

Antoine de Daruvar

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CURRENT POSITION

Full professor in bioinformatics at the University of Bordeaux (<http://www.u-bordeaux.fr/>), France, where I teach bioinformatics.

Member of the Fruit Biology and Pathology Unit (UMR 1332)

EDUCATION

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| 2001 | University Bordeaux Segalen, France: Accreditation to supervise research (HDR) |
| 1987 | University Pierre and Marie Curie, Paris 6, France: Master Degree ("DESS") in computer science applied to biology |
| 1986 | AgroParisTech, Institut National Agronomique Paris-Grignon, Paris, France : engineer in agronomy |
| 1984 | University Pierre and Marie Curie (Paris 6, France)), Graduate degree ("Maitrise") in Biochemistry |

PROFESSIONAL CAREER

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| As from 2002 | Full professor at the University Bordeaux Segalen, France. |
| 2000/2002 | Associated professor at the University Bordeaux Segalen, France. |
| 1997/2002 | Senior Manager in Bioinformatics, LION bioscience (biotech company), Heidelberg, Germany. |
| 1994/97 | Scientist at the European Molecular Biology Laboratory (EMBL - Chris Sander group) Heidelberg, Germany. |
| 1990/94 | Software engineer/project manager in various companies: Bull SA, Sanders SA and Marben SA, Paris, France. |

ACADEMIC ACTIVITIES

Teaching

I was recruited by the university Bordeaux Segalen, with the aim of promoting bioinformatics as a discipline to be taught in various biology courses at the Faculty of Life Sciences.

My teaching covered basic programming for biologists and the concepts and use of bioinformatics methods and tools. I coordinated the setting up and was responsible (2003-2007) for the Master of Bioinformatics.

I also taught at the "Ecole Nationale Supérieure de Technologie des Biomolécules de Bordeaux" (ENSTBB, Bordeaux) and occasionally at the "University of Applied Sciences" in Bremen, Germany.

Scientific activities and responsibilities

My scientific interests relate to the design and development of methods and tools for the:

- analysis of genomes, comparative genomics;
- integration of functional genomics data;
- storage and analysis of metabolomics data.

I have set-up and headed (2001-2010) the center for bioinformatics of Bordeaux (<http://www.cbib.u-bordeaux2.fr/>). The Center for Bioinformatics provides access to high-performance computing resources, data analysis and programming expertise. The resources serve scientists to fulfill the bioinformatics needs of their research.

Until 2008 I was in charge of coordinating the national network of bioinformatics platforms (ReNaBI: <http://www.renabi.fr/>) and was a member until 2011 of the steering committee of the preparatory phase of ELIXIR project (<http://www.elixir-europe.org/>). This project aims at constructing and operating a sustainable infrastructure for biological information in Europe, to support life science research and its translation to medicine and the environment, the bio-industries and society.

Other main academic responsibilities

From 2003 until 2008 I was Managing Director of the Bordeaux Functional Genomics Center (CGFB: <http://www.cgfb.u-bordeaux2.fr/>) which brings various scientific and technological platforms together, dedicated to the study of living organisms at cellular and molecular scale. This infrastructure has four main tasks:

- support scientific and technological research activities carried by laboratories;
- educate students and spread information toward researchers on new technologies;
- promote innovation by developing new technologies.

From 2008 till 2013, I was elected vice-president in charge of administrative affairs of the Bordeaux Segalen University. As vice-president, I was in charge of the management of the resources (human resources, budget, university premises, etc.) of the university and responsible of several strategic projects.

PUBLICATIONS

1. Sansone SA, Rocca-Serra P, Field D, Maguire E, Taylor C, Hofmann O, Fang H, Neumann S, Tong W, Amaral-Zettler L, Begley K, Booth T, Bougueleret L, Burns G, Chapman B, Clark T, Coleman LA, Copeland J, Das S, **de Daruvar A**, de Matos P, Dix I, Edmunds S, Evelo CT, Forster MJ, Gaudet P, Gilbert J, Goble C, Griffin JL, Jacob D, Kleinjans J, Harland L, Haug K, Hermjakob H, Ho Sui SJ, Laederach A, Liang S, Marshall S, McGrath A, Merrill E, Reilly D, Roux M, Shamu CE, Shang CA, Steinbeck C, Trefethen A, Williams-Jones B, Wolstencroft K, Xenarios I, Hide W. Toward interoperable bioscience data. *Nat Genet.* 2012 Jan 27;44(2):121-6.
2. Ferry-Dumazet H, Gil L, Deborde C, Moing A, Bernillon S, Rolin D, Nikolski M, **de Daruvar A**, Jacob D. MeRy-B: a web knowledgebase for the storage, visualization, analysis and annotation of plant NMR metabolomic profiles. *BMC Plant Biol.* 2011 Jun 13;11:104.

