Riccardo Capelli

Born	November 19th, 1987
Birth place	Bergamo (BG), Italy
Citizenship	Italian
Work e-mail	riccardo.capelli@polito.it

Research Experience

- **Postdoctoral position in Computational Physical Chemistry**

  Nov 2019 until now — Department of Applied Science and Technology (DISAT) - Politecnico di Torino, Turin (Italy)

I work under the supervision of Prof. Giovanni M. Pavan (PoliTo, SUPSI) with computational chemistry tools like molecular dynamics, enhanced sampling techniques, machine learning, on the design and study of bioinspired materials with a multiscale approach (from all-atom to coarse-grained representation). In particular, we investigate qualitatively and quantitatively the thermodynamic and kinetic behavior of such systems. This research project is inserted in the context of the ERC-CoG grant "DYNAPOL".

My postdoc is divided in 3 main topics:
- *Estimation of kinetic features of supramolecular complexes*: I studied by means of enhanced sampling approaches the self-assembly of supramolecular polymers (refs. 16, 18, and 23) and COFs (ref. 25).
- *Data-driven study of molecular systems*: I developed in the framework of Smooth Overlap of Atomic Position (SOAP) analysis, a metrics that is able to compare 3D atomic environment. This metrics has been employed to study the performances of lipid models and their phase transition (ref. 21), as well as the formation of ice-like environments of water at room condition (ref. 29).
- *Parametrization of classical molecular models via automatic optimizers*: I contributed in the formulation of *SwarmCG* framework (refs. 19 and 24), applying it to the formulation of coarse-grained and atomistic models.

- **Postdoctoral position in Modeling of Complex Biomolecular Systems**

  Apr 2018 Oct 2019 — IAS-5 / INM-9 Computational Biomedicine - Forschungszentrum Jülich, Jülich (Germany)

I worked under the supervision of Prof. Paolo Carloni and Prof. Michele Parrinello (ETHZ/USI) exploiting and developing innovative physical chemistry techniques (enhanced sampling, non-equilibrium techniques), devoted to the computational study of allosteric regulation in different GPCR receptors. This research project was inserted in the context of the Flagship EU H2020 initiative "Human Brain Project".

My postdoc was divided in 3 main topics:
- *Study of the ligand binding interaction of human M_2 muscarinic receptor*: exploiting enhanced sampling techniques (Metadynamics, Ratchet&Pawl MD), we studied the free energy landscape of the ligand binding/unbinding transition of a radioligand, iperoxo, with the human muscarinic receptor M_2 (ref. 12 and 17).
- *Development of new enhanced sampling techniques*: I developed a new flavor of metadynamics, named Volume-based metadynamics (ref. 13), that allows the exploration of multiple binding/unbinding pathways in a host/guest system. This method allows also the identification of possible binding poses of a ligand in a protein.
- *Study of coevolutionary hotspots in G-protein coupled receptors*: we investigated the coevolutionary fingerprint and the interaction network of most of the experimentally available GPCR structures both in active and inactive site to identify the residues that triggers the activation/inactivation process (ref. 15).

- **Pre-doctoral Research fellow**

  Apr 2014 Oct 2014 — Istituto di Chimica del Riconoscimento Molecolare (now SciTec) - CNR, Milan (Italy)

Consiglio Nazionale delle Ricerche

I worked in the computational chemistry group led by Dr. Giorgio Colombo. Using computational chemistry methods (*i.e.,* molecular dynamics simulation, free energy calculation techniques), I applied these techniques for the development of a diagnostic tool/vaccine for a tropical disease, melioidosis. This research project was part of the *PROVA* project - Discovery/development of diagnostic PRObes and VAccine candidates targeting Burkholderia infections, funded by Regione Lombardia.

My research project was divided in 2 topics:

- Design of immunogenic peptides against *Burkholderia pseudomallei*, the etiological agent of melioidosis. Making use of long molecular dynamics simulations of large immunogenic proteins, we investigated the energetics related to the intermolecular interaction between antibodies-antigen.
- Application and improvement of free energy calculation methods, like Free Energy Perturbation and Thermodynamic integration on biomolecular systems.

