

Alejandro Giorgetti - Curriculum Vitae

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- Since 2018 – 2018** ***Associate Professor*** at the University of Verona. Department of Biotechnology. Verona, Italy
Italian national qualification for full professorship in Biochemistry
- Since 2015 -** ***Research associate*** at IAS-5 / INM-9: Computational Biomedicine - Institute for Advanced Simulation (IAS) / Institute of Neuroscience and Medicine (INM) - Forschungszentrum Jülich, Germany
- 2011 – 2015** ***Visiting Scientist*** at the German Research School for Simulation Sciences (GRS). Juelich, Germany
- 2007- 2017** ***Assistant Professor (tenured)*** at the University of Verona. Department of Biotechnology. Verona, Italy
- 2004 - 2007** Postdoctoral research fellow at the Department of Biochemical Sciences, University of Rome "La Sapienza". Rome, Italy.
- 2006-2009** Research fellow at the Bioinformatics Program, [CRS4](#), Pula (CA). Sardegna, Italy
- 2004** PhD in Statistical and biological Physics, cum laude. [SISSA](#) (Scuola Internazionale Superiore di Studi Avanzati. Trieste, Italy (10-10-2004)
- 1999 - 2000** Quality Control expert of the SPECT system. Sanatorio Privado del Sur. Bahia Blanca, Argentina
- 2000** Master degree in Medical Physics at the Universidad de Buenos Aires ([UBA](#)), Argentina
- 1997 - 1999** Internship for Medical Physics activities supported by the Universidad Nacional del Sur. Bahia Blanca, Argentina.
- 1996** Licenciado en Fisica (Degree in Physics) at the Universidad Nacional del Sur ([UNS](#)). Bahia Blanca, Argentina (18-12-1996).

Reference web pages:

University of Verona: <http://www.dbt.univr.it/?ent=persona&id=3845>

Computational Biomedicine (INM-9/IAS-5), Forschungszentrum Jülich (FZJ): <https://www.fz-juelich.de/en/ias/ias-5/about/staff/alejandro-giorgetti>

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RESEARCH GROUPS:

APPLIED BIOINFORMATICS GROUP. - Department of Biotechnology, University of Verona

Members:

- **Alejandro Giorgetti (Principal Investigator)**
- Rui Ribeiro Fernandes (**Assistant Professor**, Verona)
- Klevia Dishnica (PhD student)
- Francesco Fontanive (PhD student)
- Filippo Baldessari (Research assistant, Verona)
- Riccardo Vanini (Master student, Verona)
- Massimo Sossai (Master student, Verona)

Former members:

- Francesco Musiani (Visiting Postdoc - SISSA, Trieste)
- Eda Suku (PhD student, Verona)
- Mangesh Damre (visiting PhD, SISSA, Italy)
- Sergio Paul Marin Vargas (PhD and Postdoc, Verona)
- Massimo Sandal (Postdoc – Dept Biotechnology, Verona)
- Stefano Piccoli (PhD student, Verona)
- Ivan Arcangelo Sciascia (PhD student, Verona)
- Mirko Busato (PhD student, Verona)
- Caterina Calligaris (Master student, Verona)

- Katia Galentino (Master student, visiting from Bari University)
- Aldo Tocci (Master student, Verona)
- Stefano Massella (Master Student)
- Matteo Mazzocca (graduate stage)
- Emiliano Maresi (master student)
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STRUCTURAL NEUROINFORMATICS – *Computational Medicine Institute (IAS-5/INM-9) Forschungszentrum Jülich, Germany*

Members

- Prof. Paolo Carloni (Director of the Institute)
- Dr. Mercedes Alfonso Prieto (PI)
- **Prof. Alejandro Giorgetti (guest scientist)**
- Giuliano Santarpia (PhD student)

Former members

- Fabrizio Fierro (PhD student)
- Massimo Sandal (PhD student)

Publications (*: *corresponding author*, #: *'equally contributing authors'*).

- *Peer-reviewed journals: 101*

- *Citations: 2424*

- *H-index: 27*

- *Corresponding author: 28*

- *First or shared first authorship: 10*

International peer reviewed journals

1. C. Piubelli, D Treggiari, ... **A Giorgetti**, et al. Wide Real-Life Data Support Reduced Sensitivity of Antigen Tests for Omicron SARS-CoV-2 Infections. (2024) *Viruses* 16 (5), 657
2. B Kapur, F Baldessari, M Lazaratos, H Nar, G Schnapp, **A Giorgetti**, et al. Protons Taken Hostage: Dynamic H-Bond Networks of the pH-sensing GPR68. *Computational and Structural Biotechnology Journal*, 2023
3. BP Joseph, V Weber, L Knüpfer, **A Giorgetti** et al. Low Molecular Weight Inhibitors Targeting the RNA-Binding Protein HuR – (2023) *International Journal of Molecular Sciences*, 14 (32), 8651-8661

4. J Goßen, RPRR Ribeiro, DDB Bier, B Neumaier, P Carloni, **A Giorgetti** and G. Rossetti. AI-based identification of therapeutic agents targeting GPCRs: introducing ligand type classifiers and systems biology. (2023) Chemical Science
5. V Guglielmi, E Pancheri, ... **A Giorgetti**, et al. A novel in-frame deletion in myot causes an early adult onset distal myopathy. (2023). Clinical Genetics. *In press*
6. G Bisello, RP Ribeiro, M Perduca, BD Belviso, P Polverino de'Laureto ,.. **A Giorgetti** et al. Human aromatic amino acid decarboxylase is an asymmetric and flexible enzyme: implication in AADC deficiency. (2023) Protein Science
7. F Oliva, F Musiani, **A Giorgetti**, S De Rubeis, O Sorokina, DJ Armstrong, et al. Modelling eNvironment for Isoforms (MoNviso): A general platform to predict structural determinants of protein isoforms in genetic diseases.(2023) Frontiers in Chemistry 10, 105959
8. Cunha P., Petit E., Coutelier M., ... **Giorgetti, A.**, et al. Extreme phenotypic heterogeneity in non-expansion spinocerebellar ataxias. The American Journal of Human Genetics. (2023)
9. Dishnica,K, Piubelli,C, **Giorgetti, A** et al. Natalia Tiberti. Novel insights into the somatic proteome of Strongyloides stercoralis infective third-stage larvae. (2023) Parasites & Vectors 16 (1), 1-12
10. Ribeiro, R and **Giorgetti A***. pyGOMoDo: GPCRs modeling and docking with python. (2023) Bioinformatics 39 (5), btad294
11. Mango, G., Osti, N., Udali, S., Vareschi, A., Malerba, G., **Giorgetti, A.**, et al. Novel protein-truncating variant in the APOB gene may protect from coronary artery disease and adverse cardiovascular events (2022) Atherosclerosis Plus, 49, pp. 42-46.
12. Gerdol, M., Dishnica, K., **Giorgetti, A.** Emergence of a recurrent insertion in the N-terminal domain of the SARS-CoV-2 spike glycoprotein(2022) Virus Research, 310, art. no. 198674
13. Maguolo, A., Rodella, G., **Giorgetti, A.**, et al. A Gain-of-Function Mutation on BCKDK Gene and Its Possible Pathogenic Role in Branched-Chain Amino Acid Metabolism (2022) Genes, 13 (2), art. no. 233, .
14. Meyer, M., Jurek, B., Alfonso-Prieto, M., Ribeiro, R., Milenkovic, V.M., Winter, J., Hoffmann, P., Wetzel, C.H., **Giorgetti, A.**, Carloni, P., Neumann, I.D. Structure-function relationships of the disease-linked A218T oxytocin receptor variant(2022) Molecular Psychiatry, 27 (2), pp. 907-917.
15. Sitani, D., **Giorgetti, A**, Alfonso-Prieto, M., Carloni, P. Robust principal component analysis-based prediction of protein-protein interaction hot spot(2021) Proteins: Structure, Function and Bioinformatics, 89 (6), pp. 639-647.
16. Schmitz-Hübsch, T., Lux, S., Bauer, P., Brandt, A.U., Schlapakow, E., Greschus, S., Scheel, M., Gärtner, H., Kirlangic, M.E., Gras, V., Timmann, D., Synofzik, M., **Giorgetti, A.**, et al. Spinocerebellar ataxia type 14: refining clinicogenetic diagnosis in a rare adult-onset disorder (2021) Annals of Clinical and Translational Neurology, 8 (4), pp. 774-789.
17. Lai, H.T.T., **Giorgetti, A.**, Rossetti, G., Nguyen, T.T., Carloni, P., Kranjc, A. The interplay of cholesterol and ligand binding in hTSPO from classical molecular dynamics simulations (2021) Molecules, 26 (5), art. no. 1250
18. Sena, D.M., Jr, Cong, X., **Giorgetti, A.** Ligand based conformational space studies of the μ -opioid receptor(2021) Biochimica et Biophysica Acta - General Subjects, 1865 (3), art. no. 129838, .

