Dominic Philip Tölle

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Tel:	+49(0)176-31424004	**Nationality:**	Irish
E-mail:	dominic.tolle@gmail.com	**Sex:**	male
Social Networks:	https://de.linkedin.com/in/dominic-tölle-795298b2	**DoB:**	10. December 1976

Education:

2004 - 2009 **Ph.D. (Bioinformatics), University of Cambridge,** Hughes Hall College,
Predoctoral Fellowship awarded by the European Molecular Biology Laboratory to work at the European Bioinformatics Institute, Cambridge, UK.
Under the supervision of: *Nicolas Le Novère*
Work included design and development of a particle-based stochastic simulation software in Java
Project title: *Investigating the Consequences of AMPA Receptor Diffusion on Long-term Potentiation using Single-Particle Modelling Approaches*

2003 - 2004 **MRes in Bioinformatics**, **University of York**
Distinction Grade.
Coursework included: C/C++, Perl, molecular sequence and protein structure analysis, phylogeny, database mining, statistical and numerical skills, transferable skills
Work included 3 month project in the Laboratory of Computational Biology at the Universidad Nacional Autónoma de México, Cuernavaca, Mexico.

2000 – 2001 **Higher Diploma in Computer Science, University College Dublin**
Distinction Grade.
Coursework included: Programming, System Analysis and Design, Interactive Multimedia Systems, Networks, Operating Systems, Computer Architecture, Artificial Intelligence, Program Design and Verification

1994 – 1998 **B.A. (mod.) (Hons.) Biochemistry, Trinity College Dublin**
Grade 2.1.
Coursework included: Biochemistry, Bioinformatics, Genetics, Microbiology, Chemistry, Mathematics

Work Experience:

Aug ’11 – Present **IT-specialist at mgm Technology Partners, Berlin (Germany)**
Key areas of the job included development of customer (E-commerce & Insurance industry) software projects (mainly Java, Javascript, CSS, HTML, SQL, numerous frontend & backend frameworks)

July ’09 – Dec ’10 **Bioinformatician for AG Dieterich, BIMSB-MDC, Berlin (Germany)**
Key areas of the job included collection and analysis of Mass Spectrometry data. Design and implementation of tools and data repositories for experimental meta-data.

Oct ’02 – Oct ‘03 **Bioinformatics Research Assistant for MEROPS Protease Database, Sanger Institute, Cambridge (UK)**
Key areas of the job included collection and analysis of data for inclusion in the database, and the design and maintenance of computing tools for the analysis of data (Perl, SQL, HTML)

Oct ’01 – Oct ‘02 **Bioinformatics Research Assistant for MEROPS Protease Database, Babraham Institute, Cambridge (UK)**
See above

Oct. ’98 – May ‘00	**Laboratory work experience in Biochemistry, TCD, Dublin** Laboratory research into the mechanism of synaptic apoptosis. In addition, supervised Science/Medicine undergraduate students as a Biochemistry Teaching Assistant. Also provided private biochemistry tuition for Science undergraduates.

Achievements:

European Bioinformatics Institute (EBI) Predoc Representative '05 – '06.
Responsibilities included: Liaising between Students and Supervisors, organisation of training course for Predoctoral fellows, looking after interview candidates, representing EBI Predoctoral fellows.

Higher Diploma in Computer Science Class Representative ’00 – ’01.
Responsibilities included: Liaising between Students and Lecturers, organisation of various social activities.

Treasurer of Dublin University Biochemical Society ’99 – ’00.
Responsibilities included: acquisition of funding, budgeting and handling of finances, organising and entertaining guest speakers, organising social events

Languages
Bilingual English/German, basic knowledge of Spanish

Interests :

Swing dancing, hiking, diving

Selected Publications:

Tolle DP, Le Novère N; ***Current Bioinformatics*** *1: 315-320 (2006)*
Particle-based Stochastic Simulation in Systems Biology

Tolle DP, Le Novère N; ***BMC Syst Biol*** *4:24 (2010)*
Meredys, a multi-compartment reaction-diffusion simulator using multistate realistic molecular complexes

Tolle DP, Le Novère N; ***BMC Syst Biol*** *4:25 (2010)*
Brownian Diffusion of AMPA Receptors Is Sufficient to Explain Fast Onset of LTP

Complete list attached separately

References:

Neil Rawlings,
EMBL-EBI,
Wellcome Genome Campus,
Hinxton,
Cambridge CB10 1SD,
United Kingdom
email: ndr@ebi.ac.uk

Nicolas Le Novère,
Babraham Institute,
Babraham Research Campus,
CB22 3AT Cambridgeshire,
United-Kingdom
email: lenov@babraham.ac.uk

Arbeitszeugniss **AG Dietrich, BIMSB-MDC** available on demand

Publications:

Barrett AJ, **Tolle DP**, Rawlings ND; ***Biological Chemistry*** *384(6):873-82 (2003)*
Managing peptidases in the genomic era

Rawlings ND, **Tolle DP**, Barrett AJ**;** ***Biochemical Journal*** *378(3):705-16 (2004)*
Evolutionary families of peptidase inhibitors

Rawlings ND, **Tolle DP**, Barrett AJ; ***Nucleic Acids Research*** *32: D160-4(2004)*
MEROPS: The peptidase database

Le Novère N, **Tolle DP**; ***Proceedings of the 4th Workshop on Computation of Biochemical Pathways and Genetic Networks*** *(2005)*
Particle-based stochastic simulations

Tolle DP, Le Novère N; ***Current Bioinformatics*** *1: 315-320 (2006)*
Particle-based Stochastic Simulation in Systems Biology.

Tolle DP, Le Novère N; ***BMC Syst Biol*** *4:24 (2010)*
Meredys, a multi-compartment reaction-diffusion simulator using multistate realistic molecular complexes

Tolle DP, Le Novère N; ***BMC Syst Biol*** *4:25 (2010)*
Brownian Diffusion of AMPA Receptors Is Sufficient to Explain Fast Onset of LTP

Waltemath D, Adams R, Beard D, Berman F, Bhalla US, Britten R, Chelliah V, Cooling M, Cooper J, Crampin E, Garny A,Goryanin I, Hoops S, Hucka M, Hunter P, Klipp E, Kolpakov F, Laibe C, Miller A, Morau I, Nickerson D, Nielsen P,Nikolski M, Sahle S, Sauro H, Schmidt H, Snoep J, **Tolle D**, Wolkenhauer O, Zaitlen B, Le Novère N; ***PloS Comp. Biol****,7(4):e1001122 (2011)*
Minimum Information About a Simulation Experiment (MIASE)

Adamidi C, Wang Y, Gruen D, Mastrobuoni G, You X, **Tolle D**, Dodt M, Mackowiak S, Gogol-Doering A, Rybak A,Kempa S, Dieterich C, Rajewsky N, Chen W; ***Genome Research****, 21(7): 1193-200 (2011*)
De novo assembly and validation of a metazoan transcriptome by massive parallel sequencing and shotgun proteomics