

## PUBLICATIONS - SERVICE DE BIOINFORMATIQUE DES GÉNOMES ET DES RÉSEAUX (BIGRE)

Last update: Oct 26, 2009

### 2009

1. Lima-Mendez, G. and van Helden, J. (2009). The powerful law of the power law and other myths in network biology. *Molecular BioSystems*, 2009, 2009, DOI:10.1039/b908681a.
2. Faust, K., Croes, D. and van Helden, J. (2009). In response to "Can sugars be produced from fatty acids? A test case for pathway analysis tools". *Bioinformatics* 2009 Sept 23. Pubmed 19776213.
3. Sand, O., Thomas-Chollier, M. and van Helden, J. (2009). Retrieve-ensembl-seq: user-friendly and large-scale retrieval of single or multi-genome sequences from Ensembl. *Bioinformatics*, 2009. DOI:10.1093/bioinformatics/btp519. Pubmed 19720677.
4. Defrance, M. and Helden, J. V. (2009). Info-gibbs: a motif discovery algorithm that directly optimizes information content during sampling. *Bioinformatics*. Pubmed 19689955
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6. Lonz, C., Lensink, M. F., Vandenbranden, M. and Ruyschaert, J.-M. 2009. Cationic Lipids Activate Cellular Cascades. Which Receptors are Involved? *Biochim. Biophys. Acta* 1790, 425-430. Pubmed 19269309
7. Lensink, M. F., Lonz, C., Ruyschaert, J.-M. and Vandenbranden, M. 2009. Characterization of the Cationic DiC(14)-Amidine Bilayer by Mixed DMPC/DiC(14)-Amidine Molecular Dynamics Simulations shows an Interdigitated Nonlamellar Bilayer Phase. *Langmuir* 25, 5230-5238. Pubmed 19231818
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11. Lensink, M. F. 2008, Membrane-associated Proteins and Peptides. In *Molecular Modeling of Proteins. Methods in Molecular Biology*. ISBN 978-1-58829-864-5. Pubmed 18446287
12. Lensink, M. F. and Méndez, R. (2008). Recognition-induced Conformational Changes in Protein-Protein Docking. *Curr. Pharm. Biotechnol.* 9, 77-86. Review. Pubmed 18393864
13. Smeesters, P. R., Mardulyn, P., Vergison, A., Leplae, R. and Van Melderen, L. (2008). Genetic diversity of Group A Streptococcus M protein: implications for typing and vaccine development. *Vaccine* 26, 5835-42. Pubmed 18789365
14. Kontos, K., Godard, P., Andre, B., van Helden, J. and Bontempi, G. (2008). Machine learning techniques to identify putative genes involved in nitrogen catabolite repression in the yeast *Saccharomyces cerevisiae*. *BMC Proc* 2 Suppl 4, S5. Pubmed 19091052
15. Sand, O., Turatsinze, J. V. and van Helden, J. (2008). Evaluating the prediction of cis-acting regulatory elements in genome sequences. In Frishman, D. and Valencia, A. (eds.), *Modern genome annotation: the BioSapiens network*. Springer. ISBN: 978-3-211-75122-0
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21. Turatsinze, J.V., Thomas-Chollier, M., Defrance, M. and van Helden, J. (2008) Using RSAT to scan genome sequences for transcription factor binding sites and cis-regulatory modules. *Nat Protoc*, 3, 1578-1588. Pubmed 18802439
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28. Dessailly, B. H., Lensink, M. F., Orenco, C. A. and Wodak, S. J. LigASite--a database of biologically relevant binding sites in proteins with known apo-structures *Nucleic Acids Res* 36, D667-73 (2008). Pubmed 17933762.

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