

ELODIE LAINE

MAITRE DE CONFÉRENCES

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ORIGINAL ARTICLES IN INTERNATIONAL PEER-REVIEW JOURNALS

1 submitted manuscript

40. Behbahani Y. M., P. Saighi, F. Corsi, **E. Laine*** and A. Carbone* (2022). LEVELNET: diving into the multiple layers of protein-protein physical interaction networks. *bioRxiv*. doi: 10.1101/2021.07.31.453756

39 published research articles, 13 as first author, 10 as co-corresponding last or next-to-last author (supervised students or post-doc are underlined).

39. Vicedomini R., J-P. Bouly, **E. Laine**, A. Falciatore and A. Carbone (2022) Multiple probabilistic models extract features from protein sequence data and resolve functional diversity of very different protein families. *Mol Biol Evol.* (accepted) doi: 10.1101/717249

38. Zea DJ., H. Richard* and **E. Laine***. (2022) ASES: Visualising evolutionary conservation of alternative splicing in proteins. *Bioinformatics* (accepted)

37. Dequeker C., Y. M. Behbahani, L. David, **E. Laine***, and A. Carbone* (2022). From complete cross-docking to partners identification and binding sites predictions. *PLoS Comput Biol* 18: e1009825

36. Kryshtafovych A. *et al.* (2021) Modeling severe acute respiratory syndrome—coronavirus-2 proteins in the Critical Assessment of Structure Prediction-commons experiment. *Proteins* 89: 1987–1996

35. Zea DJ., S. Laskina, A. Baudin, H. Richard* and **E. Laine***. (2021) Assessing conservation of alternative splicing with evolutionary splicing graphs. *Genome Research* 31:1462-1473

34. Danko D. *et al.* (2021) A global metagenomic map of urban microbiomes and antimicrobial resistance. *Cell* 184:3376-3393.e17

33. **Laine E.*** and S. Grudinin* (2021). HOPMA: Boosting protein functional dynamics with colored contact maps. *J. Phys. Chem. B.* 125:2577–2588

32. Karami Y.*, P. Saighi, R. Vanderhaegen, S. Longhi, D. Gerlier, **E. Laine*** and A. Carbone* (2020) Predicting substitutions to modulate disorder and stability in coiled-coils. *BMC Bioinformatics* 21:1-20

31. Grudinin S.+, **E. Laine+** and A. Hoffmann (2020) Predicting protein functional motions: an old recipe with a new twist. *Biophys. J.* 118:2513-2525 (+equal contributions)

30. Ait-hamlat A., DJ. Zea, A. Labeeuw, L. Polit, H. Richard* and **E. Laine***. (2020) Transcripts' evolutionary history and structural dynamics give mechanistic insights into the functional diversity of the JNK family. *J Mol Biol* 432:2121-2140.

29. Corsi F., R. Lavery, **E. Laine*** and A Carbone*. (2019) Multiple protein-DNA interfaces unravelled by evolutionary information, physico-chemical and geometrical properties. *PLoS Comput Biol* 16:e1007624

28. Lensink MF., G. Brysbaert, N. Nadzirin, S. Velankar, RAG. Chaleil, T. Gerguri *et al.* (2019) The CASP13-CAPRI experiment. *Proteins: Structure, Function, and Bioinformatics* 87: 1200-1221.

27. **Laine E.***, Y. Karami and A. Carbone*. (2019) GEMME: a simple and fast global epistatic model predicting mutational effects. *Mol Biol Evol.* 36:2604–2619

26. Dequeker C., **E. Laine*** and A. Carbone*. (2019) Decrypting protein surfaces by combining evolution, geometry, and molecular docking. *Proteins.* 87:952-965

25. Karami Y., T. Bitard-Feildel, **E. Laine*** and A. Carbone*. (2018) "Infostery" analysis of short molecular dynamics simulations identifies highly sensitive residues and predicts deleterious mutations, *Scientific Reports.* 8 :16126

