

# Julien MAUPETIT

DEVELOPER · OPEN (SOURCE | DATA) ENTHOUSIAST

## PERSONAL DATA

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PLACE AND DATE OF BIRTH: Saint Denis (93), France · 14 October 1980  
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## EDUCATION

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Nov 2007 PhD's Degree in BIOINFORMATICS, **Paris Diderot University**, Paris, France  
Supervisor: Dr P. TUFFÉRY

JULY 2004 Master's Degree in BIOINFORMATICS, **Paris Diderot University**, Paris, France  
Grade: *magna cum laude*

JULY 2002 Bachelor's Degree in BIOCHEMISTRY, **Paris Diderot University**, Paris, France  
Grade: *magna cum laude*

## POSITIONS HELD

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<i>Current</i> MAR 2024	Self-Employed at <a href="#">PUYDATA</a> <i>Data Engineering</i> I mostly work for French public institutions to help them open their data or provide innovative services. Most significative projects: <ul style="list-style-type: none"><li>• <a href="#">QualiCharge</a> (Mar 2024 - current): collect Electric Vehicle Supply Equipment (EVSE) description, statuses and charging sessions to automate certificates calculation, provide real-time <a href="#">open data</a> and ease ecological planification.</li></ul>
<i>Mar 2024</i> JAN 2021	Chief Data Officer at <a href="#">FRANCE UNIVERSITÉ NUMÉRIQUE</a> <i>Learning Analytics</i> My second mission at FUN has been to handle the development of a complete suite to collect, store, transform, analyze and report usage data from our learning platforms.
<i>Jan 2021</i> FEB 2018	Senior Developer at <a href="#">FRANCE UNIVERSITÉ NUMÉRIQUE</a> <i>From back-end to DevOps</i> My first mission at FUN was to add quality in our open-source projects and automate its assessment using standard CI-CD tools and migrate our stack to Docker/Kubernetes.
<i>Feb 2018</i> FEB 2014	Co-Founder & CEO at TAILORDEV <i>Application development for research labs</i> The mission of TailorDev was to develop modern tools to ease scientific collaboration and promote Open Science / Data in research entities.
<i>Dec 2015</i> DEC 2011	Co-Founder & CTO at COMSOURCE <i>Front &amp; Back End Web development</i> Entrepreneurship has always been in my mind. My passion for the web and its design decided me to join the ComSource web agency to develop tailored solutions for the web.

NOV 2011 SEP 2008	<b>Frozen Position</b> Research Engineer at PARIS DIDEROT UNIVERSITY (RPBS & INSERM UMR-S973), Paris, France <i>Structural bioinformatics - Web development - System administration</i> Supervisors: DR P. TUFFÉRY and DR B. VILLOUTREIX Since I obtained my position, my principal activities have been: (i) structural bioinformatics and chemoinformatics web servers / programs development, (ii) structural bioinformatics assistance with biological wet laboratories, and (iii) platform / laboratory hosting / computing / storage resources administration.
AUG 2008 OCT 2007	Assistant Professor at IBPC (CNRS UPR9080), Paris, France <i>Bioinformatics teaching - Peptide structure prediction</i> Supervisor: PR P. DERREUMAUX The technics developed during my PhD applied to peptide structures appears strongly relevant. Hence, we designed PEP-FOLD, a fast method for large scale <i>de novo</i> peptide and miniprotein structure prediction.
SEP 2007 OCT 2004	PhD at PARIS DIDEROT UNIVERSITY (INSERM U726), Paris, France <i>Protein structure prediction</i> Supervisor: DR P. TUFFÉRY In a post-genomic context, plenty of proteins, identified by their sequence, have no experimentally resolved structure, and fall out the range of application of comparative modelling methods. The goal of my PhD was to explore a new <i>de novo</i> protein structure prediction approach.
SUMMER 2003	Summer Intern at PARIS DIDEROT UNIVERSITY (INSERM U726) and PASTEUR INSTITUTE, Paris, France <i>Molecular visualization</i> Supervisor: DR P. TUFFÉRY Development and integration of a PDB files parser in a molecular visualization widget.
MAY 2003 JAN 2003	Intern at PARIS DIDEROT UNIVERSITY (EA3508), Paris, France <i>Molecular biology</i> Supervisor: PR J. LONDON Transgenic mice genotyping.
SUMMER 2002	Summer Intern at HOSPITAL BICHAT (INSERM U409), Paris, France <i>Molecular biology</i> Supervisor: DR M.E. MARTIN Hepcidin involvement in particular hemochromatosis – IRE/IRP system in transgenic mice over-expressing the superoxyde dismutase.

