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November 2018

Agenda

1. Spolupráca s Google Scholar (len vo WOS CC)
2. Nastavenie OPEN URL
3. Prístup k Open Access publikáciám
4. Kopernio

Odkazy na plný text v plnom zázname



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A mammalian microRNA expression atlas based on small RNA library sequencing

Associated Data

By: Landgraf, P (Landgraf, Pablo); Rusu, M (Rusu, Mirabela); Sheridan, R (Sheridan, Robert); Sewer, A (Sewer, Alain); Iovino, N (Iovino, Nicola); Aravin, A (Aravin, Alexei); Pfeffer, S (Pfeffer, Sebastien); Rice, A (Rice, Amanda); Kamphorst, AO (Kamphorst, Alice O.); Landthaler, M (Landthaler, Markus)...More

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CELL

Volume: 129 Issue: 7 Pages: 1401-1414

DOI: 10.1016/j.cell.2007.04.040

Published: JUN 29 2007

Document Type: Article

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Abstract

MicroRNAs (miRNAs) are small noncoding regulatory RNAs that reduce stability and/or translation of fully or partially sequence-complementary target mRNAs. In order to identify miRNAs and to assess their expression patterns, we sequenced over 250 small RNA libraries from 26 different organ systems and cell types of human and rodents that were enriched in neuronal as well as normal and malignant hematopoietic cells and tissues. We present expression profiles derived from clone count data and provide computational tools for their analysis. Unexpectedly, a relatively small set of miRNAs, many of which are ubiquitously expressed, account for most of the differences in miRNA profiles between cell lineages and tissues. This broad survey also provides detailed and accurate information about mature sequences, precursors, genome locations, maturation processes, inferred transcriptional units, and conservation patterns. We also propose a subclassification scheme for miRNAs for assisting future experimental and computational functional analyses.

Keywords: MURKIN; MURKIN-INTERACTING PROTEIN; POST-TRANSCRIPTIONAL REGULATION; C-ELEGANS; CAENORHABDITIS-ELEGANS; ANIMAL DEVELOPMENT; GENE-EXPRESSION; IDENTIFICATION; TARGETS; MIRNAS; ZEBRAFISH

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4. Ďalšie varianty Open Access
5. Kopernio

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By: Hanahan, D; Weinberg, RA
CELL Volume: 100 Issue: 1 Pages: 57-70 Published: JAN 7 2000
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3. **Global Cancer Statistics**
By: Jemal, Ahmedin; Bray, Freddie; Center, Melissa M.; et al.
CA-A CANCER JOURNAL FOR CLINICIANS Volume: 61 Issue: 2 Pages: 69-90 Published: MAR-APR 2011
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4. **Global cancer statistics, 2002**
By: Parkin, DM; Bray, F; Ferlay, J; et al.
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A mammalian microRNA expression atlas based on small RNA library sequencing

Associated Data

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DOI: 10.1016/j.cell.2007.04.040

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- 2017 (10,634)
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- 2015 (6,602)
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By: Xu, Xiaofei; Yang, Jiguo; Ning, Zhengxiang; et al.

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By: Burgos-Edwards, Alberto; Jimenez-Aspee, Felipe; Theoduloz, Cristina; et al.

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- 4. **Responses of stream microbes to multiple anthropogenic stressors in a mesocosm study**

By: Nuy, Julia K.; Lange, Anja; Beermann, Arne J.; et al.

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Associated Data Citation Network

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P. Landgraf et al., *Cell*(2007) % Share Download

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Volume: 129 Issue: 7 Pages: 1401-1414
DOI: 10.1016/j.cell.2007.04.040
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Abstract
MicroRNAs (miRNAs) are small noncoding regulatory RNAs that reduce stability and/or translation of fully or partially translated mRNAs. In order to identify miRNAs and to assess their expression patterns, we sequenced over 250 small RNA libraries from 16 different cell types of human and rodents that were enriched in neuronal as well as normal and malignant hematopoietic lineages and tissue-specific profiles derived from clone count data and provide computational tools for their analysis. Unexpectedly, a set of miRNAs that are ubiquitously expressed, account for most of the differences in miRNA profiles between cell lineages and tissue types. This information provides accurate information about mature sequences, precursors, genome locations, maturation processes, inferred target sites, and potential functions, which will be useful for identifying future experimental and computational approaches to study miRNAs.