3. Ueno S, Le Provost G, Léger V, Klopp C, Noirot C, Frigerio JM, Salin F, Salse J, Abrouk M, Murat F, Brendel O, Derory J, Abadie P, Léger P, Cabane C, Barré A, **de Daruvar A**, Couloux A, Wincker P, Reviron MP, Kremer A, Plomion C. Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. *BMC Genomics*. 2010 Nov 23;11:650.
4. Durand J, Bodénès C, Chancerel E, Frigerio JM, Vendramin G, Sebastiani F, Buonamici A, Gailing O, Koelewijn HP, Villani F, Mattioni C, Cherubini M, Goicoechea PG, Herrán A, Ikarán Z, Cabané C, Ueno S, Alberto F, Dumoulin PY, Guichoux E, **de Daruvar A**, Kremer A, Plomion C. A fast and cost-effective approach to develop and map EST-SSR markers: oak as a case study. *BMC Genomics*. 2010 Oct 15;11:570.
5. Bourbeillon J, Orchard S, Benhar I, Borrebaeck C, **de Daruvar A**, Dübel S, Frank R, Gibson F, Gloriam D, Haslam N, Hiltker T, Humphrey-Smith I, Hust M, Juncker D, Koegl M, Konthur Z, Korn B, Krobitch S, Muyldermans S, Nygren PA, Palcy S, Polic B, Rodriguez H, Sawyer A, Schlapshy M, Snyder M, Stoevesandt O, Taussig MJ, Templin M, Uhlen M, van der Maarel S, Wingren C, Hermjakob H, Sherman D. Minimum information about a protein affinity reagent (MIAPAR). *Nat Biotechnol*. 2010 Jul;28(7):650-3.
6. Garcia V, Stevens R, Gil L, Gilbert L, Gest N, Petit J, Faurobert M, Maucourt M, Deborde C, Moing A, Poessel JL, Jacob D, Bouchet JP, Giraudel JL, Gouble B, Page D, Alhaghdow M, Massot C, Gautier H, Lemaire-Chamley M, **de Daruvar A**, Rolin D, Usadel B, Lahaye M, Causse M, Baldet P, Rothan C. An integrative genomics approach for deciphering the complex interactions between ascorbate metabolism and fruit growth and composition in tomato. *C R Biol*. 2009 Nov;332(11):1007-21.
7. Pereyre S, Sirand-Pugnet P, Beven L, Charron A, Renaudin H, Barré A, Avenaoud P, Jacob D, Couloux A, Barbe V, **de Daruvar A**, Blanchard A, Bébéar C. Life on arginine for *Mycoplasma hominis*: clues from its minimal genome and comparison with other human urogenital mycoplasmas. *PLoS Genet*. 2009 Oct;5(10):e1000677.
8. Gloriam DE, Orchard S, Bertinetti D, Björling E, Bongcam-Rudloff E, Borrebaeck CA, Bourbeillon J, Bradbury AR, **de Daruvar A**, Dübel S, Frank R, Gibson TJ, Gold L, Haslam N, Herberg FW, Hiltke T, Hoheisel JD, Kerrien S, Koegl M, Konthur Z, Korn B, Landegren U, Montecchi-Palazzi L, Palcy S, Rodriguez H, Schweinsberg S, Sievert V, Stoevesandt O, Taussig MJ, Ueffing M, Uhlén M, van der Maarel S, Wingren C, Woollard P, Sherman DJ, Hermjakob H. A community standard format for the representation of protein affinity reagents. *Mol Cell Proteomics*. 2010 Jan;9(1):1-10.
9. Bon E, Delaherche A, Bilhère E, **de Daruvar A**, Lonvaud-Funel A, Le Marrec C. *Oenococcus oeni* genome plasticity is associated with fitness. *Appl Environ Microbiol*. 2009 Apr;75(7):2079-90
10. Schwartz JM, Gaugain C, Nacher JC, de Daruvar A, Kanehisa M. Observing metabolic functions at the genome scale. *Genome Biol*. 2007;8(6):R123.
11. Toulza E, Mattiuzzo NR, Galliano MF, Jonca N, Dossat C, Jacob D, **de Daruvar A**, Wincker P, Serre G, Guerrin M. Large-scale identification of human genes implicated in epidermal barrier function. *Genome Biol*. 2007;8(6):R107.
12. Sirand-Pugnet P, Lartigue C, Marena M, Jacob D, Barré A, Barbe V, Schenowitz C, Mangenot S, Couloux A, Segurens B, **de Daruvar A**, Blanchard A, Citti C. Being pathogenic, plastic, and sexual while living with a nearly minimal bacterial genome. *PLoS Genet*. 2007 May 18;3(5):e75.
13. Taussig MJ, Stoevesandt O, Borrebaeck CA, Bradbury AR, Cahill D, Cambillau C, **de Daruvar A**, Dübel S, Eichler J, Frank R, Gibson TJ, Gloriam D, Gold L, Herberg FW, Hermjakob H, Hoheisel JD, Joos TO, Kallioniemi O, Koegl M, Konthur Z, Korn B, Kremmer E, Krobitch S, Landegren U, van der Maarel S, McCafferty J, Muyldermans S, Nygren PA, Palcy S, Plückthun A, Polic B, Przybylski M, Saviranta P, Sawyer A, Sherman DJ, Skerra A, Templin M, Ueffing M, Uhlén M. ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. *Nat Methods*. 2007 Jan;4(1):13-7.
14. Plomion C, Lalanne C, Claverol S, Meddour H, Kohler A, Bogeat-Triboulot MB, Barre A, Le Provost G, Dumazet H, Jacob D, Bastien C, Dreyer E, **de Daruvar A**, Guehl JM, Schmitter JM, Martin F, Bonneu M. Mapping the proteome of poplar and application to the discovery of drought-stress responsive proteins. *Proteomics*. 2006 Dec;6(24):6509-27.
15. Delaherche A, Bon E, Dupe A, Lucas M, Arveiler B, **De Daruvar A**, Lonvaud-Funel A. Intraspecific diversity of *Oenococcus oeni* strains determined by sequence analysis of target genes. *Appl Microbiol Biotechnol*. 2006 Nov;73(2):394-403. Epub 2006 Aug 16.

