

CURRICULUM VITAE

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Part I: General Information

Name: Marc Vidal
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Education:

1985 Ingénieur Agronome (B.S.), Faculté des Sciences Agronomiques, Gembloux, Belgium
1991 Docteur en Sciences Agronomiques (Ph.D.), Faculté des Sciences Agronomiques, Gembloux, Belgium

Postdoctoral Training:

1992-1997 Research Fellow in Medicine in the Laboratory of Dr. E. Harlow, Massachusetts General Hospital Cancer Center, Charlestown, MA and Harvard Medical School, Boston, MA

Academic Appointments:

1997-2000 Instructor in Medicine, Harvard Medical School, Boston, MA
2000-2003 Assistant Professor of Genetics, Dana-Farber Cancer Institute and Department of Genetics, Harvard Medical School, Boston, MA
2003-present Associate Professor of Genetics, Dana-Farber Cancer Institute and Department of Genetics, Harvard Medical School, Boston, MA

Other Professional Positions:

1986-1991 Graduate Student in the Laboratory of Dr. F. Hilger, Faculté des Sciences Agronomiques, Gembloux, Belgium
1988-1991 Predoctoral Visiting Scientist in the Laboratory of Dr. R.F. Gaber, Northwestern University, Evanston, IL
1993 Visiting Scientist in the Laboratory of Dr. J.D. Boeke, Johns Hopkins University School of Medicine, Baltimore, MD
1994-1999 Consultant, Life Technologies Inc. (now Invitrogen), Gaithersburg, MD
1997-2000 Assistant in Genetics, Principal Investigator position, Massachusetts General Hospital Cancer Center, Charlestown, MA
2004-present Director, Center for Cancer Systems Biology (CCSB), Dana-Farber Cancer Institute, Boston, MA

Editorial Boards:

- 1999-present *Current Genomics*
- 2001-present *Molecular & Cellular Proteomics*
- 2002-present *Nature Reviews in Genetics* (Highlight Advisory Panel)
- 2004-present *Genome Research*
- 2005-present *Molecular Systems Biology*
- 2005-present *BMC Genomics*
- 2005-present *Biology Direct*
- 2005-present *The Scientist*
- 2007-present *BMC Systems Biology*

Awards and Honors:

- 1986-1988 Bourse de Spécialisation Fellowship, Institut de la Recherche Scientifique dans l'Industrie et l'Agriculture (IRSIA), Brussels, Belgium
- 1991-1993 Collaborateur Scientifique Fellowship, Fonds National de la Recherche Scientifique (FNRS), Brussels, Belgium
- 1992-1993 Scientific Research Award, North Atlantic Treaty Organization (NATO), Brussels, Belgium
- 1993-1994 Fund for Medical Discovery, Massachusetts General Hospital, Boston, MA
- 1995-1997 Senior Postdoctoral Fellowship, American Cancer Society (ACS), Atlanta, GA
- 1997-2005 Chercheur Qualifié, Fonds National de la Recherche Scientifique (FNRS), Brussels, Belgium
- 2003 Abbott Bioresearch Award, Boston, MA
- 2005 International Francqui Chair, Francqui Foundation, Brussels, Belgium
- 2006 Elected Associate Member, Royal Academy of Sciences, Humanities and Fine Arts of Belgium, Brussels, Belgium

Part II: Research and Teaching Contributions

A. Narrative Report of Research:

The long-term goal of our laboratory is to understand how macromolecular networks control development, and how perturbations in such networks can lead to human disease.

Physical protein-protein interactions are crucial for most biological processes. In this context, we address the following questions. How are protein interactions organized at the scale of the whole cell, considering the fact that thousands of proteins are present in a cell at any given moment, most of them interacting with each other, either to form molecular machines or to participate in various regulatory mechanisms? Are there global principles that organize such complex networks of interactions? If so, how can we start tackling such global topological features of networks? And importantly, could it be that such organizational principles are disrupted in human disease?

We have focused most of our work on the multi-cellular model organism, *Caenorhabditis elegans*. The complete genome sequence of *C. elegans* is available and predicts ~19,000 protein-

encoding open reading frames (ORFs). To determine how proteins work together in complex cellular networks in this model organism, we have been mapping and characterizing protein-protein interactions in a systematic manner, an approach referred to as “interactome” modeling. In short, we have:

- experimentally tested genome-wide models of the *C. elegans* “ORFeome”, i.e. its complete set of ORFs, thereby generating a resource for proteome-wide protein expression (Walhout *et al Methods in Enzymology* 2000; Reboul *et al Nat Genet* 2001; Reboul *et al Nat Genet* 2003; Lamesch *et al Genome Res* 2004),

- generated first-draft maps of the *C. elegans* interactome network (Walhout *et al Science* 2000; Davy *et al EMBO Rep* 2001; Matthews *et al Genome Res* 2001; Walhout *et al Curr Biol* 2002; Boulton *et al Science* 2002; Li *et al Science* 2004),

- derived functional and dynamic models of interactome networks by combining interactome maps with various functional genomic information such as expression profiling and large-scale phenotypic profiling (Vidal *Cell* 2001; Ge *et al Nat Genet* 2001; Walhout *et al Current Biol* 2002; Boulton *et al Science* 2002; Tewari *et al Mol Cell* 2004),

- discovered global properties of interactome networks (Han *et al Nature* 2004; Han *et al Nat Biotechnol* 2005; Gunsalus *et al Nature* 2005)

- developed experimental strategies based on the reverse two-hybrid system (Vidal *et al Proc Natl Acad Sci USA* 1996a; 1996b) to systematically study the logic of interactome networks by disturbing specific protein-protein interactions (Endoh *et al Methods in Enzymology* 2000; 2002).