19. Micheli, P., Ribeiro, R., **Giorgetti, A***. A mechanistic model of nmda and ampa receptor-mediated synaptic transmission in individual hippocampal ca3-ca1 synapses: A computational multiscale approach (2021) International Journal of Molecular Sciences, 22 (4), art. no. 1536, pp. 1-24.
20. Marchetto, A., Chaib, Z.S., Rossi, C.A., Ribeiro, R., Pantano, S., Rossetti, G., **Giorgetti, A***. CGMD Platform: Integrated Web Servers for the Preparation, Running, and Analysis of Coarse-Grained Molecular Dynamics Simulations(2020) Molecules, 25 (24), art. no. 5934, .
21. Lira Zidanes, A., Marchi, G., Busti, F., Marchetto, A., Fermo, E., **Giorgetti, A.**, et al. A Novel ALAS2 Missense Mutation in Two Brothers With Iron Overload and Associated Alterations in Serum Hepcidin/Erythroferrone Levels (2020) Frontiers in Physiology, 11, art. no. 581386, .
22. Schneider, J., Korshunova, K., Chaib, Z.S., **Giorgetti, A.**, Alfonso-Prieto, M., Carloni, P. Ligand pose predictions for human G protein-coupled receptors: Insights from the Amber-based hybrid molecular mechanics/coarse-grained approach(2020) Journal of Chemical Information and Modeling, 60 (10), pp. 5103-5116.
23. De Rosa, C., Melchior, A., Sanadar, M., Tolazzi, M., **Giorgetti, A.**, Ribeiro, R.P., Nardon, C., Piccinelli, F. Effect of the Heteroaromatic Antenna on the Binding of Chiral Eu(III) Complexes to Bovine Serum Albumin (2020) Inorganic Chemistry, 59 (17), pp. 12564-12577.
24. Schneider, J., Ribeiro, R., Alfonso-Prieto, M., Carloni, P., **Giorgetti, A***. Hybrid MM/CG Webserver: Automatic Set Up of Molecular Mechanics/Coarse-Grained Simulations for Human G Protein-Coupled Receptor/Ligand Complexes (2020) Frontiers in Molecular Biosciences, 7, art. no. 576689,
25. Chaib, Z.S., Marchetto, A., Dishnica, K., Carloni, P., **Giorgetti, A***, Rossetti, G Impact of cholesterol on the stability of monomeric and dimeric forms of the translocator protein TSPO: A molecular simulation study (2020) Molecules, 25 (18), art. no. 4299, .
26. Guaitoli, V., Alvarez-Ginarte, Y.M., Montero-Cabrera, L.A., Bencomo-Martínez, A., Badel, Y.P., **Giorgetti, A.**, Suku, E. A computational strategy to understand structure-activity relationship of 1,3-disubstituted imidazole [1,5- α] pyrazine derivatives described as ATP competitive inhibitors of the IGF-1 receptor related to Ewing sarcoma (2020) Journal of Molecular Modeling, 26 (8), art. no. 222
27. F Baldessari, R Capelli, P Carloni, A **Giorgetti**. Coevolutionary data-based interaction networks approach highlighting key residues across protein families: The case of the G-protein coupled receptors. Computational and Structural Biotechnology Journal, 2020 (6,018)
28. Giuliari, B., Kösters, M., Zhou, J., Dingersen, T., Heissmann, A., Rotzoll, R., Krüger, J., **Giorgetti, A.**, Sommers, B. The Vesicle Builder - A Membrane Packing Algorithm for the CELLmicrocosmos MembraneEdito(2020) MolVA 2020 - Workshop on Molecular Graphics and Visual Analysis of Molecular Data, pp. 7-15
29. Cuenca, MV, Marchi, G, [...], Marchetto, A., **Giorgetti, A** et al. Genetic and Clinical Heterogeneity in Thirteen New Cases with Aceruloplasminemia. Atypical Anemia as a Clue for an Early Diagnosis (2020) Int. J. Mol. Sci., 21, 2374 (4.183)
30. Damre, M, Marchetto, A., **Giorgetti A***. MERMAID: dedicated web server to prepare and run coarse-grained membrane protein dynamics (2019) Nucleic Acid Res. 47(W1), pp. W456-W461 (11,797)
31. Amundarain, M.J., Viso, J.F., Zamarreño, F., **Giorgetti, A.***, Costabel, M. Orthosteric and benzodiazepine cavities of the $\alpha 1\beta 2\gamma 2$ GABAA receptor: insights from experimentally validated in silico methods (2019) Journal of Biomolecular Structure and Dynamics, 37 (6), pp. 1597-1615.(4,986)