Education

Dottorato di Ricerca (Ph.D) in Physics, Astrophysics and Applied Physics

Nov 2014 – Nov 2017 Università degli Studi di Milano, Milan (Italy)

Thesis title: "Computational modeling of proteins: from statistical mechanics to immunology"
Supervisors:

- Guido Tiana (Università degli Studi di Milano)
- Giorgio Colombo (ICRM-CNR)

My PhD was divided in 3 main topics:

- *Enhancement of free energy calculation techniques*: we studied the confinement simulation technique, which permits to compute conformational free energies exploiting thermodynamic integration. In particular, we improved its performance in terms of computational time needed (ref. 4) and we applied it to the calculation of single-point mutations $\Delta\Delta G$ in a small peptide (ref. 3).
- *Data-driven simulation of non-equilibrium processes*: we implemented the principle of Maximum Caliber (the non-equilibrium extension of the Maximum Entropy principle) using replica-averaged simulations in PLUMED (ref. 8). This technique permits to insert time-resolved ensemble experimental data in a simulation to correct a perfectible force field in a given non-equilibrium process.
- *Protein design for immunology*: we implemented a structural vaccinology approach, based on the study of the energetics of the biomolecules involved with the aim to find a suitable diagnostic tool (refs 6,7) and a candidate vaccine (ref 9) for *Burkholderia pseudomallei*, the etiological agent of meliodosis. We also developed a computational tool for epitope grafting on a target protein, called SAGE (ref. 5).

The PhD thesis is available **here**.

Laurea Magistrale (M.Sc.) in Physics (grade: 110/110)

Oct 2011 – Feb 2014 Università degli Studi di Milano, Milan (Italy)

Thesis title: "Building a model to describe the equilibrium state of small proteins"
Supervisors:

- Guido Tiana (Università degli Studi di Milano)
- Carlo Camilloni (University of Cambridge)

During my thesis I developed a multi-core implementation of a Monte Carlo polymer simulation software, MonteGrappa, adding also a new term in the potential that takes into account the propensity to form α and β structures in proteins (ref. 2). We exploited this software to study $\Delta\Delta G$ of single point mutations in small proteins (ref. 1).

Laurea Triennale (B.Sc.) in Physics (grade: 100/110)

Oct 2006 – Jul 2011 Università degli Studi di Milano, Milan (Italy)

Thesis title:"Valutazione di ampiezze di scattering su scheda grafica" (Scattering amplitude evaluation on GPU)
Supervisor:
- Alessandro Vicini (Università degli Studi di Milano)

Scholarship and awards

2014 - PhD scholarship (2014/2017 - ∼ 40 k€), Università degli Studi di Milano

Grants

2018 - HPC Computing time on JURECA (11/2018 - 10/2019 - 2 Mcore-h), JARA/FZ Jülich - PI

2019 - *Innovative high-performance computing approaches for molecular neuromedicine* (2020/2022 - 750k€), Helmholtz Society European Partnering project - Investigator

Supervised Students

2017 - Piero Valena - M.Sc. in Physics, Università degli Studi di Milano (co-supervised with G. Tiana)
Thesis project: Development of a model to study the thermodynamics of large protein systems

Teaching Experience

A.Y. 2021/22 - Tutor (15 hours) for the course "Chemistry", Bachelor in Aerospace Eng., Politecnico di Torino.

A.Y. 2016/17 - Exercise class (16 hours) for the course "Physics", B.Sc. in Natural Sciences, Università degli Studi di Milano, held by Prof. Alberto Vailati.
- Exercise class (24 hours) for the course "Physics", B.Sc. in Biotechnology, Università degli Studi di Milano, held by Prof. Guido Tiana.

A.Y. 2015/16 - Exercise class (16 hours) for the course "Physics", B.Sc. in Natural Sciences, Università degli Studi di Milano, held by Prof. Alberto Vailati.

Publications

∗ indicates corresponding author,
† indicates equal contribution.

26. L. Hoang Gia†, J. Goßen†, **R. Capelli***, T. T. Nguyen, Z. Sun, K. Zuo, J. Schulz, G. Rossetti*, P. Carloni
Multiple poses and thermodynamics of ligands targeting protein surfaces: the case of furosemide binding to mitoNEET in aqueous solution
Accepted, Front. Cell Dev. Biol. (2022). (2020 IF: 6.684)

25. K. Koner, S. Karak, S. Kandambeth, S. Karak*, N. Thomas, L. Leanza, C. Perego, L. Pesce, **R. Capelli**, M. Moun, M. Bhakar, T. G. Ajithkumar, G. M. Pavan*, and R. Banerjee*
Porous covalent organic nanotubes and their assembly in loops and toroids
Nat. Chem. (2022), DOI:10.1038/s41557-022-00908-1 (2020 IF: 24.427)

24. C. Empereur-mot*, **R. Capelli**, M. Perrone, C. Caruso, G.Doni, and G. M. Pavan*.
Automatic Multi-Objective Optimization of Coarse-Grained Lipid Force Fields Using SwarmCG
J. Chem. Phys. 156 (2), 024801 (2022), DOI:10.1063/5.0079044 (2020 IF: 3.488)