We have now started to analyze the human interactome network (Rual *et al Genome Res* 2004; Rual *et al Nature* 2005). Our goals are to: i) study the evolution of interactome networks, by comparing those of yeast, *C. elegans* and humans, and ii) understand how global interactome network features are perturbed in human disease.

C. Report of Current Research Activities:

Vidal Laboratory:

Genetic analyses of interactome networks; PI, project of:
Stuart Milstein, Ph.D. (Research Fellow)
Matija Dreze (Visiting Graduate Student)

Domain-domain interactome modeling; PI, project of:
Mike Boxem, Ph.D. (Instructor)
Xinping Yang, Ph.D. (Research Fellow)
Na Li (Senior Research Assistant)
Danny Mou (Undergraduate Student)

Interactome networks and human disease; PI, project of:
Kavitha Venkatesan, Ph.D. (Research Fellow)
Quan Zhong, Ph.D. (Research Fellow)
Qianru Li (BBS Graduate Student)
Han Yan (BBS Graduate Student)
Anne-Ruxandra Carvunis (Visiting Graduate Student)

Stanley Tam (Research Assistant)
Amélie Dricot (Visiting Graduate Student)
Haiyuan Yu, Ph.D. (Research Fellow)
Nicolas Simonis, Ph.D. (Research Fellow)
Muhammed Yildirim (DEAS Graduate Student)

C. elegans spatiotemporal promoter activity modeling; PI, project of:
Denis Dupuy, Ph.D. (Research Fellow)
Nenad Svrzikapa (Research Assistant)

DFCI Center for Cancer Systems Biology (CCSB):

The major goal of CCSB is to model the human interactome network

Management Team:

David Hill, Ph.D. (Senior Research Scientist, CCSB Associate Director)
Michael Cusick, Ph.D. (Information Manager)
Tong Hao (Systems Manager)

Bioinformatics:

Changyu Fan (Bioinformatics Programmer)
Niels Klitgord (Bioinformatics Analyst)
Chenwei Lin (Bioinformatics Analyst)

ORFeome projects:

Kourosch Salehi-Ashtiani, Ph.D. (Project Leader)
Tomoko Hirozane-Kishikawa (Senior Research Assistant)
Fana Gebreab (Research Assistant)

Interactome projects:

Pascal Braun, Ph.D. (Project Leader)
Julie Sahalie (Senior Research Assistant)
David Szeto (Research Assistant)
Ryan Murray (Research Assistant)

PART III: Bibliography

Original Articles

1. Gaber RF, Copple DM, Kennedy BK, **Vidal M**, Bard M. The yeast gene *ERG6* is required for normal membrane function but is not essential for biosynthesis of the cell-cycle-sparking sterol. *Mol Cell Biol* 1989;9:3447-56.
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3. **Vidal M**, Strich R, Esposito RE, Gaber RF. *RPD1 (SIN3/UME4)* is required for maximal activation and repression of diverse yeast genes. *Mol Cell Biol* 1991;11:6306-16.
4. **Vidal M**, Gaber RF. *RPD3* encodes a second factor required to achieve maximum positive and negative transcriptional states in *Saccharomyces cerevisiae*. *Mol Cell Biol* 1991;11:6317-27.
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8. **Vidal M**, Gaber RF. Selectable marker replacement in *Saccharomyces cerevisiae*. *Yeast* 1994;10:141-9.
9. Ishioka C, Ballester R, Engelstein M, **Vidal M**, Kassel J, The I, Bernards A, Gusella JF, Friend SH. A functional assay for heterozygous mutations in the GTPase activating protein related domain of the neurofibromatosis type 1 gene. *Oncogene* 1995;10:841-7.
10. **Vidal M**, Buckley AM, Yohn C, Hoepfner DJ, Gaber RF. Identification of essential nucleotides in an upstream repressing sequence of *Saccharomyces cerevisiae* by selection for increased expression of *TRK2*. *Proc Natl Acad Sci USA* 1995;92:2370-4.
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14. Du W, **Vidal M**, Xie JE, Dyson N. *RBF*, a novel RB-related gene that regulates E2F activity and interacts with *cyclin E* in *Drosophila*. *Genes Dev* 1996;10:1206-18.
15. **Vidal M**, Brachmann RK, Fattaey A, Harlow E, Boeke JD. Reverse two-hybrid and one-hybrid systems to detect dissociation of protein-protein and DNA-protein interactions. *Proc Natl Acad Sci USA* 1996;93:10315-20.

16. **Vidal M**, Braun P, Chen E, Boeke JD, Harlow E. Genetic characterization of a mammalian protein-protein interaction domain by using a yeast reverse two-hybrid system. *Proc Natl Acad Sci USA* 1996;93:10321-6.
17. Kim SS, Chen YM, O'Leary E, Witzgall R, **Vidal M**, Bonventre JV. A novel member of the RING finger family, KRIP-1, associates with the KRAB-A transcriptional repressor domain of zinc finger proteins. *Proc Natl Acad Sci USA* 1996;93:15299-304.
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