24. Raucci R., **E. Laine**, A. Carbone. (2018) Local Interaction Signal Analysis Predicts Protein-Protein Binding Affinity. *Structure*. 26:905-915
23. Dequeker C., **E. Laine*** and A. Carbone*. (2017) INTerface Builder: A Fast Protein-Protein Interface Reconstruction Tool. *J Chem Inf Model.*, 57:2613-2617
22. **Laine E.** and A. Carbone. (2017) Protein social behaviour gives a stronger signal for protein partner identification than geometrical docking, *Proteins*, 85:137-154
21. Ripoche H.⁺, **E. Laine⁺**, N. Ceres and A. Carbone. (2017) JET2 Viewer: a database of predicted multiple, possibly overlapping, protein-protein interaction sites for PDB structures, *Nucl. Acids Res. (database issue)*, 45:D236-D242 (+equal contributions)
20. T. Delaveau, D. Davoine, A. Jolly, A. Vallot, J.O. Rouviere, A. Gerber, S. Brochet, M. Plessis, R. Roquigny, J. Merhej, T. Leger, C. Garcia, G. Lelandais, **E. Laine**, B. Palancade, F. Devaux and M. Garcia. (2016) Tma108, a putative M1 aminopeptidase, is a specific nascent-chain associated protein in *Saccharomyces cerevisiae*. *Nucl. Acids Res.*, 44:8826-8841
19. Champeimont R., **E. Laine**, S.-W. Hu, F. Penin and A. Carbone. (2015) Coevolution analysis of Hepatitis C virus genotypes to identify the structural and functional dependency network of viral proteins, *Sci. Reports*, 6:26401
18. **Laine E.*** and A. Carbone*. (2015) Local geometry and evolutionary conservation of protein surfaces reveal the multiple recognition patches in protein-protein interactions. *PLoS Comput Biol*, 11: e1004580
17. Karami Y., **E. Laine*** and A. Carbone*. (2015) Dissecting protein architecture with communication blocks and communicating segment pairs. *BMC Bioinformatics*, 17:13
16. Couve S., C. Ladroue, **E. Laine**, K. Mahtouk, J. Guégan, S. Gad, H. Lejeune, M. Le Gentil, G. Nuel *et al.* (2014) Genetic evidence of a precisely tuned dysregulation in the hypoxia signaling pathway during oncogenesis. *Cancer Research* 74:6554-64
15. Chauvot de Beauchêne I., A. Allain, N. Panel, **E. Laine**, A. Trouve, P. Dubreuil and L. Tchertanov. (2014) Hotspot mutations in KIT receptor differentially modulate its allosterically coupled conformational dynamics: impact on activation and drug sensitivity. *PLoS Comput Biol* 10:e1003749
14. Da Silva Figueiredo Celestino Gomes P., N. Panel, **E. Laine**, P.G. Pascutti, E. Solary and L. Tchertanov. (2014) Differential effects of CSF-1R D802V and KIT D816V homologous mutations on receptor tertiary structure and allosteric communication. *PLoS ONE* 9:e97519
13. Allain A., I. C. de Beauchêne, F. Langenfeld, Y. Guarracino, **E. Laine**, L. Tchertanov (2014) Allosteric pathway identification through network analysis: from molecular dynamics simulations to interactive 2D and 3D graphs. *Faraday discussions* 169:303-321
12. Lopes A., S. Sacquin-Mora, V. Dimitrova, **E. Laine**, Y. Ponty and A. Carbone. (2013) Protein-protein interactions in a crowded environment: an analysis via cross-docking simulations and evolutionary information. *PLoS Comput Biol*. 9:e1003369
11. Arora R., I.C. de Beauchene, J. Polanski, **E. Laine** and L. Tchertanov. (2013) Raltegravir flexibility and its impact on recognition by the HIV-1 IN targets. *J Mol Recognit.* 26:383-401
10. **Laine E.**, C. Auclair and L. Tchertanov. (2012) Allosteric Communication across the Native and Mutated KIT Receptor Tyrosine Kinase. *PLoS Comput Biol*. 8:e1002661
9. Ni X.⁺, S. Abdel-Azeim⁺, **E. Laine⁺**, R. Arora, O. Osemwota, AG. Marcelin, V. Calvez, JF. Mouscadet and L. Tchertanov. (2012) *In silico* and *in vitro* Comparison of HIV-1 Subtypes B and CRF02_AG Integrase Susceptibility to Integrase Strand Transfer Inhibitors. *Adv Virol*. 2012:548657 (+equal contributions)
8. Selwa E., **E. Laine** and TE. Malliavin. (2011) Differential role of Calmodulin and Calcium ions in the stabilization of the catalytic domain of adenyl cyclase CyaA from *Bordetella pertussis*. *Proteins*. 80:1028-40
7. Serafin K., P. Mazur, A. Bak, **E. Laine**, L. Tchertanov, JF. Mouscadet, J. Polanski. (2011) Ethyl malonate amides: A diketo acid offspring fragment for HIV integrase inhibition. *Bioorg Med Chem*. 19:5000-5

