

Morgane THOMAS-CHOLLIER (36)

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Short CV

Associate Professor in Bioinformatics at the *Ecole Normale Supérieure* (ENS) in Paris (FRANCE), Morgane Thomas-Chollier has obtained her Ph.D in 2008 as a joint work between the Université Libre de Bruxelles and the Vrije Universiteit Brussels in Belgium, under the joint direction of Luc LEYNS and Jacques van HELDEN. MTC then worked as a postdoc in Brussels for a year, followed by three years in Germany (MPIMG Martin VINGRON, Berlin, 2009-2012) thanks to an Alexander von Humboldt fellowship. MTC has joined the lab of Denis Thieffry in 2012, to reinforce the bioinformatics section of the Computational Systems Biology group at the Institute of Biology of the ENS (IBENS).

Research topics

MTC research interests mainly involve regulation of transcription, high-throughput functional genomics and evolution/development of metazoans. She is specialized in the detection of binding regions for transcription factors (motif detection, de-novo motif discovery, ChIP-seq, ChIP-exo) and is actively developing new computational methods and software, in particular within the RSAT suite (<http://rsat.eu>) in collaboration with Jacques van Helden. She has several collaborations with experimental groups, focusing on the glucocorticoid receptor, osteoporosis and evolution/development in sea urchin.

Publications

Articles in peer-reviewed international journals

1. Medina-Rivera A*, Defrance M*, Sand O*, Herrmann C, Castro-Mondragon J, Delerce J, Jaeger S, Blanchet C, Vincens P, Caron C, Staines DM, Contreras-Moreira B, Artufel M, Charbonnier – Khamvongsa L, Hernandez C, Thieffry D, Thomas-Chollier M#, van Helden J# "RSAT 2015 : Regulatory Sequence Analysis Tools", *Nucleic Acid Research* 43(W1):W50-W56 2015
2. Starick S*, Ibn-Salem J*, Jurk M*, Hernandez C, Love MI, Chung H, Vingron M, Thomas-Chollier M#, Meijnsing SH# "ChIP-exo signal associated with DNA-binding motifs provide insights into the genomic binding of the glucocorticoid receptor and cooperating transcription factors", *Genome Research*, 25(6):825-35 2015
3. Hudry B, Thomas-Chollier M, Volovik Y , Duffraisse M, Dard A, Dale F, Technau U, Merabet S. "Molecular insights into the origin of the Hox-TALE patterning System", *eLife* 3:e01939 2014
4. Thomas-Chollier M*, Watson L*, Cooper S, Pufall MA, Liu JS, Borzym K, Vingron M, Yamamoto K.R, Meijnsing SH. "A naturally occurring single amino acid insertion rewires transcriptional regulation by Glucocorticoid receptor isoforms", *Proc. Natl. Acad. Sci. U. S. A.* 110(44):17826-31 2013
5. Thomas-Chollier M, Darbo E, Herrmann C, Defrance M, Thieffry D, van Helden J. "From peaks to motifs: a complete workflow for the analysis of full-size ChIP-seq (and similar) datasets", *Nature Protocols* 7:1551-1568 2012
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7. Thomas-Chollier M, Hufton A, Heinig M, O'Keeffe S, El Masri N, Roider HG, Manke T, Vingron M. "Transcription factor binding predictions using TRAP for the analysis of ChIP-seq data and regulatory SNPs", *Nature Protocols* 6(12):1860-9 2011
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9. Medina-Rivera A, Abreu-Goodger C, Thomas-Chollier M, Salgado H, Collado-Vides J, van Helden J. "Theoretical and empirical quality assessment of transcription factor-binding motifs", *Nucleic Acids Res.* 39(3):808-24 2011
10. Thomas-Chollier M, Ledent V, Leyns L, Vervoort M "A non-tree-based comprehensive study of metazoan Hox and ParaHox genes prompts new insights into their origin and evolution ", *BMC Evol Biol* 10:73 2010 (*highly accessed*)
11. Sand O, Thomas-Chollier M, van Helden J. "Retrieve-ensembl-seq: user-friendly and large-scale retrieval of single or multi-genome sequences from Ensembl.", *Bioinformatics*, 15;25(20):2739-40 2009
12. Thomas-Chollier M*, Sand O*, Turatsinze J-V, Janky R, Defrance M, Vervisch E, van Helden J "RSAT: Regulatory Sequence Analysis Tools", *Nucleic Acids Research* 36:W119-W127 2008
13. Sand O, Thomas-Chollier M, Vervisch E , van Helden J. "Analyzing multiple datasets by inter-connecting RSAT programs via SOAP Web Services – an example with ChIP-chip data", *Nature Protocols*, 3:10 2008
14. Turatsinze J-V*, Thomas-Chollier M*, Defrance M, van Helden J. "Using RSAT to scan genome sequences for transcription factor binding sites and cis-regulatory modules", *Nature Protocols*, 3:10 2008
15. Thomas-Chollier M, Ledent V "Comparative phylogenomic analyses of teleost fish Hox gene clusters: lessons from the cichlid fish *Astatotilapia burtoni*: comment", *BMC Genomics*, 9:35 2008
16. Thomas-Chollier M, Leyns L, Ledent V "HoxPred: automated classification of Hox proteins using combinations of generalised profiles", *BMC Bioinformatics*, 8:247 2007
17. Simionato E, Ledent V, Richards G, Thomas-Chollier M, Kerner P, Coornaert D, Degnan BM, Vervoort M. "Origin and diversification of the basic helix-loop-helix gene family in metazoans: insights from comparative genomics.", *BMC Evol Biol*, 7:33 2007 (*highly accessed*)

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