32. Alfonso-Prieto, M., **Giorgetti, A.**, Carloni, P. Multiscale simulations on human Frizzled and Taste2 GPCRs (2019) *Current Opinion in Structural Biology*, 55, pp. 8-16. (6,908)
33. Fierro F, **Giorgetti A**, Carloni P, Meyerhof W, Alfonso-Prieto M. Dual binding mode of "bitter sugars" to their human bitter taste receptor target. *Sci Rep*. 2019 Jun 11;9(1):8437 (4,525)
34. Amundarain, M.J., Ribeiro, R.P., Costabel, M.D., **Giorgetti, A.***. GABA A receptor family: Overview on structural characterization (2019) *Future Medicinal Chemistry*, 11 (3), pp. 229-246. (3,617)
35. Cao, R.; **Giorgetti, A.**; Bauer, A.; Neumaier, B.; Rossetti, G.; Carloni, P. Role of Extracellular Loops and Membrane Lipids for Ligand Recognition in the Neuronal Adenosine Receptor Type 2A: An Enhanced Sampling Simulation Study. (2018) *Molecules* 23, 2616 (3,06)
36. Capaldi, S., Suku, E., Antolini, M., Di Giacobbe, M., **Giorgetti, A.***, Buffelli, M. Allosteric sodium binding cavity in GPR3: a novel player in modulation of A β production (2018) *Scientific Reports*, 8 (1), art. no. 11102 (4,525)
37. Busato M, Distefano R, Bates F, Karim K, Bossi AM, López Vilariño JM, Piletsky S, Bombieri N, **Giorgetti A.*** MIRATE: Mlps RAtional dEsign Science Gateway. *J Integr Bioinform*. 2018 Jun 13. [Epub ahead of print]
38. Mechaly, A.S., Tovar-Bohórquez, M., Mechaly, A.E., Suku, E., **Giorgetti, A.**, Pérez, M., Ortí, G., Viñas, J., Somoza, G.M. Evidences of alternative splicing as a regulatory mechanism for Kissr2 in pejerrey fish. (2018) *Frontiers in Endocrinology* 9, 604 (3,675)
39. Zeng, J., Guareschi, R., Damre, M., Cao, R., Kless, A., Neumaier, B., Bauer, A., **Giorgetti, A.***, Carloni, P., Rossetti, G. Structural prediction of the dimeric form of the mammalian translocator membrane protein TSPO: A key target for brain diagnostics (2018) *International Journal of Molecular Sciences*, 19 (9), art. no. 2588. (4,183)
40. Amundarain, M.J., Viso, J.F., Zamarreño, F., **Giorgetti, A.***, Costabel, M. Orthosteric and benzodiazepine cavities of the $\alpha 1 \beta 2 \gamma 2$ GABAA receptor: insights from experimentally validated in silico methods. (2018) *Journal of Biomolecular Structure and Dynamics*, pp. 1-19. Article in Press. (4,986)
41. Schneider, J., Korshunova, K., Musiani, F., Alfonso-Prieto, M., **Giorgetti, A.**, Carloni, P. Predicting ligand binding poses for low-resolution membrane protein models: Perspectives from multiscale simulations (2018) *Biochemical and Biophysical Research Communications*, 498 (2), pp. 366-374. (1,133)
42. Zamarreño, F., **Giorgetti, A.**, Amundarain, M.J., Viso, J.F., Córscico, B., Costabel, M.D. Conserved charged amino acids are key determinants for fatty acid binding proteins (FABPs)-membrane interactions. A multi-methodological computational approach (2018) *Journal of Biomolecular Structure and Dynamics*, 36 (4), pp. 861-877.(4,986))
43. Tarenzi T, Calandrini V, Potestio R, **Giorgetti A**, Carloni P. Open Boundary Simulations of Proteins and Their Hydration Shells by Hamiltonian Adaptive Resolution Scheme. *J Chem Theory Comput*. (2017) 13 (11), pp. 5647-5657.
44. Fierro F, Suku E, Alfonso-Prieto M, **Giorgetti A.***, Cichon S, Carloni P. Agonist binding to chemosensory receptors: a systematic bioinformatics analysis (2017) *Frontiers in Molecular Biosciences* 4 (SEP), art. no. 63
45. Radu BM, Osculati AMM, Suku E, Banciu A, Tsenov G, Merigo F, Di Chio M, Banciu DD, Tognoli C, Kacer P, **Giorgetti A**, Radu M, Bertini G, Fabene PF. All muscarinic acetylcholine receptors (M1-M5) are expressed in murine brain microvascular endothelium (2017) *Scientific Reports* 7(1): 5083
46. Ponzoni, L., Rossetti G., Maggi, L., **Giorgetti A.**, Carloni P. and Micheletti C. Unifying view of mechanical and functional hotspots across class A GPCRs. (2017) *PLOS Comp. Biology* Feb 3;13(2): e1005381

47. Minnerop, M., Kurzwelly, D., [...], **Giorgetti, A.**, et al. Hypomorphic mutations in POLR3A are a frequent cause of sporadic and recessive spastic ataxia. (2017) *BRAIN* 140 (6): 1561-1578
48. Suku, E., Fierro, F., **Giorgetti, A.***, Alfonso-Prieto, M. and Carloni, P. Multi-scale simulations of membrane proteins: The case of bitter taste receptors. (2017) *Journal of Science: Advanced Materials and Devices* (*in press*)
49. Sena, D. Jr, Cong, X., **Giorgetti, A.**, Kless, A., and Carloni, P. Structural heterogeneity of the μ -opioid receptor's conformational ensemble in the apo state. (2017) *Scientific Reports* 8: 45761
50. Piubelli C., Castagna A., Marchi G., Rizzi M., Busti F., Badar S., Marchetti M., De Gobbi M., Roetto A., Xumerle L., Suku E., **Giorgetti A.**, Delledonne M., Olivieri O., Girelli D. Identification of New BMP6 Pro-Peptide Mutations in Patients with Iron-Overload (2017) *American Journal of Hematology* 92 (6), pp. 562-568
51. Bates F., Busato M., Piletska E., Whitcombe MJ., Karim K., Guerreiro A., Del Valle M., **Giorgetti A.**, and Piletsky S. Computational design of molecularly imprinted polymer for direct detection of melamine in milk. (2017) *Separation Science and Technology* 52 (8), pp. 1441-1453
52. Ariani, P., Regaiolo, A., Lovato, A., **Giorgetti, A.**, Wong, D., Porceddu, A., Camiolo, S., Castellarin, S., Vandelle, A., Polverari, A. Genome-wide characterisation and expression profile of the grapevine ATL ubiquitin ligase family reveal biotic and abiotic stress-responsive and development-related members (2016). *Scientific Reports*; 6:38260
53. Dindo M, Montioli R, Busato M, **Giorgetti A**, Cellini B, Voltattorni CB. Effects of interface mutations on the dimerization of alanine glyoxylate aminotransferase and implications in the mistargeting of the pathogenic variants F152I and I244T (2016) *Biochimie*, pii: S0300-9084(16)30230-9
54. Busato, M., **Giorgetti, A.***. Structural modeling of G-protein coupled receptors: An overview on automatic web-servers (2016) *International Journal of Biochemistry and Cell Biology* 77, pp. 264-274.
55. Vallone, R., La Verde, V., D'Onofrio, M., **Giorgetti, A.**, Dominici, P., Astegno, A. Metal binding affinity and structural properties of calmodulin-like protein 14 from *Arabidopsis thaliana* (2016) *Protein Science*, pp. 1461-1471.
56. Kumar, N., Astegno, A., Chen, J., **Giorgetti, A.**, Dominici, P. Residues in the distal heme pocket of arabidopsis non-symbiotic hemoglobins: Implication for nitrite reductase activity (2016) *International Journal of Molecular Sciences*, 17 (5), art. no. 640
57. Sousa, S.A., Leitão, J.H., Martins, R.C., Sanches, J.M., Suri, J.S., **Giorgetti, A.** Bioinformatics Applications in Life Sciences and Technologies (2016) *BioMed Research International*, 2016, art. no. 3603827 (Editorial)
58. Serena, M., **Giorgetti, A.**, Busato, M., Gasparini, F., Diani, E., Romanelli, M.G., Zipeto, D. Molecular characterization of HIV-1 Nef and ACOT8 interaction: Insights from in silico structural predictions and in vitro functional assays (2016) *Scientific Reports*, 6, art. no. 22319.
59. Badar, S., Busti, F., Ferrarini, A., Xumerle, L., Bozzini, P., Capelli, P., Pozzi-Mucelli, R., Campostrini, N., De Matteis, G., Marin Vargas, S., **Giorgetti, A.**, Delledonne, M., Olivieri, O., Girelli, D. Identification of novel mutations in hemochromatosis genes by targeted next generation sequencing in Italian patients with unexplained iron overload (2016) *American Journal of Hematology*, 91 (4), pp. 420-425.

