

Thomas Rolland

Human Genetics and Cognitive Functions unit
Institut Pasteur, CNRS UMR3571
25, rue du Docteur Roux 75015 Paris.
Email: thomas.rolland@pasteur.fr

Research

2015 – Now: Research Assistant (CR-CN CNRS), Human Genetics and Cognitive Functions unit, Institut Pasteur, CNRS UMR3571, Paris, France.

Advisor: Thomas Bourgeron

Integrative approaches to study disease heterogeneity in autism spectrum disorders.

2011 – 2014: Postdoctoral research fellow, Center for Cancer Systems Biology (CCSB), Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA.

Advisor: Marc Vidal

Genotype-phenotype relationships in the human protein interaction network.

2007 – 2010: Graduate student, Yeast Molecular Genetics unit, Institut Pasteur, Paris, France.

Advisor: Bernard Dujon

Synteny and evolution of genes in hemiascomycetous yeasts.

2007: Master thesis student, Systems Biology lab, Institut Pasteur, Paris, France.

Advisor: Benno Schwikowski

Evaluation of biochemical network modularization techniques.

2005: Intern, Physics and Chemistry Unit, Institut Curie, Paris, France.

Advisor: Hervé Isambert

Visualization tool for genetic interactions in the yeast *Saccharomyces cerevisiae*.

2005: Bsc thesis student, INSERM U511, Analytical Genomics unit, Paris, France.

Advisor: Alessandra Carbone

Protein sequence database and interfacing with a multiple sequence alignment tool.

2003: DUT intern, Oncology-Radiology unit, Hopital Tenon, Paris, France.

Advisor: Jean-Noël Foulquier

Radioactive source management software for use in curietherapy treatments.

Education

2007 – 2010: Ph.D. in Genome Analysis.

Université Paris VI – UPMC, Paris, France.

2004 – 2007: Master degree in Bioinformatics.

Université Paris VII – D. Diderot, Paris, France.

2005 – 2007: Engineer diploma in Bioinformatics and Modeling.

INSA de Lyon, Lyon, France.

2003 – 2004: Bsc degree in Bioinformatics.

Université Paris VII – Denis Diderot, Paris, France.

2001 – 2003: DUT in Computer Science.

Université Paris V – René Descartes, Paris, France.

Publications

*Symbols * and # indicate co-first and co-second authors*

Tabet AC*, **Rolland T***, Ducloy M, Lévy J, Buratti J, Mathieu A, Haye D, Perrin L, Dupont C, Passemard S, Capri Y, Verloes A, Drunat S, Keren B, Mignot C, Marey I, Jacqueline A, Whalen S, Pipiras E, Benzacken B, Chantot-Bastaraud S, Afenjar A, Héron D, Le Caignec C, Beneteau C, Pichon O, Isidor B, David A, El Khattabi L, Kemeny S, Gouas L, Vago P, Mosca-Boidron AL, Faivre L, Missirian C, Philip N, Sanlaville D, Edery P, Satre V, Coutton C, Devillard F, Dieterich K, Vuillaume ML, Rooryck C, Lacombe D, Pinson L, Gatinois V, Puechberty J, Chiesa J, Lespinasse J, Dubourg C, Quelin C, Fradin M, Journal H, Toutain A, Martin D, Benmansour A, Leblond C, Toro R, Amsellem F, Delorme R, Bourgeron T (2017) A framework to identify contributing genes in patients with Phelan-McDermid syndrome. *npj Genomic Medicine* 2:32.

Benabou M, **Rolland T**, Leblond CS, Millot GA, Huguet G, Delorme R, Leboyer M, Pagan C, Callebert J, Maronde E, Bourgeron T (2017) Heritability of the melatonin synthesis variability in autism spectrum disorders. *Sci. Rep.* 7(1):17746.

Mercati O*, Huguet G*, Danckaert A, André-Leroux G, Maruani A, Bellinzoni M, **Rolland T**, Gouder L, Mathieu A, Buratti J, Amsellem F, Benabou M, Van-Gils J, Beggiano A, Konyukh M, Bourgeois J-P, Gazzellone MJ, Yuen RKC, Walker S, Delépine M, Boland A, Régnault B, Francois M, Van Den Abbeele T, Mosca-Boidron AL, Faivre L, Shimoda Y, Watanabe K, Bonneau D, Rastam M, Leboyer M, Scherer SW, Gillberg C, Delorme R, Cloëz-Tayarani I, Bourgeron T (2016) *CNTN6* mutations are risk factors for abnormal auditory sensory perception in autism spectrum disorders. *Mol. Psy.* 22(4):625-633.