## TEACHING EXPERIENCE

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2005-2011, PARIS DIDEROT UNIVERSITY (300h)

MASTER	Introduction to XHTML/CSS	Protein structure prediction
	Introduction to $\LaTeX$	Microarray data analysis
	Introduction to BioPython	Molecular phylogeny
	Python programming	Bioinformatics tools
	C programming	
	Interfacing C and Python with Swig	
BACHELOR	Bioinformatics tools	

2006, 1<sup>st</sup> MEDILS SUMMER SCHOOL, SPLIT, CROATIA (4h)

PHD	Comparative protein modelling	Normal modes analysis
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## PUBLICATIONS

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### Peer reviewed articles

Denecker, T., W. Durand, J. Maupetit, C. Hébert, J.-M. Camadro, P. Poulain, and G. Lelandais (2019). "Pixel: a content management platform for quantitative omics data". In: *PeerJ* 7, e6623. DOI: [10.7717/peerj.6623](https://doi.org/10.7717/peerj.6623).

Shen, Y., J. Maupetit, P. Derreumaux, and P. Tufféry (2014). "Improved PEP-FOLD Approach for Peptide and Miniprotein Structure Prediction". In: *Journal of Chemical Theory and Computation* 10.10. PMID: 26588162, pp. 4745–4758. DOI: [10.1021/ct500592m](https://doi.org/10.1021/ct500592m).

Thévenet, P., Y. Shen, J. Maupetit, F. Guyon, P. Derreumaux, and P. Tufféry (July 2012). "PEP-FOLD: an updated de novo structure prediction server for both linear and disulfide bonded cyclic peptides". In: *Nucleic Acids Res* 40.Web Server issue, W288–93. DOI: [10.1093/nar/gks419](https://doi.org/10.1093/nar/gks419).

Tudor, D., H. Yu, J. Maupetit, A.-S. Drillet, T. Bouceba, I. Schwartz-Cornil, L. Lopalco, P. Tuffery, and M. Bomsel (July 2012). "Isotype modulates epitope specificity, affinity, and antiviral activities of anti-HIV-1 human broadly neutralizing 2F5 antibody". In: *Proc Natl Acad Sci U S A* 109.31, pp. 12680–5. DOI: [10.1073/pnas.1200024109](https://doi.org/10.1073/pnas.1200024109).

Lagorce, D., J. Maupetit, J. Baell, O. Sperandio, P. Tufféry, M. A. Miteva, H. Galons, and B. O. Villoutreix (July 2011a). "The FAF-Drugs2 server: a multistep engine to prepare electronic chemical compound collections". In: *Bioinformatics* 27.14, pp. 2018–20. DOI: [10.1093/bioinformatics/btr333](https://doi.org/10.1093/bioinformatics/btr333).

Regad, L., A. Saladin, J. Maupetit, C. Geneix, and A.-C. Camproux (July 2011). "SA-Mot: a web server for the identification of motifs of interest extracted from protein loops". In: *Nucleic Acids Res* 39.Web Server issue, W203–9. DOI: [10.1093/nar/gkr410](https://doi.org/10.1093/nar/gkr410).

Maupetit, J., P. Derreumaux, and P. Tufféry (Mar. 2010). "A fast method for large-scale de novo peptide and miniprotein structure prediction". In: *J Comput Chem* 31.4, pp. 726–38. DOI: [10.1002/jcc.21365](https://doi.org/10.1002/jcc.21365).

Maupetit, J., A. Saladin, and P. Tufféry (Nov. 2010). "Prédiction en ligne de la structure des protéines : un état des lieux". In: *Spectra Analyse* 39.276, pp. 27–33.

Schmidtke, P., V. Le Guilloux, J. Maupetit, and P. Tufféry (July 2010). "fpocket: online tools for protein ensemble pocket detection and tracking". In: *Nucleic Acids Res* 38 Suppl, W582–9. DOI: [10.1093/nar/gkq383](https://doi.org/10.1093/nar/gkq383).