60. Rossetti, G., Dibenedetto, D., Calandrini, V., **Giorgetti, A.***, Carloni, P. Structural predictions of neurobiologically relevant G-protein coupled receptors and intrinsically disordered proteins. (2015) *Archives of Biochemistry and Biophysics*, 582, art. no. 6948, pp. 91-100.
61. Lovato P, **Giorgetti A**, Bicego M. A Multimodal Approach for Protein Remote Homology Detection. *IEEE/ACM Trans Comput Biol Bioinform.* 2015 Sep-Oct;12(5):1193-8
62. Ceccon, A., Busato, M., Pérez Santero, S., D'Onofrio, M., Musiani, F., **Giorgetti, A.***, Assfalg, M. Transient interactions of a cytosolic protein with macromolecular and vesicular cosolutes: Unspecific and specific effects (2015) *ChemBioChem*, 16 (18), pp. 2633-2645.
63. Sandal, M., Behrens, M., Brockhoff, A., Musiani, F., **Giorgetti, A.***, Carloni, P., Meyerhof, W. Evidence for a Transient Additional Ligand Binding Site in the TAS2R46 Bitter Taste Receptor. (2015) *Journal of Chemical Theory and Computation*, 11 (9), pp. 4439-4449.
64. Pizzolo, F., Friso, S., Morandini, F., Antoniazzi, F., Zaltron, C., Udali, S., Gandini, A., Cavarzere, P., Salvagno, G., **Giorgetti, A.**, Speziali, G., Choi, S.-W., Olivieri, O. Apparent mineralocorticoid excess by a novel mutation and epigenetic modulation by HSD11B2 promoter methylation. (2015) *Journal of Clinical Endocrinology and Metabolism*, 100 (9), pp. E1234-E1241.
65. Costantini, S., Malerba, G., Contreas, G., Corradi, M., Marin Vargas, S.P., **Giorgetti, A.**, Maffei, C. Genetic and bioinformatics analysis of four novel GCK missense variants detected in Caucasian families with GCK MODY phenotype. (2015) *Clinical Genetics*, 87 (5), pp. 440-447.
66. Astegno, A., Allegrini, A., Piccoli, S., **Giorgetti, A.**, Dominici, P. Role of active-site residues Tyr55 and Tyr114 in catalysis and substrate specificity of *Corynebacterium diphtheriae* C-S lyase. (2015) *Proteins: Structure, Function and Bioinformatics*, 83 (1), pp. 78-90.
67. Grison A, Zucchelli S, Urzi A, Zamparo I, Lazarevic D, Pascarella G, Roncaglia P, **Giorgetti A**, Garcia-Esparcia P, Vlachouli C, Simone R, Persichetti F, Forrest AR, Hayashizaki Y, Carloni P, Ferrer I, Lodovichi C, Plessy C; FANTOM Consortium, Carninci P, Gustincich S. Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. *BMC Genomics*. 2014 Aug 27;15:729.
68. Montioli R, Dindo M, **Giorgetti A**, Piccoli S, Cellini B, Voltattorni CB. A comprehensive picture of the mutations associated with aromatic amino acid decarboxylase deficiency: from molecular mechanisms to therapy implications. *Hum Mol Genet.* 2014 Oct 15;23(20):5429-40.
69. **Giorgetti, A.***. Membrane Proteins: Insights from computational biology. (2014) *Biology and Medicine*, 6 (1), art. no. 1000e101.
70. Piccoli, S., Musiani, F., **Giorgetti, A.***. Dynamic characterization and substrate binding of cis-2,3 dihydrobiphenyl-2,3-diol dehydrogenase—an enzyme used in bioremediation. (2014) *Journal of Molecular Modeling*, 20 (12), 6 p.
71. Musiani, F., Rossetti, G., **Giorgetti, A.***, Carloni, P. Chemosensorial G-proteins-coupled receptors: A perspective from computational methods. (2014) *Advances in Experimental Medicine and Biology*, 805, pp. 441-457.
72. Piccoli, S., Andreolli, M., **Giorgetti, A.**, Zordan, F., Lampis, S., Vallini, G. Identification of aldolase and ferredoxin reductase within the dbt operon of *Burkholderia fungorum* DBT1. (2014) *Journal of Basic Microbiology*, 54 (5), pp. 464-469.
73. **Giorgetti, A.***. Multi-scale computational biology (2014) *Biology and Medicine*, 6 (1), art. no. 1000e102.

