEXT-GENERATION SEQUENCING

This series highlights the breadth of next-generation sequencing applications and the importance of the insights that are being gained through these methods.
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► **COVER:** 'You social insects' by Patrick Morgan, inspired by the Review on p677.



Research Highlight on transient Darwinian selection p642

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