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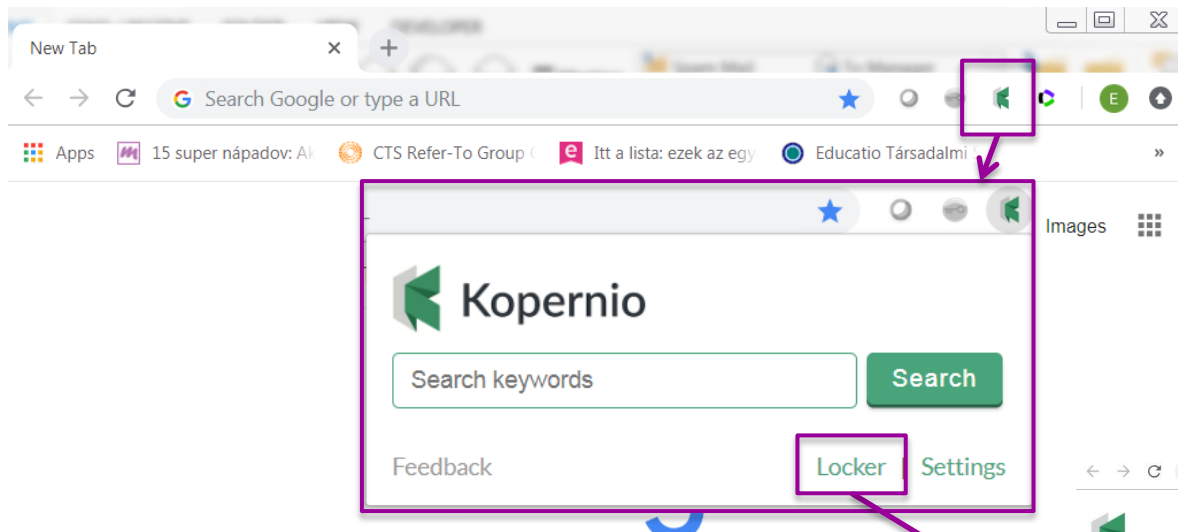
A Mammalian microRNA Expression Atlas Based on Small RNA Library Sequencing

Pablo Landgraf,¹ Mirabela Rusu,² Robert Sheridan,³ Alan Sewer,^{2,19,29} Nicola Iovino,^{1,27} Alexei Aravin,^{1,26} Sébastien Pfeffer,^{1,25} Amanda Rice,¹ Alice O. Kamphorst,¹ Markus Landthaler,¹ Carolina Lin,¹ Nicholas D. Socci,³ Leandro Hermida,² Valerio Fulci,⁴ Sabina Chiaretti,⁴ Robin Foà,⁴ Julia Schliwka,⁵ Uta Fuchs,⁶ Astrid Novosel,^{6,28} Roman-Ulrich Müller,^{1,7} Bernhard Schermer,⁷ Ute Bissels,⁸ Jason Inman,⁹ Quang Phan,¹⁰ Minchen Chien,¹¹ David B. Weir,¹¹ Ruchi Choksi,¹¹ Gabriella De Vita,¹² Daniela Frezzetti,¹² Hans-Ingo Trompeter,¹³ Veit Hornung,²³ Grace Teng,¹⁴ Gunther Hartmann,¹⁴ Miklos Palkovits,¹⁵ Roberto Di Lauro,^{15,12,20} Peter Wernet,¹³ Giuseppe Macino,¹ Charles E. Rogler,¹⁶ James W. Nagle,¹⁷ Jingyue Ju,^{1,21} F. Nina Papavasiliou,¹⁴ Thomas Benzing,¹ Peter Lichter,² Wayne Tam,¹⁷ Michael J. Brownstein,¹⁰ Andreas Bosio,⁸ Arndt Borkhardt,^{6,28} James J. Russo,¹¹ Chris Sander,³ Mihaela Zavolan,^{2,19,*} and Thomas Tuschl^{1,*}

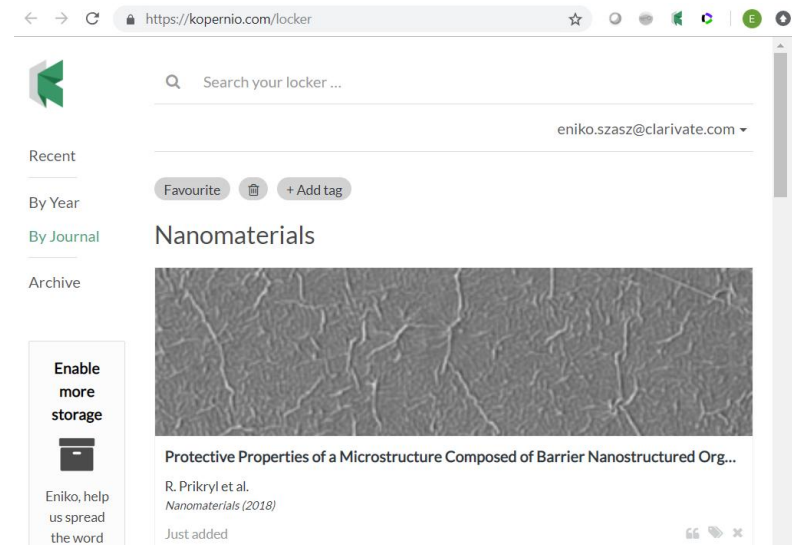
¹Howard Hughes Medical Institute, Laboratory of RNA Molecular Biology, Box 186, The Rockefeller University, New York, NY 10021, USA
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¹⁷Department of Pathology and Laboratory Medicine, the Joan and Sanford I. Weill Medical College of Cornell University, New York, NY 10021, USA
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