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EDITORIAL

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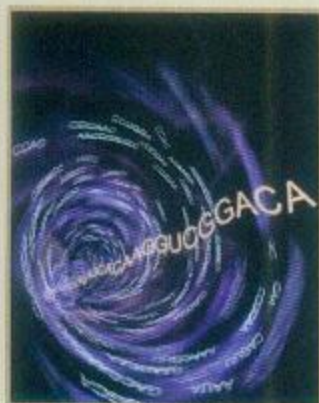
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Emerging order from RNA-Seq data.

Regev and colleagues describe algorithms for assembling hundreds of millions of short reads into full-length alternatively spliced transcripts without the aid of a reference genome (p 644). Credit: ©Kenneth Eward.



Protease inhibitors for hepatitis C treatment, p 553



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Nature Biotechnology (ISSN 1087-0156) is published monthly by Nature Publishing Group, a trading name of Nature America Inc., located at 75 Varick Street, F19, New York, NY 10013-1917. Periodicals postage paid at New York, NY and additional mailing post offices. **Editorial Office:** 75 Varick Street, F19, New York, NY 10013-1917. Tel: (212) 726-9335. Fax: (212) 696-9753. **Annual subscription rates:** USA/Canada: US\$250 (personal), US\$4,048 (institution), US\$4,658 (corporate institution). Canada add 5% GST #104911596R7001. Euro-zone: €202 (personal), €3,214 (institution), €4,011 (corporate institution). Rest of world (excluding China, Japan, Korea): €130 (personal), €2,077 (institution), €2,588 (corporate institution). Japan: Contact NPG Nature Asia-Pacific, Chiyoda Building, 2-37 Ichigayefemachi, Shinjuku-ku, Tokyo 162-0843. Tel: 81 (03) 3267-8751, Fax: 81 (03) 3267-8746. **POSTMASTER:** Send address changes to Nature Biotechnology, Subscriptions Department, 75 Varick Street, 9th Floor, New York, NY 10013-1917. **Authorization to photocopy** material for internal or personal use, or internal or personal use of specific clients, is granted by Nature Publishing Group to libraries and others registered with the Copyright Clearance Center (CCC) Transactional Reporting Service, provided the relevant copyright fee is paid direct to CCC, 222 Rosewood Drive, Danvers, MA 01923, USA. Identification code for Nature Biotechnology: 1087-0156/04. **Back issues:** US\$45, Canada add 7% for GST. CPC PUB AGREEMENT #40032744. Printed by Publishers Press, Inc., Lebanon Junction, KY, USA. Copyright © 2011 Nature America, Inc. All rights reserved. Printed in USA.

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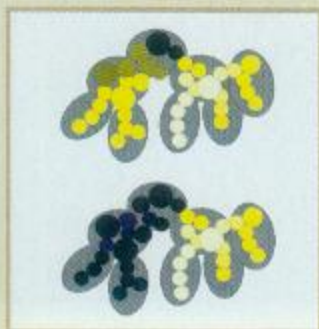
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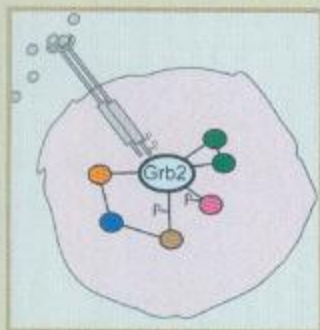
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