- 6. Laine E.***, I. Chauvot de Beauchêne, D. Perahia, C. Auclair, L. Tchertanov*. (2011) Mutation D816V alters the internal structure and dynamics of KIT cytoplasmic region: implications for dimerization and activation mechanisms. *PLoS Comput Biol.* 7:e1002068
- 5. Laine E.**, L. Martínez, A. Blondel and TE. Malliavin. (2010) Activation of the edema factor of *Bacillus anthracis* by calmodulin: evidence of an interplay between the EF-calmodulin interaction and calcium binding. *Biophys J.* 99:2264-72
- 4. Laine E.**, C. Goncalves, J. Karst, A. Lesnard, S. Rault, W.-J. Tang, TE. Malliavin, D. Ladant and A. Blondel. (2010) Use of allostery to identify inhibitors of calmodulin-induced activation of *Bacillus anthracis* edema factor. *Proc. Natl. Acad. Sci. U.S.A.* 107:11277-82
- 3. Martínez L., E. Laine**, TE. Malliavin, M. Nilges and A. Blondel. (2009) ATP conformations and ion binding modes in the active site of anthrax edema factor: A computational analysis. *Proteins.* 77:971-83
- 2. Laine E.**, A. Blondel and TE. Malliavin. (2009) Dynamics and energetics: a consensus analysis of the impact of calcium on EF-CaM protein complex. *Biophys. J.* 96:1249-63
- 1. Laine E.**, JD. Yoneda, A. Blondel and TE. Malliavin. (2008) The conformational plasticity of calmodulin upon calcium complexation gives a model of its interaction with the oedema factor of *Bacillus anthracis*. *Proteins.* 71:1813-29

REVIEW ARTICLES IN INTERNATIONAL PEER-REVIEW JOURNALS

- Laine E.**+, S. Eismann+, A. Elofsson+, S. Grudinin+. (2021) Protein sequence-to-structure learning: Is this the end (-to-end revolution)? *Proteins* (+equal contributions)
- Colas C., **E. Laine.** (2020) Targeting Solute Carrier Transporters through Functional Mapping. *Trends Pharmacol Sci.* 21:S0165-6147(20)30255-8.
- Laine E.**, L. Martínez, D. Ladant, TE. Malliavin and A. Blondel. (2012) Functional Molecular Motions in Edema Factor of Anthrax Toxin: a Structural and Energetic Interplay to Target for Drug Design (review). *Toxins* 4:580-604

EDUCATION ARTICLES IN INTERNATIONAL PEER-REVIEW JOURNALS

- N. Abdollahi, A. Albani, E. Anthony, A. Baud, M. Cardon, ..., **E. Laine*** and A. Lopes*. (2018) Meet-U: Educating through research immersion. *PLoS Comput Biol.* 14:e1005992 (*co-corresponding authors)

PATENTS

- Tchertanov L., **E. Laine**, A. Allain and I. Chauvot de Beauchêne (2013) MOdular NETwork Analysis (MONETA) version 2.0. *IDDN.FR.001.020012.000.S.P.2014.000.31235*
- Malliavin T.E., **E. Laine**, A. Blondel, D. Ladant, J. Karst, S. Rault and A. Lesnard (2011) Methods of identifying compounds that inhibit the activation of a biomolecule and methods of treatment using the compounds. *US Patent* n° 20110065782