- Maupetit, J., P. Derreumaux, and P. Tufféry (July 2009). "PEP-FOLD: an online resource for de novo peptide structure prediction". In: *Nucleic Acids Res* 37.Web Server issue, W498–503. DOI: [10.1093/nar/gkp323](https://doi.org/10.1093/nar/gkp323).
- Néron, B., H. Ménager, C. Maufrais, N. Joly, J. Maupetit, S. Letort, S. Carrere, P. Tufféry, and C. Letondal (Nov. 2009). "Mobyle: a new full web bioinformatics framework". In: *Bioinformatics* 25.22, pp. 3005–11. DOI: [10.1093/bioinformatics/btp493](https://doi.org/10.1093/bioinformatics/btp493).
- Regad, L., F. Guyon, J. Maupetit, P. Tufféry, and A. C. Camproux (Feb. 2008). "A Hidden Markov Model applied to the protein 3D structure analysis". In: *Computational Statistics and Data Analysis* 52.6, pp. 3198–3207. DOI: [10.1016/j.csda.2007.09.010](https://doi.org/10.1016/j.csda.2007.09.010).
- Maupetit, J., P. Tufféry, and P. Derreumaux (Nov. 2007). "A coarse-grained protein force field for folding and structure prediction". In: *Proteins* 69.2, pp. 394–408. DOI: [10.1002/prot.21505](https://doi.org/10.1002/prot.21505).
- Maupetit, J., R. Gautier, and P. Tufféry (July 2006). "SABBAC: online Structural Alphabet-based protein BackBone reconstruction from Alpha-Carbon trace". In: *Nucleic Acids Res* 34.Web Server issue, W147–51. DOI: [10.1093/nar/gkl289](https://doi.org/10.1093/nar/gkl289).

## Proceedings

- Ménager, H., V. Gopalan, B. Néron, S. Larroudé, J. Maupetit, A. Saladin, P. Tufféry, Y. Huyen, and B. Caudron (2011). "Bioinformatics applications discovery and composition with the Mobyle suite and MobyleNet". In: *RED 2010*. Vol. [Accepted]. Lecture Notes in Computer Science.
- Shen, Y., J. Maupetit, P. Derreumaux, and P. Tufféry (2011c). "PEP-FOLD: biased approach for the de novo prediction of peptide and miniprotein structure". In: *JOBIM 2011*. URL: <http://www.pasteur.fr/ip/easysite/pasteur/fr/recherche/communication-scientifique/conferences-et-congres-scientifiques/conferences-service-colloques-institut-pasteur/jobim-2011>.
- Strauser, E., M. Naveau, H. Ménager, J. Maupetit, Z. Lacroix, and P. Tufféry (2011). "Semantic Map for Structural Bioinformatics: enhanced service discovery based on high level concept ontology". In: *RED 2010*. Vol. [Accepted]. Lecture Notes in Computer Science. Springer.

## Oral communications

- Maupetit, J. (Sept. 2013a). *Django mérite bien un oscar*. DjangoCong 2013. URL: <http://comsource.github.io/Oscar-DjangoCong-2013/>.
- (Sept. 2013b). *MicroGeno - Towards an advanced and open web-based platform for bacterial genotyping*. DjangoCong 2013. URL: <http://comsource.github.io/MicroGeno-DjangoCong-2013/>.
  - (June 2013c). *MicroGeno - Towards an open web-based platform for genotyping data*. MLVA Workshop. URL: <http://comsource.github.io/MicroGeno-MLVA-Workshop-2013/>.
- Maupetit, J., A. Saladin, and P. Tufféry (2011a). *La plate-forme RPBS : analyse fonctionnelle des structures protéiques in silico*. APLIBIO day. URL: <http://renabi.genouest.org/platforms/aplibio/>.
- (2011b). *The RPBS Platform - in silico functional analysis & prediction of protein structures ... and molecular 3D printing!* GGMM. URL: <http://ggmm2011.wordpress.com>.
- Maupetit, J. and P. Tufféry (2009). *Mobyle @ RPBS // MobyleNet*. MobyleNet. URL: <http://mobylenet.rpbs.univ-paris-diderot.fr>.
- Maupetit, J., B. Néron, H. Ménager, C. Maufrais, N. Joly, C. Letondal, and P. Tufféry (2008). *Mobyle @ RPBS - A web portal for structural bioinformatics and chemoinformatics*. BIOGRALE. URL: [http://pbil.univ-lyon1.fr/pf\\_bioinfo/breve86.html](http://pbil.univ-lyon1.fr/pf_bioinfo/breve86.html).