74. Sandal, M., Paltrinieri, D., Carloni, P., Musiani, F., **Giorgetti, A.*** Structure/Function Relationships of Phospholipases C Beta. (2013) *Current Protein and Peptide Science*, 14 (8), pp. 650-657.
75. Astegno, A., **Giorgetti, A.**, Allegrini, A., Cellini, B., Dominici, P. Characterization of C-S lyase from *C. diphtheriae*: A possible target for new antimicrobial drugs. (2013) *BioMed Research International*, 2013, art. no. 701536.
76. Sandal, M., Duy, T.P., Cona, M., Zung, H., Carloni, P., Musiani, F., **Giorgetti, A.***. GOMoDo: A GPCRs Online Modeling and Docking Webserver. (2013) *PLoS ONE*, 8 (9), art. no. e74092.
77. Piccoli, S., Suku, E., Garonzi, M., **Giorgetti, A.***. Genome-wide membrane protein structure prediction. (2013) *Current Genomics*, 14 (5), pp. 324-329.
78. Marchiori, A., Capece, L., **Giorgetti, A.#**, Gasparini, P., Behrens, M., Carloni, P., Meyerhof, W. Coarse-Grained/Molecular Mechanics of the TAS2R38 Bitter Taste Receptor: Experimentally-Validated Detailed Structural Prediction of Agonist Binding. (2013) *PLoS ONE*, 8 (5), art. no. e64675.
79. Bisha, I., Laio, A., Magistrato, A., **Giorgetti, A.**, Sgrignani, J. A candidate ion-retaining state in the inward-facing conformation of sodium/galactose symporter: Clues from atomistic simulations. (2013) *Journal of Chemical Theory and Computation*, 9 (2), pp. 1240-1246.
80. Leguèbe, M., Nguyen, C., Capece, L., Hoang, Z., **Giorgetti, A.***, Carloni, P. Hybrid Molecular Mechanics/Coarse-Grained Simulations for Structural Prediction of G-Protein Coupled Receptor/Ligand Complexes. (2012) *PLoS ONE*, 7 (10), art. no. e47332.
81. **Giorgetti, A.**, Ruggerone, P., Pantano, S., Carloni, P. Advanced computational methods in molecular medicine. (2012) *Journal of Biomedicine and Biotechnology*, 2012, art. no. 709085, .
82. Zanzoni, S., Assfalg, M., **Giorgetti, A.**, D'Onofrio, M., Molinari, H. Structural requirements for cooperativity in ileal bile acid-binding proteins. (2011) *Journal of Biological Chemistry*, 286 (45), pp. 39307-39317.
83. Biarnés, X., Marchiori, A., **Giorgetti, A.***, Lanzara, C., Gasparini, P., Carloni, P., Born, S., Brockhoff, A., Behrens, M., Meyerhof, W. Insights into the binding of phenyltiocarbamide (PTC) agonist to its target human TAS2R38 bitter receptor. (2010) *PLoS ONE*, 5 (8), art. no. e12394.
84. Griguoli, M., Maul, A., Nguyen, C., **Giorgetti, A.**, Carloni, P., Cherubini, E. Nicotine blocks the hyperpolarization-activated current I_h and severely impairs the oscillatory behavior of oriens-lacunosum moleculare interneurons. (2010) *Journal of Neuroscience*, 30 (32), pp. 10773-10783.
85. Saga, G., **Giorgetti, A.**, Fufezan, C., Giacometti, G.M., Bassi, R., Morosinotto, T. Mutation analysis of violaxanthin de-epoxidase identifies substrate-binding sites and residues involved in catalysis. (2010) *Journal of Biological Chemistry*, 285 (31), pp. 23763-23770.
86. Heller, D.M., **Giorgetti, A.***. NMR constraints analyser: A web-server for the graphical analysis of NMR experimental constraints. (2010) *Nucleic Acids Research*, 38 (SUPPL. 2), art. no. gkq484, pp. W628-W632.
87. Mazzolini, M., Marchesi, A., **Giorgetti, A.**, Torre, V. Gating in CNGA1 channels. (2010) *Pflugers Archiv European Journal of Physiology*, 459 (4), pp. 547-555.
88. Maullu, C., Raimondo, D., Caboi, F., **Giorgetti, A.**, Sergi, M., Valentini, M., Tonon, G., Tramontano, A. Site-directed enzymatic PEGylation of the human granulocyte colony-stimulating factor. (2009) *FEBS Journal*, 276 (22), pp. 6741-6750.
89. Lupieri, P., Nguyen, C.H.H., Bafghi, Z.G., **Giorgetti, A.**, Carloni, P. Computational molecular biology approaches to ligand-target interactions. (2009) *HFSP Journal*, 3 (4), pp. 228-239.

90. Raimondo, D., **Giorgetti, A.**, Bernassola, F., Melino, G., Tramontano, A. Modelling and molecular dynamics of the interaction between the E3 ubiquitin ligase Itch and the E2 UbcH7. (2008) *Biochemical Pharmacology*, 76 (11), pp. 1620-1627.
91. Albiero, E., Madeo, D., Ruggeri, M., Bernardi, M., **Giorgetti, A.**, Rodeghiero, F. Loss of the JAK2 intramolecular auto-inhibition mechanism is predicted by structural modelling of a novel exon 12 insertion mutation in a case of idiopathic erythrocytosis. (2008) *British Journal of Haematology*, 142 (6), pp. 986-990.
92. Cozzetto, D., **Giorgetti, A.**, Raimondo, D., Tramontano, A. The evaluation of protein structure prediction results. (2008) *Molecular Biotechnology*, 39 (1), pp. 1-8.
93. Moutran, A., Balan, A., Ferreira, L.C., **Giorgetti, A.**, Tramontano, A., Ferreira, R.C. Structural model and ligand interactions of the *Xanthomonas axonopodis* pv. *citri* oligopeptide-binding protein. (2007) *Genetics and molecular research: GMR*, 6 (4), pp. 1169-1177.
94. Tramontano, A., Cozzetto, D., **Giorgetti, A.**, Raimondo, D. The assessment of methods for protein structure prediction. (2007) *Methods in Molecular Biology*, 413, pp. 43-57.
95. Tress, M.L., Martelli, P.L., Frankish, A., Reeves, G.A., Wesselink, J.J., Yeats, C., Ólason, P.Í., Albrecht, M., Hegyi, H., **Giorgetti, A.**, Raimondo, D., Lagarde, J., Laskowski, R.A., López, G., Sadowski, M.I., Watson, J.D., Fariselli, P., Rossi, I., Nagy, A., Kai, W., Størling, Z., Orsini, M., Assenov, Y., Blankenburg, H., Huthmacher, C., Ramírez, F., Schlicker, A., Denoué, F., Jones, P., Kerrien, S., Orchard, S., Antonarakis, S.E., Reymond, A., Birney, E., Brunak, S., Casadio, R., Guigo, R., Harrow, J., Hermjakob, H., Jones, D.T., Lengauer, T., Orengo, C.A., Patthy, L., Thornton, J.M., Tramontano, A., Valencia, A. The implications of alternative splicing in the ENCODE protein complement. (2007) *Proceedings of the National Academy of Sciences of the United States of America*, 104 (13), pp. 5495-5500.
96. Raimondo, D., **Giorgetti, A.**, Bosi, S., Tramontano, A. Automatic procedure for using models of proteins in molecular replacement. (2007) *Proteins: Structure, Function and Genetics*, 66 (3), pp. 689-696.
97. Nair, A.V., Mazzolini, M., Codega, P., **Giorgetti, A.**, Torre, V. Locking CNGA1 channels in the open and closed state. (2006) *Biophysical Journal*, 90 (10), pp. 3599-3607
98. **Giorgetti, A.**, Raimondo, D., Miele, A.E., Tramontano, A. Evaluating the usefulness of protein structure models for molecular replacement. (2005) *Bioinformatics*, 21 (SUPPL. 2), pp. ii72-ii76.
99. **Giorgetti, A.**, Carloni, P., Mistrik, P., Torre, V. A homology model of the pore region of HCN channels. (2005) *Biophysical Journal*, 89 (2), pp. 932-944.
100. **Giorgetti, A.**, Nair, A.V., Codega, P., Torre, V., Carloni, P. Structural basis of gating of CNG channels. (2005) *FEBS Letters*, 579 (9), pp. 1968-1972.
101. **Giorgetti, A.**, Carloni, P. Molecular modeling of ion channels: Structural predictions. (2003) *Current Opinion in Chemical Biology*, 7 (1), pp. 150-156.