ORAL COMMUNICATIONS WITH PROCEEDINGS

- Laine E.** (2017) Decrypting how protein move and change their shape. *16th International Symposium on Mathematical and Computational Biology, Tianjin, CN, 30 Oct. – 5 Nov. 2016, published in Mathematical Biology And Biological Physics, edited by Rubem P. Mondaini*
- Laine E.**, H. Ripoche and A. Carbone. (2016) Local geometry and evolutionary conservation of protein surfaces reveal the multiple recognition patches in protein-protein interactions *60th Annual Meeting of the Biophysical-Society, Los Angeles, CA, USA, published in Biophys J.* 110:S347A-348A
- Laine E.** and A. Carbone. (2013) Identification of protein interaction partners from shape complementarity molecular cross-docking. *New Trends in Image Analysis and Processing - ICIAP 2013, Naples, IT, published in LNCS* 8158:318-325

Laine E., I. Chauvot de Beauchêne, C. Auclair and L. Tchertanov. (2011) Propagation of D816V/H mutation effects across KIT receptor. *8th European Biophysics Congress*, August 23-27 2011, Budapest, HN, published in *Eur. Biophys. J. Biophys. Lett.* 40:S109

Laine E., JD. Yoneda, A. Blondel & TE. Malliavin. (2009) The Residue Network Architecture of a Protein-Protein Complex Reveals the Linkage between Dynamics and Energetics. *Biophysical Society 53rd Annual Meeting*, Feb. 28. - March 4 2009, Boston, MA, USA, published in *Biophys. J.* 96:S585a

Laine E., J. Huguenin & TE. Malliavin. (2007) Analysis of the calcium-dependent activation of the anthrax oedema factor by calmodulin. *6th European Biophysical Congress*, July 14-19, London, UK, published in *Eur. Biophys. J.* 36:S107

INVITED SEMINARS IN CONFERENCES, WORKSHOPS, SCHOOLS

Lessons from Protein Evolution: from Sequences through Structures to Functions, and back, *Plenary Annual Meeting of the GDR Molecular Bioinformatics*, Nov. 23 2021, Lyon, FR

Machine learning in the post CASP14 era : from protein structure to protein interactions, *algoSB Winter School*, Nov. 7-12 2021, Marseille, FR (seminar + hands-on)

Mutational scanning predictions, *INDEPTH Training School on Protein-Protein Interactions*, Feb. 10 2021, online (seminar + hands-on)

Protein sequence-structure-dynamics-function relationships: efficient tools for mining experimental and simulated data, *PDCLifeS 2020 workshop*, Aug. 24 2020, online

Prediction d'effets de mutations à partir de l'histoire évolutive des protéines, *Evolution à Paris*, Nov. 21 2019, Paris, FR

Learning about protein-molecules interactions, *MASIM kick-off meeting*, Nov. 16-17 2017, Paris, FR

Protein infostery : a new way to look into protein motions to predict deleterious mutations, *16th International Symposium on Mathematical and Computational Biology*, invitée par R. Mondaini, Oct. 30 – Nov. 5 2016, Chern Institute of Mathematics, Nankai University, Tianjin, CN

Protein evolution and structural dynamics, *Journée MESU*, invited by P. Frey, Dec. 9 2014, ICS, Paris, FR

Etude des mécanismes d'activation de cibles thérapeutiques & recherche d'inhibiteurs, *Congrès GGMM 2011*, as the recipient of the GGMM award, May 30 – June 1 2011, La Rochelle, FR

Use of allostery to identify inhibitors of calmodulin-induced activation of *Bacillus anthracis* Edema Factor, *Séminaire "EMBO Practical Course on Biomolecular Simulation"*, July 2010, Institut Pasteur, Paris, FR

ORAL PRESENTATIONS (SELECTED)

Deciphering protein sequence variations' functional outcomes, *Artificial Intelligence and Structural Biology Workshop*, Aug. 2-6 2021, CIRM, Marseille, FR

Evolutionary decomposition and structural characterization of functionally distinct protein isoforms, *MASIM colloquium @BIM meeting days*, Nov. 5 2019, Paris, FR