Maupetit, J. and P. Tufféry (2008). *Mobyle vers Playmoby - Déploiement de web services*. BioWorkflow. URL: <http://migale.jouy.inra.fr/bioworkflow/>.

Maupetit, J., F. Guyon, A. C. Camproux, P. Derreumaux, and P. Tufféry (2007). *Candidate Fragments Prediction and their Assembly with a Greedy Algorithm and a Coarse-Grained Force Field to solve Protein Folding*. JOBIM. URL: <http://crfb.univ-mrs.fr/jobim2007>.

## Posters

Lagorce, D., J. Maupetit, J. Baell, O. Sperandio, P. Tufféry, M. A. Miteva, H. Galons, and B. O. Villoutreix (2011b). *The FAF-Drugs2 server: a multi-step engine to prepare electronic chemical compound collections*. BABE. URL: <http://www.omicsonline.org/BABE2011/>.

Saladin, A., J. Maupetit, H. Ménager, B. Néron, B. Caudron, and P. Tufféry (2011). *MobyleNet: a network of trusted platforms for seamlessly sharing a large spectrum of services*. GGMM. URL: <http://ggmm2011.wordpress.com>.

Shen, Y., J. Maupetit, P. Derreumaux, and P. Tufféry (2011a). *Mini protein fast fold de novo generation using biased conformation search*. PepCon. URL: <http://www.bitlifesciences.com/PepCon2011/>.

– (2011b). *PEP-FOLD: biased approach for the de novo prediction of peptide and miniprotein structure*. GGMM. URL: <http://ggmm2011.wordpress.com>.

Larroudé, S., J. Maupetit, H. Ménager, B. Néron, A. Saladin, B. Caudron, and P. Tufféry (2010). *MobyleNet: user-centered large spectrum service integration over distributed sites*. ISMB. URL: <http://www.iscb.org/ismb2010>.

Maupetit, J., B. O. Villoutreix, and P. Tufféry (2010a). *3D Printing service @ RPBS*. JOBIM 2010. URL: <http://www.jobim2010.fr>.

– (2010b). *3D Printing service @ RPBS*. Obernai 2010. URL: <http://infochim.u-strasbg.fr/new/spip.php?rubrique15>.

Maupetit, J., P. Derreumaux, and P. Tufféry (2006). *A Greedy Algorithm for Protein Structure Reconstruction: Improvements and Applications*. GCB. URL: <http://www.gcb2006.de/>.

Maupetit, J., F. Guyon, J. Martin, A. C. Camproux, P. Derreumaux, and P. Tufféry (2006). *Assessing a New Approach for Protein Structure Modeling Combining Structural Alphabet Local Conformation Prediction and Greedy Algorithm for Reconstruction*. CASP7. URL: <http://predictioncenter.org/casp7/>.

## INTERN SUPERVISION

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2011 3 MONTHS	<b>SbMAP3, STRUCTURAL BIOINFORMATICS SEMANTIC MAP REDESIGN</b> <i>B. Delepine, Bachelor in Bioinformatics</i> Redesign SbMap interface with modern javascript tools instead of a Java Applet.
2010 5 MONTHS	<b>SbMAP2, STRUCTURAL BIOINFORMATICS SEMANTIC MAP</b> <i>E. Strauser, Master of Bioinformatics</i> SbMAP Java applet user interface and graphical navigation improvements.  <b>PYPDB, A TOOLBOX TO WORK WITH PDB FILES</b> <i>F. Briand, Master of Bioinformatics</i> Design of a command line tool to manipulate PDB files, its packaging and integration in the RPBS MOBYLE portal.
2009 3 MONTHS	<b>PYPDB, A PYTHON CLASS TO WORK WITH PDB FILES</b> <i>C. Habib, Bachelor in Bioinformatics</i> PYTHON code cleanup and documentation, integration of PDB-XML files support.
2008 5 MONTHS	<b>SbMAP, STRUCTURAL BIOINFORMATICS SEMANTIC MAP</b> <i>M. Naveau, Master of Bioinformatics</i> Structural bioinformatics concepts ontology automatic update integration in an web administration interface.

## INTERESTS AND ACTIVITIES

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- Wannabe musician (guitar, drums, singing)
- Actor in a theater company
- Open-Source advocate
- Co-Founder & first President of [Clermont'ech](#) – a developers association made in Auvergne – from february 2012 to may 2016.
- Treasurer of a [local association](#) that provides affordable sports activities for young citizens.