# Access and citation statistics, current as of June 2011

- ***A novel sensitive microarray approach for differential screening using probes labeled with two different radio-elements*** by Salin H, Vujasinovic T, Mazurie A, Maitrejean S, Menini C, Mallet J and Dumas S. Published in *Nucleic Acids Research*, Feb 2002; 30(4):e17
  - Number of accesses (downloads from the journal's website): data not available
  - Number of citations in scholarly journals publications: **22** (sources: ISI Web of Knowledge[1] and CrossRef[2]); complete list in appendix A (p. 3).

- ***Gene networks inference using dynamic bayesian networks*** by Perrin BE, Ralaivola L, Mazurie A, Bottani S, Mallet J and d'Alché-Buc F. Published in *Bioinformatics*, Oct 2003; 19(2):II138-II148
  - Number of accesses (downloads from the journal's website): data not available
  - Number of citations in scholarly journals' publications: **128** (source: Google Scholar[3]); complete list in appendix B (p. 5).

- ***An evolutionary and functional assessment of regulatory network motifs*** by Mazurie A, Bottani S and Vergassola M. Published in *Genome Biology*, Mar 2005; 6(4):R35
  - Number of accesses (downloads from the journal's website): **6961** (source: BioMed Central[4])
  - Number of citations in scholarly journals' publications: **49** (sources: Google Scholar[5], ISI Web of Knowledge[6], PubMed[7]); complete list in appendix C (p. 16).
  - Tagged as '**must read**' by the Faculty of 1000[8]

- ***Integrating genome-scale data for gene essentiality prediction*** by Roberts SB, Mazurie A and Buck GA. Published in *Chemistry and Biodiversity*, 2007; 4(11):2618-2630
  - Number of accesses (downloads from the journal's website): data not available
  - Number of citations in scholarly journals' publications: **2** (source: Google Scholar[9]); complete list in appendix D (p. 20).

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[1] http://goo.gl/JgOM5

[2] http://goo.gl/mFxdU

[3] http://goo.gl/jG7Js

[4] http://goo.gl/gDtkB

[5] http://goo.gl/FfT8v

[6] http://goo.gl/RgU4d

[7] http://goo.gl/swssY

[8] See document #5 provided as initial evidence under section 2.A.3

[9] http://goo.gl/GpzMs

- ***Phylogenetic distances are encoded in networks of interacting pathways*** by Mazurie A, Bonchev D, Schwikowski B and Buck GA. Published in *Bioinformatics*, Nov 2008; 24(22):2579-2585
    - Number of accesses (downloads from the journal's website): **1698** (source: Bioinformatics[10])
    - Number of citations in scholarly journals' publications: **16** (sources: ISI Web of Knowledge[11] and Google Scholar[12]); complete list in appendix E (p. 21).

- ***Path-a-Way: a strategy for network analysis of microarray data*** by Arasappan D, Mazurie A, Alves J, Bonchev D and Buck GA. Presented at *International Conference on BioMedical Engineering and Informatics* and published in proceedings, p. 432-436 (2008)
    - Number of accesses (downloads from the journal's website): data not available
    - Number of citations in scholarly journals' publications: 0.

- ***Evolution of metabolic network organization*** by Mazurie A, Bonchev D, Schwikowski B and Buck GA. Published in *BMC Systems Biology*, May 2010; 4(1):59
    - Number of accesses (downloads from the journal's website): **2670** (source: BioMed Central[13])
    - Number of citations in scholarly journals' publications: **3** (sources: ISI Web of Knowledge[14] and Google Scholar[15]); complete list in appendix F (p. 23)
    - Tagged as '**Highly accessed**' (source: BMC Systems Biology[16])

- ***Physiology of Pseudomonas aeruginosa in biofilms as revealed by transcriptome analysis*** by Folsom JP, Richards L, Pitts B, Roe F, Ehrlich GD, Parker A, Mazurie A and Stewart PS. Published in *BMC Microbiology*, Nov 2010; 10:294
    - Number of accesses (downloads from the journal's website): **3008** (source: BioMed Central[17])
    - Number of citations in scholarly journals' publications: 0.
    - Tagged as '**Highly accessed**' (source: BMC Microbiology[18])

**Note**: the two latest publications in BMC Systems Biology and BMC Microbiology are too recent (2010) to have been significantly cited in any other publication, due to the average length for a publication to be peer-reviewed and published (about a year). However, their tagging as 'Highly accessed' by the journal's website demonstrate the interest shown by scientists in the field for the content of this work.