Meet-U: education through research immersion, *ISMB-ECCB 2019*, July 21-25 2019, Basel, CH

Towards a large-scale prediction of protein partners, *MAPPING conference – Understanding protein interactions: from molecules to organisms*, April 24-26 2017, Lyon, FR

The impact of alternative splicing evolution on protein structure and conformational dynamics, *1st qBio mini-Workshop*, Feb. 20-21 2017, Milan, IT

Accurately predicting and dissecting protein-protein interfaces with Joint Evolutionary Trees, *Bringing Maths to Life Meeting*, Oct. 27-29 2014, Naples, IT

A Modular Network Analysis (MONETA) of Protein Structures for Exploring and Predicting Allosteric Communication, *JOBIM 2012*, 2012, Rennes, FR

Propagation de perturbation à travers les structures protéiques : le récepteur tyrosine kinase KIT, *Atelier "Modélisation Gros Grains des Système Biologiques"*, Nov. 23-24 2011, Paris, FR

Role of Mutation D816V in the deregulation of KIT receptor: hypotheses & perspectives, *Modeling and Beyond, 2nd ENSC-Schrödinger Meeting/Workshop*, May 10-11 2011, Cachan, FR

Mutation D816V alters the internal structure and dynamics of KIT cytoplasmic region, *CECAM "Dynamics and Thermodynamics of Biomolecular Recognition"*, May 5-7 2011, Palaiseau, FR

Effect of the D816V mutation on c-Kit kinase domain: implications for the receptor molecular recognition, *1st Aegean International Conference on Molecular Recognition*, June 6-11 **2010**, Heraklion, GR

Structural mobility of the anthrax toxin and search for inhibitors, *MGMS Annual Molecular Modelling Workshop*, Sept. 6-7 **2009**, Erlangen, DE

Mobilité Structurale de la Toxine de l'Anthrax et Recherche d'Inhibiteurs, *16^{ème} Congrès Annuel du GGMM*, May 5-7 **2009**, Mittelwihr, FR

Modeling the effect of Ca²⁺ through the residue network of the complex between EF and calmodulin, *Computer Simulation and Theory of Macromolecules*, April 18-20 **2008**, Hünfeld, DE

The conformational plasticity of CaM upon Ca²⁺ complexation gives a model of its interaction with EF, *CCPB Annual Conference: frontiers of biomolecular simulation*, Jan. 7-9 **2008**, Bristol, UK

Analyse de l'activation de facteur oedémateux de *Bacillus anthracis* par dynamique moléculaire, *Atelier "Modélisation Gros-Grains pour la Biologie et la Matière Molle"*, Feb. **2007**, Evry, FR

POSTER PRESENTATIONS (SELECTED)

DLA-Ranker: Evaluating protein docking conformations with many locally oriented cubes. Machine Learning for Structural Biology Workshop at the Thirty Fifth Conference on Neural Information Processing Systems (NeurIPS), Dec. 13 **2021**, online

Assessing conservation of alternative splicing with evolutionary splicing graph, CSHL Virtual Meeting: Eukaryotic mRNA Processing, Aug. 24-27 **2021**, online

GEMME: a simple and fast global epistatic model predicting mutational effects, *ISMB-ECCB 2019*, July 21-25 **2019**, Basel, CH

Decrypting protein surfaces using evolutionary information, geometry and docking. *7th CAPRI evaluation meeting*, April 3-5 **2019**, Cambridge, UK

Local geometry and evolutionary conservation of protein surfaces reveal the multiple recognition patches in protein-protein interactions, *6th CAPRI evaluation meeting*, 17-19 avril **2016**, Tel-Aviv, IL

Accurate prediction of protein-protein contacts: from patches to sites, *ISMB/ECCB Conference*, July 21-23 **2013**, Berlin, DE

Propagation of point mutation effect throughout tyrosine kinase c-Kit structure, probed by MD, *2nd NaBi Workshop, CNRS-Weizmann*, Nov. 20-23 **2010**, Annecy, FR

Propagation of point mutation effect throughout tyrosine kinase c-Kit structure, probed by MD, **TAGp 2010**, Oct. 20-22 **2010**, Annecy-le-Vieux, FR