Book chapters

1. Musiani, F., **Giorgetti, A.** *Protein Aggregation and Molecular Crowding: Perspectives From Multiscale Simulation. In: Early Stage Protein Misfolding and Amyloid Aggregation, 2017 . Vol 329, IRCMB, UK: Academic Press, 2017, pp. 49-77*

2. **Giorgetti A.** and Carloni P. "*Molecular Mechanics/Coarse-Grained models*". **2014** pag 165 - 174. In '*Protein Modelling*'; editor: Gábor Náray-Szabo. Springer. ISBN: 978-3-319-09975-0
3. **Giorgetti A.**, Piccoli S., *Knowledge Based Membrane Protein Structure Prediction: From X-Ray Crystallography to Bioinformatics and Back to Molecular Biology*, in *Current Trends in X-Ray Crystallography*, edited by Annamalai Chandrasekaran, InTech Publisher (**2011**).
4. Tress M., Casadio R., **Giorgetti A.**, Hallin PF., Juncker AS., Kulberkyte E., Martelli PL., Raimondo D., Reeves GA., Thornton JM., Tramontano A., Wang K., Wesselink JJ., Valencia A., **Alternative Splicing in the ENCODE Protein-Complement**, Frishman D., Valencia A. *Modern Genome Annotation: the Biosapiens Network*, Wienn, Springer-Verlag, **2008**
5. Tramontano A., Jones D., Rychlewski L., Casadio R., Martelli PL., Raimondo D., **Giorgetti A.**, **Protein structure prediction**, Frishman D., Valencia A. *Modern Genome Annotation: the Biosapiens Network*, Wienn, Springer-Verlag, **2008**

Editorial and evaluation activities

- **Member of the editorial board** of the international journal: **Scientific Reports** (Nature group).
- **Member of the editorial board** of: **Journal of Integrative Bioinformatics**.
- **Guest editor**: special issue in "Advanced Computational Methods in Molecular Medicine". Journal of Biomedicine and Biotechnology.
- **Guest editor**: special issue on "Bioinformatics Applications in Life Sciences and Technologies". **BioMed Research International**.
- **Reviewer**: 23rd CINECA CLASS B IS CRA call – 2021
- **Reviewer**: 26th CINECA CLASS B IS CRA call – 2022
- **Reviewer**: 29th CINECA CLASS B IS CRA call – 2024
- **Reviewer**: *FEBS journal*; *Bioinformatics*; *Proteins*; *Biophysical journal*; *Amino Acids*; *EBJO*; *Protein Engineering, Design, and Selection (PEDS)*; *Current Bioinformatics*; *Plos Computational Biology*; *Plos One*, *Nature Communications*; *Biochimie*
- **Expert Reviewer** for the French National Research Agency "Blanc SVSE 5" call for proposals.
- **Expert Reviewer** for the French National Research Agency "Generic Call 2017" call for proposals.
- **Expert reviewer** for the Consejo Nacional De Investigaciones Cientificas y Tecnicas (CONICET) Ministerio De Ciencia, Tecnologia E Innovacion Productiva della Repubblica Argentina, 2017

- **Expert reviewer** for the Consejo Nacional De Investigaciones Cientificas y Tecnicas (CONICET) Ministerio De Ciencia, Tecnologia E Innovacion Productiva della Repubblica Argentina, 2019

Funding

- FIRB 'Future in research 2010', national italian project (RBFR08R7OU_001). Title: "Dalla comprensione dell'attivazione allosterica di fatty acid binding proteins modulata dall'interazione con membrane cellulari e leganti, al disegno di nuovi inibitori della cattura di lipidi". 36 months. **Participant**
- PRIN (National Italian funding system) (2009): "Meccanismi di riconoscimento molecolare in sistemi a molte componenti costituiti da proteine trasportatrici di lipidi, i loro leganti specifici, recettori e membrane fosfolipidiche". 24 months. **Participant**
- International call for HPC time: RWTH Computer Cluster (University of Aachen, Germany), Germany. Project: Ligand screening in G-protein coupled receptors: Insights from bioinformatics and MM/CG simulations (2013). **P.I.**
- International call for HPC time: RWTH Computer Cluster (University of Aachen, Germany), Germany. Project: Agonist binding to human bitter taste receptors: insights from molecular simulation (2013). **P.I.**
- International call for HPC time: RWTH Computer Cluster (University of Aachen, Germany), Germany. Project: Agonist binding to human bitter taste receptors: insights from molecular simulation (extension) (2014). **P.I.**
- International call for HPC time: RWTH Computer Cluster (University of Aachen, Germany), Germany. Project: Binding of oxytocin to the oxytocin receptor, a key interaction for social behavior. (1300000 core/hours) (2014). **P.I.**
- International call for HPC time: RWTH Computer Cluster (University of Aachen, Germany), Germania. Project: Ligand binding to the OR7D4 odorant receptor studied by multiscale molecular simulations. (2016). **P.I.**
- International call for HPC time: RWTH Computer Cluster (University of Aachen, Germany), Germania. Project: Molecular basis of agonist "access control" across bitter taste receptors. (2017). **P.I.**
- OCPC (Office of the China Postdoctoral Commission) Postdoc position - 24 months (2016-2018). Project: 'Multi-scale simulation based-structural predictions of human odorant receptors: The case of the OR7D4 receptor in complex with its agonists androstenone and androstadienone' (72000 euro). **P.I.**
- Development of NeuroDrug Design web-portal for design and synthesis of ligands for brain imaging and drug leads for neurodegenerative diseases. Foreign Talents STI Grants. Germany – Vietnam (€ 200,000) (2017-2019) **Participant (foreign talent)**
- **DFG** - Deutsche Forschungsgemeinschaft - Research Unit: Functional dynamics of ion channels and transporters (Dynlon) (2017-2020). (€ 240,000) **Participant**
- Project funded by the Università degli Studi di Verona: 'In silico and in vitro characterization of the orphan G protein coupled receptor 3 (GPR3)' (2017 - 2019) (€ 35.294). **P.I.**
- 2019-2021: BMBF Förderung der bilateralen Zusammenarbeit mit Vietnam.co- **PIs:** Jun. Prof. Dr. Rossetti, Prof. Dr. Carloni (FZJ), Jun. Prof. Dr. Alfonso-Prieto (FZJ), **Prof. Dr. Giorgetti** "Molecular simulation-based rational design of Painkillers Targeting the Opioid Receptor (PaTOR)", **€ 235.021,31**

- Project funded by the Center for Simulation and Data Sciences co-funded by FZJ and RWTH Aachen University. Title: 'Prediction of protein-protein ligand interactions and brain signaling cascades using machine learning approaches: Olfaction as a test scenario'. One Ph.D. position **P.I.**
- PRIN (National Italian funding system). 'The aroma diversity of Italian white wines. Study of chemical and biochemical pathways underlying sensory characteristics and perception mechanisms for developing models of precision and sustainable enology'. (2019 - 2022) € 836.975,16 **Participant**
- European Union's Horizon 2020 Framework Programme for Research and Innovation under the Specific Grant Agreement No. 945539 (Human Brain Project SGA3). P.I.
- #NEXTGENERATIONEU (NGEU) and the Ministry of University and Research (MUR), National Recovery and Resilience Plan (NRRP), project MNESYS [PE0000006]—A Multiscale integrated approach to the study of the nervous system in health and disease [DN. 1553 11.10.2022]. €170000 Task leader
- PRIN (National Italian funding system: 'Protein-protein interactions in Autism Spectrum Disorder' 2022. €290000. Research Unit leader