16. Ferry-Dumazet H, Houel G, Montalent P, Moreau L, Langella O, Negroni L, Vincent D, Lalanne C, **de Daruvar A**, Plomion C, Zivy M, Joets J. PROTiCdb: a web-based application to store, track, query, and compare plant proteome data. *Proteomics*. 2005 May;5(8):2069-81.
17. Gion JM, Lalanne C, Le Provost G, Ferry-Dumazet H, Paiva J, Chaumeil P, Frigerio JM, Brach J, Barre A, **de Daruvar A**, Claverol S, Bonneu M, Sommerer N, Negroni L, Plomion C. The proteome of maritime pine wood forming tissue. *Proteomics*. 2005 Sep;5(14):3731-51.
18. Iragne, F., A. Barre, N. Goffard, and **A. De Daruvar**. 2004. AliasServer: a web server to handle multiple aliases used to refer to proteins. *Bioinformatics* 20: 2331-2.
19. Dujon, B., D. Sherman, G. Fischer, P. Durrens, S. Casaregola, I. Lafontaine, J. de Montigny, C. Marck, C. Neugeglise, E. Talla, N. Goffard, L. Frangeul, M. Aigle, V. Anthouard, A. Babour, V. Barbe, S. Barnay, S. Blanchin, J.-M. Beckerich, E. Beyne, C. Bleykasten, A. Boisrame, J. Boyer, L. Cattolico, F. Confanioleri, **A. de Daruvar**, L. Despons, E. Fabre, C. Fairhead, H. Ferry-Dumazet, A. Groppi, F. Hantraye, C. Hennequin, N. Jauniaux, P. Joyet, R. Kachouri, A. Kerrest, R. Koszul, M. Lemaire, I. Lesur, L. Ma, H. Muller, J.-M. Nicaud, M. Nikolski, S. Oztas, O. Ozier-Kalogeropoulos, S. Pellenz, S. Potier, G.-F. Richard, M.-L. Straub, A. Suleau, D. Swennen, F. Tekaiia, M. Wesolowski-Louvel, E. Westhof, B. Wirth, M. Zeniou-Meyer, I. Zivanovic, M. Bolotin-Fukuhara, A. Thierry, C. Bouchier, B. Caudron, C. Scarpelli, C. Gaillardin, J. Weissenbach, P. Wincker, and J.-L. Souciet. 2004. Genome evolution in yeasts. *Nature* 430: 35-44.
20. Dantec, L. L., D. Chagne, D. Pot, O. Cantin, P. Garnier-Gere, F. Bedon, J. M. Frigerio, P. Chaumeil, P. Leger, V. Garcia, F. Laignet, **A. De Daruvar**, and C. Plomion. 2004. Automated SNP detection in expressed sequence tags: statistical considerations and application to maritime pine sequences. *Plant Mol Biol* 54: 461-70.
21. Barriot, R., J. Poix, A. Groppi, A. Barre, N. Goffard, D. Sherman, I. Dutour, and **A. de Daruvar**. 2004. New strategy for the representation and the integration of biomolecular knowledge at a cellular scale. *Nucleic Acids Res* 32: 3581-9.
22. Barriot, R., Poix, J., Groppi, A., Barre, A., Goffard, N., Sherman, D., Dutour, I. & **de Daruvar, A.** New strategy for the representation and the integration of biomolecular knowledge at a cellular scale. (soumis).
23. Barre A, **de Daruvar A**, Blanchard A. (2004) MolliGen, a database dedicated to the comparative genomics of Mollicutes. *Nucleic Acids Res.* 1;32:D307-10.
24. Goffard, N., Garcia, V., Iragne, F., Groppi, A. and **de Daruvar, A.** (2003) IPPRED : server for proteins interactions inference. *Bioinformatics* 1;19(7):903-4.