Analysis of the activation of the edema factor of *Bacillus anthracis*, probed by molecular dynamics, *20th Pasteur Weizmann Symposium: Structural Biology*, June 21-23 **2006**, Paris, FR

INVITED SEMINARS

Functional protein sites deciphered by evolution and conformational dynamics, Genopole seminar, invited by C. Maroun, Feb. 24 **2020**, Evry, FR

Functional protein sites deciphered by evolution and conformational dynamics, Structural Biology Institute seminar, invited by S. Grudinin, Jan. 27 **2020**, Grenoble, FR

Functional protein sites deciphered by evolution and conformational dynamics, Guest lecture at University of Vienna/MolTag Doctoral Program, invited by C. Colas, Dec. 19 **2019**, Vienna, AU

Modeling protein-protein interactions at large scale, *Séminaire CMLA*, invited by L. Tchertanov, Nov. 22 **2018**, CMLA, Cachan, FR

Modeling protein-protein interactions at large scale, Première journée de Biologie Structurale à l'UPMC, Oct. 2 **2017**, Paris, FR

Protein evolution and structural dynamics, *Séminaire EMC2*, invited par Y. Maday, April 24 **2015**, LIP6, Paris, FR

Méthodes de modélisation moléculaire pour extraire des réseaux fonctionnels de résidus dans les protéines, *Séminaire Math-Bio*, invited by V. Milisik, March 1 **2013**, LAGA, Paris 13, FR

Mécanismes d'activation des récepteurs tyrosine kinases par des mutations oncogènes, *Séminaire LERMIT*, invited by R. Fischmeister, Dec. 5 **2011**, UMR-S 769, Châtenay-Malabry, FR

Modeling the regulatory impact of cancer mutation on c-Kit kinase structure, dynamics and stability *Séminaire LBT*, invited by S. Sacquin-Mora, 14 oct. 2010, LBT, IBPC, Paris, FR

Interview at D.E. Shaw Research, invited by Y. Shan, Oct. 6 **2010**, New York, NY, USA

Mobilité structurale de la toxine de l'anthrax et recherche d'inhibiteurs, *Séminaire 3Bio*, invited by M. Marchi, Dec 3 **2008**, CEA de Saclay, FR

INTERNAL OR WORK GROUP SEMINARS

All letters are not equal, *IBPS Day*, 6 décembre **2018**, Paris, FR

Protein social behaviour makes a stronger signal for partner identification than surface geometry, *6th MAPPING Meeting*, Jan. 25 **2016**, Lyon, FR

Wait and see: JET2 false positives are true positives, *5th MAPPING Meeting*, July 3 **2015**, Paris, FR

The geometry of protein-protein interfaces reveals the multiple origins of recognition patches, *Séminaire Institut de Biologie Paris-Seine*, March 27 **2015**, IBPS, Paris, FR

Accurately predicting and dissecting protein-protein interfaces with Joint Evolutionary Trees, *4th MAPPING Meeting*, Dec 3 **2014**, Lyon, FR

Accurate prediction of protein-protein contacts with JET: from patches to sites, *3rd MAPPING Meeting*, May 6 **2014**, Paris, FR

Identification of protein interaction partners from shape complementarity molecular docking, *2nd MAPPING Meeting*, Sept. 16 **2013**, Lyon, FR

Predicting protein binding patches by combining evolutionary signals, physico-chemical and structural properties, *Kickoff Meeting of the MAPPING Project*, Jan. 23 **2013**, Paris, FR

Mobilité structurale de la toxine de l'anthrax et recherche d'inhibiteurs, *Journées Dép. de Biologie Structurale et Chimie*, Institut Pasteur, Dec. 13-14 **2007**, Paris, FR

ORGANISATION OF SYMPOSIA OR CONFERENCES

Artificial intelligence and structural biology, August 2-6 **2021**, Marseille, FR — with K. Fidelis, S. Grudinin and J. Moulton

Integrative Structural Modeling Symposium, July 7 **2021**, Paris, FR — with J. Andreani, G. André-Lerou, B. Bardiaux, S. Baud, I. Chauvot de Beauchêne and J. Martin