Invited speaker

1. 108° RAFA Reunión Anual de Física 2023 (with International participation). Title: "From physics to drug discovery". Dates: September 19th – 22nd 2023 – Bahia Blanca, **Argentina**
2. 2nd German workshop on structural predictions of membrane proteins, from ion channels to G-protein coupled receptor. Title: "SSB Platform: from receptor's structural modeling to signaling cascades". Dates: February 7th–8th, **2023** - Forschungszentrum Jülich, **Germany**
3. 'Structural bioinformatics and multi-scale simulations of GPCRs: it takes two to tango' 17th National Conference of Biophysics (with International Participation) (CNB 2022) September 23-25 2022, **Târgu Mureș, Romania**
4. "Systems biology and molecular networks", Corso di Laurea in Medicina High Technology, cicli di seminari: BIOLOGIA E GENETICA E PRINCIPI DI OTTIMIZZAZIONE. 6 maggio 2021- **Rome, Italy**
5. 'Structural bioinformatics and multi-scale simulations of GPCRs: it takes two to tango' 4th ERNEST meeting: "Insights from structures of signaling complexes and mathematical modelling of GPCR signaling" Online. Monday April 12th – Wednesday 14th, 2021
6. German workshop on structural predictions of membrane proteins, from ion channels to G-protein coupled receptor. Title: "A computational platform for structural systems biology". Dates: November 26th–27th, **2019** - Forschungszentrum Jülich, **Germany**
7. Molecular Dynamics Today. Title: "Protein bioinformatics and multi-scale simulations: it takes two to tango". Dates: 14-15 March **2019**. Bologna, **Italy**
8. Winter School 'Understanding human genome variations and their influence on human traits – Bioinformatics insights'. Title: 'In silico protein analyses for functional interpretation'. Canazei, **Italy**. 13 – 18 Gennaio **2019**.

9. 7th International Conference on the Development of Biomedical Engineering “Recent computational and experimental advances in molecular medicine”. Title: Bioinformatics and Multi-scale simulations of membrane proteins: the case of bitter taste receptors. Dates: June 27th-29th, **2018**. Venue: Biomedical Engineering Department, International University & Vietnam National University HCMC, **Ho Chi Minh City (Vietnam)**.
10. Membrane protein modelling. Courses and Seminars - 11th Symposium on Molecular Design and Bioinformatics. 10 – 11 Luglio **2017**, La Havanna, **Cuba**
11. Bioinformatics and Multi-scale simulations of bitter taste receptors. Scientific meeting - 11th Symposium on Molecular Design and Bioinformatics (SEADIM). 12 – 14 Luglio **2017**, Varadero, **Cuba**
12. First International Conference on "Multiscale simulations in complex biomolecular systems: linking computations to experimental validation". Title: Bioinformatics and Multi-scale simulations of membrane proteins: the case of bitter taste receptors. April 10th–12th, **2017**, in Hanoi, **Vietnam**
13. Membrane Protein Modelling: Bitter taste receptors. Biophysics-colloquium of the Institute of Biophysics, Johannes Kepler University. 9th November **2016**, Linz, **Austria**
14. Evidence for a Transient Additional Ligand Binding Site in the TAS2R46 Bitter Taste Receptor 6th International Conference on the Development of Biomedical Engineering. 27th-29th June **2016**, Ho Chi Min City, **Vietnam**
15. **Closing Lecture**: "Evidence for a Transient Additional Ligand Binding Site in Bitter Taste Receptors". VI Argentinian Conference on Bioinformatics and Computational Biology. 14–16 October **2015**, Bahía Blanca, **Argentina**.
16. 'Ligand binding mechanisms of bitter taste receptors: Insights from multiscale computational approaches'. 9th International Conference on Computational Physics; Symposia on Multiscale Modeling and Simulations. 7 - 11 January **2015**, Singapore National University, **Singapore**.
17. “Ligand binding mechanisms of bitter taste receptors: Insights from multiscale simulation approaches”. XLIII Annual meeting of the Sociedad Argentina de Biofísica, 3rd–5th December **2014**, Sierra de la Ventana, Buenos Aires, **Argentina**
18. 'Multiscale simulation approaches: Insights into the ligand binding mechanisms of bitter taste receptors'. IBBI14 Conference on Isolated Biomolecules and Biomolecular Interactions. May 18th-23rd, **2014**. Location: Porquerolles, **France**.
19. 'Molecular mechanics/coarse-grained simulations: Insights into the ligand binding mechanisms of GPCRs'. Computational Driven Drug Discovery. 3rd Meeting, March 4th-5th-6th, **2014**. Location: Verona, **Italy**.

20. 'Bitter taste sensing: Insights from computational biology'. CECAM meeting: Molecular Simulations of Membrane Proteins: From Biophysics to Pharmacological Application, March 7, 2012 to March 9, **2012**. Location: CECAM-HQ-EPFL, Lausanne, **Switzerland**.
21. 'Structural Bioinformatics approaches to chemical senses'. The International Conference in Computational Medicine *Ho Chi Minh City, Vietnam, January 11-12th, 2012*
22. 'Chemical Senses: Insights from Structural Bioinformatics'. AIMS seminar series. AICES RWTH Aachen University, Aachen, **Germany**. 5th December **2011**.
23. 'Insights into the Structural Determinants of Bitter Taste Receptors from a Combined *in silico* and *in vitro* Study'. Conference on Molecular Aspects of Cell Biology: A Perspective from Computational Physics. 11th – 15th October **2010**. ICTP. Trieste, **Italy**
24. 'Structural determinants of bitter taste perception: insights from a combined *in silico* and *in vitro* Study ' 25th August **2010**. German Research School (GRS), Jülich, **Germany**.
25. 'Applicazioni biomediche e farmaceutiche'. Sessione di Dinamica Molecolare nel Master in Comunicazione della Scienza. International School for Advanced Studies (SISSA), 24th June. **2010**, Trieste, **Italy**.
26. "Membrane Transporters: Insights from Bioinformatics". International Workshop: From Structure to Function: Influx and Efflux Systems. 6th - 8th May **2009**, Cagliari (IT)
27. Perspectives on Computational Structural/Molecular Systems Biology. March 31st **2009**. Dept. of Informatics, University of Verona, Verona, **Italy**.
28. 'Hands on Session on Bioinformatics'. 2nd Conference on Drug Development for the Third World: from Computational Molecular Biology to Experimental Approaches. 1st -5th June **2009**. Trieste, **Italy**
29. 'Molecular Systems Biology Insights from Bioinformatics'. Computer Design and Discovery of Potential Drugs for Developing Countries'. ICS-UNIDO, 8th - 12nd June. **2009**, Trieste, **Italy**.
30. 'El Proyecto ENCODE: Desde el genoma a las proteínas: un viaje de ida y vuelta'. July 11th **2008**. Universidad del Sur, Bahia Blanca, **Argentina**
31. 'New perspectives in protein landscape of the human genome: the Encode project'. April 11th **2008**. University of Padova, Padova , **Italy**
32. Bioinformatica: dalla genomica alla farmacogenomica. XVII Settimana della cultura scientifica e tecnologica. April 20th **2007**. Cagliari, **Italy**
33. "Aspetti chiave nella bioinformatica delle proteine e la loro utilità pratica". 12 Maggio **2006** Villa Mondragone, Frascati (Roma). Università degli Studi di Roma 'Tor vergata'. PhD symposia.
34. "Evaluating the usefulness of protein structure models for molecular replacement. ECCB **2005** - Madrid, **Spain**.