25. **de Daruvar, A.**, Collado-Vides, J., and Valencia, A. (2002). Characterization of cellular functions of Escherichia coli operons and their conservation in Bacillus subtilis. *Journal of Molecular Evolution.* 55(2):211-21.
26. Binz PA, Martin A, Taussig M and De **Daruvar A.** (2002) Conference report : the EFS programme on Integrated approaches for functional genomics. Workshop on "data integration in functional genomics and proteomics". *Comparative and Fonctionnal Genomics*; 3 : 16-21
27. Rice P, Jassal B and de **Daruvar A** (2002) RIBDB : an SRS based infrastructure for REALIS. *Comparative and Fonctionnal Genomics*; 3 : 35-36
28. Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A., Baquero, F., Berche, P., Bloecker, H., Brandt, P., Chakraborty, T., Charbit, A., Chetouani, F., Couvé, E., **de Daruvar, A.**, Dehoux P, Domann E, Domínguez-Bernal G, Duchaud E, Durant L, Dussurget O, Entian KD, Fsihi H, García-del Portillo F, Garrido P, Gautier L, Goebel W, Gómez-López N, Hain T, Hauf J, Jackson D, Jones LM, Kaerst U, Kreft J, Kuhn M, Kunst F, Kurapkat G, Madueno E, Maitournam A, Vicente JM, Ng E, Nedjari H, Nordtsiek G, Novella S, de Pablos B, Pérez-Díaz JC, Purcell R, Remmel B, Rose M, Schlueter T, Simoes N, Tierrez A, Vázquez-Boland JA, Voss H, Wehland J, Cossart P.. (2001). Comparative genomics of Listeria species. *Science* 294, 849-852.
29. Andrade, M. A., Brown, N. P., Leroy, C., Hoersch, S., **de Daruvar, A.**, Reich, C., Franchini, A., Tamames, J., Valencia, A., Ouzounis, C., and Sander, C. (1999). Automated genome sequence analysis and annotation. *Bioinformatics* 15, 391-412.
30. Schneider, R., **de Daruvar, A.**, and Sander, C. (1997). The HSSP database of protein structure-sequence alignments. *Nucleic Acids Res* 25, 226-230.
31. Andrade, M. A., **Daruvar, A.**, Casari, G., Schneider, R., Termier, M., and Sander, C. (1997b). Characterization of new proteins found by analysis of short open reading frames from the full yeast genome. *Yeast* 13, 1363-1374.

32. Andrade, M., Casari, G., **de Daruvar, A.**, Sander, C., Schneider, R., Tamames, J., Valencia, A., and Ouzounis, C. (1997a). Sequence analysis of the *Methanococcus jannaschii* genome and the prediction of protein function. *Comput Appl Biosci* 13, 481-483.
33. Casari, G., **De Daruvar, A.**, Sander, C., and Schneider, R. (1996). Bioinformatics and the discovery of gene function. *Trends Genet* 12, 244-245.
34. Casari, G., Andrade, M. A., Bork, P., Boyle, J., **Daruvar, A.**, Ouzounis, C., Schneider, R., Tamames, J., Valencia, A., and Sander, C. (1995). Challenging times for bioinformatics. *Nature* 376, 647-648.