Meet-4EU+ Symposium, Jan. 25 **2021**, online — with L. Carron, J. Bernardes, C. Herrmann, M. Novotny and B. Wilczynski

Non-canonical amino acids Symposium, Oct. 21-22 **2019**, Paris, FR — with F. Bihel, T. Brigaud, G. Chaume, O. Lequin, E. Miclet and S. Ye-Lehmann

Meet-U Symposia, Jan. 2017, **2018 (@SU)**, 2019, 2020, Ile-de-France, FR — with A. Lopes and J-C. Gelly

UPMC Young Researchers' Meeting: Modeling Complex Biological Systems, Dec. 13 **2017**, Paris, FR — with A. Carbone

Symposium « Biomath: Formal methods in the eyes of biological data », *SMAI 2017*, June 5-7 **2017**, Ronce-les-Bains, FR — with A. Carbone

Symposium on the « Evolution of Alternative Splicing », *Society for Molecular Biology and Evolution (SMBE) annual congress*, July 12-16 **2015**, Vienne, AT — with J. Roux and H. Richard

ORGANISATION OF SUMMER SCHOOLS

Summer school « Scientific Trends at the Interfaces », Institut des Sciences du Calcul et des Données, 17 juil-11 août **2017**, Roscoff, FR (avec A. Carbone et P. Frey)

Summer school « Scientific Trends at the Interfaces – Bioinformatics and Visualization », Institut du Calcul et de la Simulation, 15 juil-8 août **2014**, Roscoff, FR (avec A. Carbone, P. Frey, C. O. Ausoni et J. Tierny)

DIFFUSION OF SCIENTIFIC CULTURE

Sharing of experience with young women, Sorbonne Université and Rêv'Elles, 11 Feb. 2021, online

Participation to articles for the general public in Sciences et Vie Junior (11/2021), La Recherche (07/2021), [Sciences et Avenir](#), [Sciences et Vie](#) and in the [Data Analytics Post](#)

Participation to the design of a [video for the general public](#), realized by La Bande Destinée (2019)

Sharing of experience with high school students, Institut Henri Poincaré, 17 Dec. 2015, Paris, France

PARTICIPATION IN RECRUITMENT OR PHD JURYS

PhD defences: Nicolas Guillaudeux, Dec. 16 2021, *reviewer*; Nicolas Scalzitti, Sept. 29 2021, *reviewer*; Irène Pitard, Oct. 23 2020, Paris, *examiner*; Guillaume Pagès, Sept. 12 2019, Grenoble, *examiner*; Akhila Melarkode Vattekatte, March 25 2019, Paris, *examiner*

Recruitment of a Maître de Conférences at the University of Lille 1 (64 MCF 1248, May 2 2017)

PARTICIPATION IN EDITORIAL BOARDS

Review Editor of *Frontiers in Molecular Biosciences*, section *Mathematics of Biomolecules*

REVIEWING OF ARTICLES AND GRANT APPLICATIONS

Manuscripts submitted to Molecular Biology and Evolution, Bioinformatics, PLoS Computational Biology, Nucleic Acids Research, Proteins: Structure, Function and Bioinformatics, NAR Genomics and Bioinformatics, PLoS ONE, Scientific Reports, Frontiers in Molecular Biosciences, Computational Biology and Chemistry, Journal of Complex Networks, Journal of Chemical Information and Modeling

Grant applications submitted to the French National Research Agency, the Austrian Science Fund, the Medical Research Council and PRACE

Contributions submitted to WABI 2022, 2021 (+ chairing of a session), ISMB-ECCB 2021, 2019, ACM-BCB 2019

PARTICIPATION IN PHD COMMITTEES

Barthélémy Meynard (Oct. 8 2021, 1st year), Adam Bellaïche (July 21 2021, 2nd year), Blandine Baudon (May 19 2021, 1st year), Martin Romei (Oct. 8 2020, 2nd year, Sept. 17 2019, 1st year), Kai Shimagaki (Jan. 8 2021, 3rd year, Nov. 7 2019, 1st year), Chloé Quignot (July 4 2019, 2nd year)