23. E. Weyandt, L. Leanza, **R. Capelli**, G. M. Pavan, G. Vantomme, and E.W. Meijer*.
Controlling the length of porphyrin-based supramolecular polymers via coupled equilibria and dilution induced self-assembly
Nat. Commun. 13, 248 (2022), DOI:10.1038/s41467-021-27831-2 (2020 IF: 14.919)

22. Q. Zhao, **R. Capelli***, P. Carloni, B. Lüscher, J. Li, and G. Rossetti*.
Enhanced Sampling Approach to the Induced Fit Docking Problem in Protein-Ligand Binding: the case of mono-ADP-ribosylation hydrolases inhibitors
J. Chem. Theory Comput. 17, 7899–7911 (2021), DOI:10.1021/acs.jctc.1c00649 (2020 IF: 6.006)

21. **R. Capelli***, A. Gardin, C. Empereur-mot, G. Doni, and G. M. Pavan*.
A Data-Driven Dimensionality Reduction Approach to Compare and Classify Lipid Force Fields
J. Phys. Chem. B 125, 7785–7796 (2021), DOI:10.1021/acs.jpcb.1c02503 (2020 IF: 2.991)

20. M. Crippa†, D. Andreghetti†, **R. Capelli**, and G. Tiana*.
Evolution of Frustrated and Stabilising Contacts in Reconstructed Ancient Proteins
Eur. Biophys. J. 50, 699–712 (2021), DOI:10.1007/s00249-021-01500-0 (2020 IF: 1.733)

19. C. Empereur-mot*, L. Pesce, G. Doni, D. Bochicchio, **R. Capelli**, C. Perego, and G. M. Pavan*.
Swarm-CG: Automatic Parametrization of Bonded Terms in MARTINI-based Coarse-Grained Models of Simple to Complex Molecules via Fuzzy Self-Tuning Particle Swarm Optimization
ACS Omega 5, 50, 32823–32843 (2020) DOI:10.1021/acsomega.0c05469 (2020 IF: 3.512)

18. C. Perego, L. Pesce, **R. Capelli**, S. J. George, and G. M. Pavan*.
Multiscale Molecular Modelling of ATP-fueled Supramolecular Polymerisation and Depolymerisation
ChemSystemsChem 2, e2000038, (2020) DOI:10.1002/syst.202000038 (2020 IF: N/A)

17. **R. Capelli***†, W. Lyu†, V. Bolnykh, S. Meloni, J. M. H. Olsen, U. Rothlisberger, M. Parrinello, and P. Carloni.
Accuracy of Molecular Simulation-based Predictions of k_{off} Values: a Metadynamics Study
J. Phys. Chem. Lett. 11, 6373–6381, (2020) DOI:10.1021/acs.jpclett.0c00999 (2020 IF: 6.475)

16. A. Sarkar, T. Behera, R. Sasmal, **R. Capelli**, C. Empereur-mot, J. Mahato, S. S. Agasti*, G. M. Pavan*, A. Chowdhury*, and S. J. George*.
Cooperative Supramolecular Block Copolymerization for the Synthesis of Functional Axial Organic Heterostructures
J. Am. Chem. Soc. 142(26), 11528–11539 (2020) DOI:10.1021/jacs.0c04404 (2020 IF: 15.419)

15. F. Baldessari, **R. Capelli***, P. Carloni, and A. Giorgetti.
Coevolutionary Data-based Interaction Networks Approach Highlighting Key Residues across Protein Families: the Case of the G-protein Coupled Receptors
Comput. Struct. Biotechnol. J. 18, 1153–1159, (2020) DOI:10.1016/j.csbj.2020.05.003 (2020 IF: 7.271)

14. *The PLUMED consortium.*
Promoting transparency and reproducibility in enhanced molecular simulations
Nat. Methods 16(8), 670–673, (2019) DOI:10.1038/s41592-019-0506-8 (2020 IF: 28.547)

13. **R. Capelli***, P. Carloni, and M. Parrinello.
Exhaustive Search of Ligand Binding Pathways via Volume-based Metadynamics
J. Phys. Chem. Lett. 10, 3495–3499, (2019) DOI:10.1021/acs.jpclett.9b01183 (2020 IF: 6.475)