35. "Structural models of HCN ion channels". CECAM Discussion Meeting 'Ion Channels: from Biology to Physics'. Lyon -**France (2002)**

Teaching activities (see Teaching Portfolio – Appendix II of the application)

PhD thesis director.

- PhD thesis tutor: Dr. Stefano Piccoli, Università degli Studi di Verona (2010 - 2013)
- PhD thesis tutor: Ivan Sciascia, Università degli Studi di Verona (2012 - 2015)
- PhD thesis tutor: Sergio Marin Vargas, Università degli Studi di Verona (2013 - 2016)
- PhD thesis tutor: Mirko Busato, Università degli Studi di Verona (2014 - 2017)
- PhD thesis tutor: Eda Suku, Università degli Studi di Verona (2016 - 2019)
- PhD thesis tutor: Rui Ribeiro, Università degli Studi di Verona (2018 - 2021)
- PhD thesis tutor: Klevia Dishnica, Università degli studi di Verona (2021- 2024)
- PhD thesis tutor: Francesco Fontanive, Università degli studi di Verona (2023-)
- Co-tutor PhD thesis: Chuong Nguyen. German Research School for Atomistic Simulations and University of Aachen, Germany.(2009 -2012)
- Co-tutor PhD thesis: Massimo Sandal. German Research School for Atomistic Simulations and University of Aachen, Germany
- Co-tutor PhD thesis: Fabrizio Fierro. INM-9/IAS-5 and University of Aachen, Germany
- Co-tutor PhD thesis: Divya Sitani. INM-9/IAS-5 and University of Aachen, Germany
- Co-tutor PhD thesis: Somayeh Asghapour. INM-9/IAS-5 and University of Aachen, Germany
- Co-tutor PhD thesis: Giuliano Santarpia. INM-9/IAS-5 and University of Aachen, Germany

PhD evaluation committee

- Member of the evaluation committee of the PhD in "Biotechnologie molecolari industriali ed ambientali" (examination 16/04/2010) Decreto Rettoriale n. 603/2010. Università degli Studi di Verona.
- Member of the evaluation committee of the PhD in Condensed matter Physics. University of Cagliari Cagliari, Italy. (11/02/2010). Decreto Rettoriale 103 del 4.12.2009. Dr. Amit Kumar. 'Transport of Antibiotics Through Bacterial Porins'.

- Member of the evaluation committee of Dr. Kamil Khafizov. "Computational studies on GPCR's transduction cascade: the case of olfaction". Scuola Superiore di Studi Avanzati (SISSA), Marzo 04, 2008, Trieste, Italia.
- Member of the evaluation committee of Dr. Fernando Herrera. "Computational approaches to the investigation of proteins involved in Parkinson's Disease". Scuola Superiore di Studi Avanzati (SISSA), Marzo 04, 2008, Trieste, Italia.
- Member of the evaluation committee of Francesco Pontiggia. 'Protein Structure and Functionally-oriented Dynamics: From Atomistic to Coarse-grained Models' Scuola Superiore di Studi Avanzati (SISSA), Gennaio 14, 2008, Trieste, Italia.
- Member of the evaluation committee of Dr. Fabio Simona. 'Metallo- β -lattamasi (M β L): studi computazionali della reattività enzimatica' Scuola Superiore di Studi Avanzati (SISSA), Novembre 12, 2008, Trieste, Italia.

Bachelor thesis director

- Veronica Mattioli, Francesco Pezzini, Davide M. Heller, Davide Modena, Alberto Pontalto, Jacopo Fedrigo, Francesco Pezzini, Maddalena Zucchotto, Michela Dallera, Sergio Marin, Matteo Corsini, Francesco Gastaldello, Matteo Trentini, Carlo Perale, Marianna Garonzi, Simone Carli, Daniele Paltrinieri, Andrea Pegoraro, Damiano Stanzial, Altea Zucca, Filippo Baldesarri, Alessandro Marchiori, Pietro Micheli, Ana Weber (Maastricht), Eda Suku

Master thesis director

- Francesco Pezzini, Alberto Dai Prè, Marianna Garonzi, Davide Modena, Francesca Gasparini, Caterina Calligaris, Beatrice Giuliani, Mirko Busato, Aldo Tocci, Eda Suku, Alessandro Marchiori, Pietro Micheli, Irene Noro, Ludovico Modenese, Carlo Alberto Rossi, Alessandro Marchetto, Pietro Micheli, Filippo Baldessari, Riccardo Vanini, Massimo Sossai

Postdoc director:

- Dr. Massimo Sandal (2012-2013). Project: 'Web server development for the automatic modeling of GPCRs' (AdR1942/12) University of Verona
- Dr. Sergio Marin Vargas (2016 - 2017). Project: "Computational characterization of structure/function relationships in olfactory receptors " (AdR2731/16) University of Verona
- Dr. Giovanna Paolone (2017 - 2018). Project: "In silico and in vitro characterization of the orphan GPCR receptor 3 (GPR3)", Funded by the University of Verona
- Dr. Juan Zeng (anno 2016-2018). Funded by the China and Germany Postdoctoral Exchange Program- OCPC.
- Kelvia Dishnica (2019-2020). Funded by the Verona Brain Foundation, Italy
- Dr. Maria Julia Amundarain. CONICET - Argentina. Postdoctoral position: 'Atomistic and quantum calculation applied to the study of iron metabolism'. 2019-2021.

Organizing committee:

- CECAM workshop 2015 on 'Computational approaches to chemical senses'. Juelich, 9-11 September 2015.
- ECCB08, September 2008, Cagliari, Italy
- 2018: Member of the organizing committee of the Meeting 'Proteine 2018' (Italian Society of Biochemistry), May 28-30, Verona.
- 2018: Member of the organizing Committee of the Winter School in Applied Bioinformatics, January 21-25, Alba di Canazei (TN), Italy.
- 2019: Member of the organizing Committee of the Winter School 'Understanding human genome variations and their influences on human traits. Bioinformatics Insights', January 13-18, Alba di Canazei (TN), Italy.

June - 7th - 2024

Verona, Italia



Alejandro Giorgetti