Zhong Q*, Pevzner SJ*, Hao T, Wang Y, Mosca R, Menche J, Taipale M, Tasan M, Fan C, Yang X, Haley P, Murray RR, Mer F, Gebreab F, Tam S, MacWilliams A, Dricot A, Reichert P, Santhanam B, Ghamsari L, Calderwood MA, **Rolland T**, Charlotheaux B, Lindquist S, Barabasi AL, Hill DE, Aloy P, Cusick ME, Xia Y, Roth FP, Vidal M (2016) An inter-species protein-protein interaction network across vast evolutionary distance. *Mol. Syst. Biol.* 12 (4):865.

Descorps-Declère S*, Saguez C*, Cournac A, Marbouty M, **Rolland T**, Ma L, Bouchier C, Moszer I, Dujon B, Koszul R, Richard GF (2015) Genome-wide replication landscape of *Candida glabrata*. *BMC Biol.* 13:69.

Yang F, Petsalakis E, **Rolland T**, Hill DE, Vidal M, Roth FP (2015) Protein domain-level landscape of cancer-type-specific somatic mutations. *PLoS Comput. Biol.* 11(3):e1004147.

Rolland T*, Taşan M*, Charlotheaux B*, Pevzner SJ*, Zhong Q*, Sahni N*, Yi S*, Lemmens I, Fontanillo C, Mosca R, Kamburov A, Ghiassian S, Yang X, Ghamsari L, Balcha D, Begg BE, Braun P, Brehme M, Broly MP, Carvunis AR, Convery-Zupan D, Corominas R, Coulombe-Huntington J, Dann E, Dreze M, Dricot A, Fan C, Franzosa E, Gebreab F, Gutierrez BJ, Hardy MF, Jin M, Kang S, Kiros R, Lin GN, Luck K, MacWilliams A, Menche J, Murray RR, Poulin MM, Rambout X, Rasla J, Reichert P, Romero V, Ruysinck E, Sahalie JM, Scholz A, Shah AA, Sharma A, Shen Y, Spirohn K, Tam S, Tejada AO, Trigg SA, Twizere J-C, Vega K, Walsh J, Cusick ME, Xia Y, Barabási A-L, Iakoucheva L, Aloy P, De Las Rivas J, Tavernier J, Calderwood MA, Hill DE, Hao T, Roth FP, Vidal M (2014) A proteome-scale map of the human interactome network. *Cell* 159(5):1212-26.

Brehme M*, Voisine C*, **Rolland T**, Wachi S, Soper JH, Zhu Y, Orton K, Vilella A, Garza D, Vidal M, Ge H, Morimoto RI (2014) A chaperome subnetwork safeguards proteostasis in aging and neurodegenerative disease. *Cell Reports* 9(3):1135-50.

Hill SJ, **Rolland T**, Adelmant G, Xia X, Owen MS, Dricot A, Zack TI, Sahni N, Jacob Y, Hao T, McKinney KM, Clark AP, Reyon D, Tsai SQ, Joung JK, Gaudet S, Beroukhim R, Marto JA, Vidal M, Hill DE, Livingston DM (2014) Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. *Genes Dev.* 28(17):1957-75.

Munier S, **Rolland T**, Diot C, Jacob Y, Naffakh N (2013) Exploration of binary virus-host interactions using an infectious protein complementation assay. *Mol. Cell. Proteomics* 12(10):2845-55.

Rozenblatt-Rosen O*, Deo RC*, Padi M*, Adelmant G*, Calderwood MA#, **Rolland T**#, Grace M#, Dricot A#, Askenazi M#, Tavares M#, Pevzner S#, Abderazzaq F, Byrdsong D, Carvunis AR, Chen AA, Cheng J, Correll M, Duarte M, Fan C, Feltkamp MC, Ficarro SB, Franchi R, Garg BK, Gulbahce N, Hao T, Holthaus AM, James R, Korkhin A, Litovchick L, Mar JC, Pak TR, Rabello S, Rubio R, Shen Y, Singh S, Spangle JM, Tasan M, Wanamaker S, Webber JT, Roecklein-Canfield J, Johannsen E, Barabasi AL, Beroukhim R, Kieff E, Cusick ME, Hill DE, Munger K, Marto JA, Quackenbush J, Roth FP, DeCaprio JA, Vidal M (2012) Interpreting cancer genomes using systematic host perturbations by tumour virus proteins. *Nature* 487(7408):491-5.