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[10] http://goo.gl/ctwaB
[11] http://goo.gl/EL94q
[12] http://goo.gl/OON1w
[13] http://goo.gl/676Y0
[14] http://goo.gl/qW5VM
[15] http://goo.gl/G36tw
[16] http://goo.gl/DxFsq
[17] http://goo.gl/O4Lmh
[18] http://goo.gl/clzxr

**Appendix A.** Publications in scholarly journals citing the manuscript '*A novel sensitive microarray approach for differential screening using probes labeled with two different radio-elements*'

1. Huang, T.D. et al. Gene expression analysis with an integrated CMOS microarray by time-resolved fluorescence detection. BIOSENSORS & BIOELECTRONICS 26, 2660–2665 (2011).

2. Siau, A. et al. Temperature Shift and Host Cell Contact Up-Regulate Sporozoite Expression of Plasmodium falciparum Genes Involved in Hepatocyte Infection. PLOS PATHOGENS 4, e1000121 (2008).

3. Marquette, C.A., Corgier, B.P., Heyries, K.A. & Blum, L.J. Biochips: non-conventional strategies for biosensing elements immobilization. FRONTIERS IN BIOSCIENCE 13, 382–400 (2008).

4. Siau, A. et al. Whole-Transcriptome Analysis of Plasmodium falciparumField Isolates: Identification of New Pathogenicity Factors. J INFECT DIS 196, 1603–1612 (2007).

5. Rachman, H. & Kaufmann, S.H.E. Exploring functional genomics for the development of novel intervention strategies against tuberculosis. INTERNATIONAL JOURNAL OF MEDICAL MICROBIOLOGY 297, 559–567 (2007).

6. Marquette, C.A., Cretich, M., Blum, L.J. & Chiari, M. Protein microarrays enhanced performance using nanobeads arraying and polymer coating. TALANTA 71, 1312–1318 (2007).

7. Marquette, C.A., Lawrence, M.F. & Blum, L.J. DNA Covalent Immobilization onto Screen-Printed Electrode Networks for Direct Label-Free Hybridization Detection of p53 Sequences. ANALYTICAL CHEMISTRY 78, 959–964 (2006).

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9. Honore, P. et al. MicroArray Facility: a laboratory information management system with extended support for Nylon based technologies. BMC Genomics 7, (2006).

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11. Marquette, C. et al. Latex bead immobilisation in PDMS matrix for the detection of p53 gene point mutation and anti-HIV-1 capsid protein antibodies. ANALYTICAL AND BIOANALYTICAL CHEMISTRY 381, 1019–1024 (2005).

12. Marquette, C.A. & Blum, L.J. Conducting elastomer surface texturing: a path to electrode spotting. Application to the biochip production. BIOSENSORS \& BIOELECTRONICS 20, 197–203 (2004).

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22. Wierling, C. et al. Simulation of DNA array hybridization experiments and evaluation of critical parameters during subsequent image and data analysis. BMC Bioinformatics 3, (2002).

## **Appendix B.** Publications in scholarly journals citing the manuscript ‘*Gene networks inference using dynamic bayesian networks*’

1. Kentzoglanakis, K. & Poole, M. A Swarm Intelligence Framework for Reconstructing Gene Networks: Searching for Biologically Plausible Architectures. IEEE/ACM Trans. Comput. Biol. and Bioinf. PP, 1–1 (2011).

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3. Emmert-Streib, F. Large-Scale Statistical Inference of Gene Regulatory Networks: Local Network-Based Measures. Intelligent Systems Reference Library 11, 179–193 (2011).

4. Chun, H. et al. Reverse Engineering of Gene Regulation Networks with an Application to the DREAM4 in silico Network Challenge. Springer Handbooks of Computational Statistics 461–477 (2011).doi:10.1007/978-3-642-16345-6_22

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11. Zhou, T. & Wang, Y.L. Causal relationship inference for a large-scale cellular network. Bioinformatics 26, 2020–2028 (2010).

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**Appendix E**. Publications in scholarly journals citing the manuscript '*Phylogenetic distances are encoded in networks of interacting pathways*'

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**Appendix F**. Publications in scholarly journals citing the manuscript ‘*Evolution of metabolic network organization*’

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