Mikael Trellet

phD student in Bioinformatics engineering

Work experience

Sept. 2011 – Sept. 2012 **Research/Educational assistant**, *Computational and Structural Biology group*, Utrecht university - NETHERLANDS.
Under Pr. Alexandre Bonvin supervision
- Research project for protein-peptide docking with HADDOCK software [TMB13]
- European grid-computing administration in the WeNMR project
- New clustering method for protein-protein complexes assess [RTS+12]

June 2011 – Aug. 2011 **Developer at Google Summer of Code 2011**.
Project for Biopython initiative. "Interface analysis module" leading to new features in the biopython module for protein-protein interfaces analysis.
`http://biopython.org/wiki/GSoC2011_mtrellet`

Aug. 2011 – Dec. 2011 **Developer**, *AROBAS unit, IBISC/CNRS*, Evry university - FRANCE.
Under Pr. Fariza Tahi supervision Development of TFold (Pseudoknot detection in RNA; 5600 lines ; JAVA) and web-portal creation to port the software. [TBC+12]
`http://tfold.ibisc.univ-evry.fr/TFold/`

Academic

Formation

2009 – 2011 **Master's degree**, *Evry university - FRANCE.*
Biology and Informatics engineering

2006 – 2009 **Bachelor's degree**, *Evry university - FRANCE.*
Biology, specializing in biuoinformatics

2007 – 2010 **Baccalauréat**, *Mennecy Highschool - FRANCE.*
Science, specializing in Physics/Chemistry

Research

Oct. 2015 – Today **phD student**, *VENISE group, LIMSI/CNRS*, Paris-Sud university - FRANCE.
Visualization and analyses of molecular simulation in virtual environments.
- Visualization of molecular structures with stereoimages based on depthmaps/textures smartphones and tablets
- Content-based navigation of molecules in virtual environments [TFBB14]
- High-level representation of structural biology for Visual Analytics

Jan. 2011 – July 2011 **Master student**, *Computational and Structural Biology group*, Utrecht university - NETHERLANDS.
Under Pr. Alexandre Bonvin supervision
Docking of protein-peptide complexes using HADDOCK approach + Development of post-analysis module for HADDOCK web server

June 2010 – Aug. 2010 **Master student**, *AROBAS unit, IBISC/CNRS*, Evry university - FRANCE.
Under Pr. Fariza Tahi supervision
Improvement of TFold for the prediction of RNA pseudoknots

7 rue marguerite – 91200 Athis-Mons

☏ *06 50 60 71 72* • ✉ *mikael.trellet@gmail.com*
✆ *https://perso.limsi.fr/trellet/* • *27 years old – driver licence*

June 2009 – Aug. 2009	**Master student**, *Structural Bioinformatics research group*, Institut Pasteur, Paris - FRANCE.
	Under Pr. Michael Nilges supervision Homology modelling of pilin, structural subunit of N. Meningitidis and N. Gonorrhoeae pili [CRMM$^+$11]

Computer skills

Bioinfo tools	PyMol, VMD, Biopython, GROMACS
Game Engine	Unity3D, Blender
Langages	C/C++/C#, Python, Bash, Javascript, Java, HTML, PHP, SQL, SPARQL, RDF(S), OWL
Base de données	MySQL, Oracle
Systèmes	MacOSX 10.5-10.10, Linux (Ubuntu,Debian)
Administration	Nagios, Virtuoso, UMD (from EGI)
Réseaux	Websocket, Protocole IP/UDP
Logiciels	Microsoft office, Open Office, Adobe Suite (Photoshop, Illustrator, Dreamweaver)

Languages

Français	**Native**
Anglais	**Fluent**
Allemand	**School level**

Other

Private tutoring	Math, Biology, Physics and Chemistry for hischool students (4 years)
Sport	Badminton (FFBA and FFSU for 10 years) – France Championship in 2009 with the Evry university team as captain / Jogging / Tennis / Squash
Scouts	Animator for 5 years and Director for 3 years
Social activities	2-years project to build 3 classrooms in Madagaskira - summer 2007

Publications

[CRMM$^+$11]	Julia Chamot-Rooke, Guillain Mikaty, Christian Malosse, Magali Soyer, Audrey Dumont, Joseph Gault, Anne-Flore Imhaus, Patricia Martin, Mikael Trellet, Guilhem Clary, et al. Posttranslational modification of pili upon cell contact triggers n. meningitidis dissemination. *Science*, 331(6018):778, 2011.
[RTS$^+$12]	João PGLM Rodrigues, Mikaël Trellet, Christophe Schmitz, Panagiotis Kastritis, Ezgi Karaca, Adrien SJ Melquiond, and Alexandre MJJ Bonvin. Clustering biomolecular complexes by residue contacts similarity. *Proteins: Structure, Function, and Bioinformatics*, 80(7):1810–1817, 2012.
[TBC$^+$12]	Fariza Tahi, Mederich Besnard, Gabriel Chandesris, Sébastien Tempel, Mikael Trellet, et al. Evryrna: bioinformatics platform for non-coding rna. *Proc. de la 13ème Journées Ouvertes en Biologie, Informatique et Mathématiques (JOBIM 2012)*, pages 493–494, 2012.
[TFBB14]	Mikael Trellet, Nicolas Férey, Marc Baaden, and Patrick Bourdot. Content-guided navigation in multimeric molecular complexes. In *BIOIMAGING*, pages 76–81, 2014.
[TMB13]	Mikael Trellet, Adrien SJ Melquiond, and Alexandre MJJ Bonvin. A unified conformational selection and induced fit approach to protein-peptide docking. *PloS one*, 8(3):e58769, 2013.