Carvunis AR, **Rolland T**, Wapinski I, Calderwood MA, Yildirim MA, Simonis N, Charloteaux B, Hidalgo CA, Barbette J, Santhanam B, Brar GA, Weissman JS, Regev A, Thierry-Mieg N, Cusick ME, Vidal M (2012) Proto-genes and *de novo* gene birth. *Nature* 487(7407):370-4.

The Arabidopsis Interactome Mapping Consortium (2011) Evidence for network evolution in an *Arabidopsis* interactome map. *Science* 333(6042):601-7.

Rolland T, Dujon B (2011) Yeasty clocks: dating genomic changes in yeasts. *C. R. Biol.* 334(8-9):620-8.

Rolland T, Dujon B, Richard GF (2010) Dynamic evolution of megasatellites in yeasts. *Nucleic Acids Res.* 38(14):4731-9.

Rolland T, Neuvéglise C, Sacerdot C, Dujon B (2009) Insertion of horizontally transferred genes within conserved syntenic regions of yeast genomes. *PLoS ONE* 4(8):e6515.

Souciet JL, Dujon B, Gaillardin C, Johnston M, Baret PV, Cliften P, Sherman DJ, Weissenbach J, Westhof E, Wincker P, Jubin C, Poulain J, Barbe V, Ségurens B, Artiguenave F, Anthouard V, Vacherie B, Val ME, Fulton RS, Minx P, Wilson R, Durrens P, Jean G, Marck C, Martin T, Nikolski M, **Rolland T**, Seret ML, Casarégola S, Despons L, Fairhead C, Fischer G, Lafontaine I, Leh V, Lemaire M, de Montigny J, Neuvéglise C, Thierry A, Blanc-Lenfle I, Bleykasten C, Diffels J, Fritsch E, Frangeul L, Goëffon A, Jauniaux N, Kachouri-Lafond R, Payen C, Potier S, Pribylova L, Ozanne C, Richard GF, Sacerdot C, Straub ML, Talla E (2009) Comparative genomics of protoploid *Saccharomycetaceae*. *Genome Res.* 19(10):1696-709.

Book chapters

Cusick ME, Charloteaux B, **Rolland T**, Calderwood MA, Hill DE, Vidal M (2017) Human Interactomes in Network Medicine. In *Network Medicine: Complex Systems in Human Disease and Therapeutics*. *Harvard University Press*.

Luck K, Jaikhani N, Cusick ME, **Rolland T**, Calderwood MA, Vidal M (2015) Interactomes – Scaffolds of Cellular Systems, in *Encyclopedia of Cell Biology*, edited by RA Bradshaw and PD Stahl, *Academic Press*.

Teaching

April 2017: Bioinformatics of protein-protein interactions for wet lab scientists course, Institut Pasteur.

Co-organizer of the course, 5 days including theoretical and practical sessions.

November 2015 / 2016 / 2017: Molecular Genetics and Epigenetics course, Institut Pasteur.

Lecture "Protein-protein interaction networks to study human diseases", 3 hours.

July 2014: Department of Genetics, Harvard Medical School.

Assisting Prof. Marc Vidal for the course "Molecular and systems level cancer cell biology", 1 hour lecture and 2 hours paper review practice.

July – August 2012 and 2013: Program "Bioinformatics and Integrative Genomics" of Harvard and MIT.

Supervising 2 students for 8 weeks:

- Seerat Hassan, Benedictine University, Lisle, Illinois
- Mike Jin, Yale University New Haven, Connecticut

Awards

February 2016 - 2017: Postdoctoral program, Labex Bio-Psy

Postdoctoral fellowship to study autism using interaction network approaches.

January 2011: Prix Jacques Monod de la Fondation de France

Awarding my thesis work on genome evolution in hemiascomycetous yeasts.

December 2007 – 2010: Ministère de l'Enseignement Supérieur et de la Recherche

Personal research fellowship for my Ph.D thesis.