12. **R. Capelli***, A. Bochicchio, GM. Piccini, R. Casasnovas, P. Carloni*, and M. Parrinello.
Chasing the full free energy landscape of neuroreceptor/ligand unbinding by metadynamics simulations
J. Chem. Theory Comput. 15, 3354–3361, (2019) DOI:10.1021/acs.jctc.9b00118 (2020 IF: 6.006)

11. F. Marchetti†, **R. Capelli**†, F. Rizzato†, A. Laio*, and G. Colombo*.
The subtle tradeoff between evolutionary and energetic constraints in protein-protein interactions
J. Phys. Chem. Lett. 10, 1489–1497, (2019) DOI:10.1021/acs.jpclett.9b00191 (2020 IF: 6.475)

10. **R. Capelli**, S. Caracciolo, A. Di Gioacchino, and E. M. Malatesta.
Exact value for the average optimal cost of bipartite traveling-salesman and 2-factor problems in two dimensions
Phys. Rev. E (2018) 98, 030101 DOI:10.1103/PhysRevE.98.030101 (2020 IF: 2.529)

9. **R. Capelli**, C. Peri, R. Villa, A. Nithichanon, O. Conchillo-Solé, D. Yero, P. Gagni, M. Chiari, G. Lertmemongkolchai, M. Cretich, X. Daura, M. Bolognesi, G. Colombo*, and L. J. Gourlay*.
BPSL1626: Reverse and Structural Vaccinology Reveal a Novel Candidate for Vaccine Design Against *Burkholderia pseudomallei*
Antibodies 7, 26 (2018) DOI:10.3390/antib7030026 (2020 IF: N/A)

8. **R. Capelli**, G. Tiana*, and C. Camilloni*.
An implementation of the maximum–caliber principle by replica–averaged time–resolved restrained simulations
J. Chem. Phys. 148, 184114 (2018) DOI:10.1063/1.5030339 (2020 IF: 3.488)

7. L. Sola†, P. Gagni†, I. D'Annessa†, **R. Capelli**, C. Bertino, A. Romanato, F. Damin, G. Bergamaschi, E. Marchisio, A. Cuzzocrea, M. Bombaci, R. Grifantini, M. Chiari, G. Colombo, A. Gori*, and M. Cretich*.
Enhancing antibody serodiagnosis using a controlled peptide co-immobilization strategy
ACS Infect. Dis. 4, 998–1006, (2018) DOI:10.1021/acsinfecdis.8b00014 (2020 IF: 5.084)

6. **R. Capelli**†, E. Matterazzo†, M. Amabili, C. Peri, A. Gori, P. Gagni, M. Chiari, G. Lertmemongkolchai, M. Cretich, M. Bolognesi, G. Colombo*, and L. J. Gourlay*.
Designing probes for immunodiagnostics: structural insights into an epitope targeting *Burkholderia* infections
ACS Infect. Dis. 3, 736–743, (2017) DOI:10.1021/acsinfecdis.7b00080 (2020 IF: 5.084)
(Cover article)

5. **R. Capelli**, F. Marchetti, G. Tiana and G. Colombo*.
SAGE: a Fast Computational Tool for Linear Epitope Grafting onto a Foreign Protein Scaffold
J. Chem. Inf. Model. 57, 6–10, (2017) DOI:10.1021/acs.jcim.6b00584 (2020 IF: 4.956)

4. F. Villemot, **R. Capelli**, G. Colombo and A. van der Vaart*.
Balancing accuracy and cost of confinement simulations by interpolation and extrapolation of confinement energies
J. Chem. Theory Comput. 12, 2779–2789, (2016) DOI:10.1021/acs.jctc.5b01183 (2020 IF: 6.006)

3. **R. Capelli**, F. Villemot, E. Moroni, G. Tiana, A. van der Vaart* and G. Colombo*.
Assessment of mutational effects on peptide stability through confinement simulations
J. Phys. Chem. Lett. 7 (1), 126-130, (2016) DOI:10.1021/acs.jpclett.5b02221 (2020 IF: 6.475)

2. G. Tiana*, F. Villa, Y. Zhan, **R. Capelli**, C. Paissoni, P. Sormanni, E. Heard, L. Giorgetti and R. Meloni
MonteGrappa: an iterative Monte Carlo program to optimize biomolecular potentials in simplified models
Comput. Phys. Commun. 186, 93–104, (2015) DOI:10.1016/j.cpc.2014.09.12 (2020 IF: 4.390)

1. **R. Capelli**, C. Paissoni, P. Sormanni and G. Tiana*.
Iterative derivation of effective potentials to sample the conformational space of proteins at atomistic scale
J. Chem. Phys. 140, 195101 (2014) DOI:10.1063/1.4876219 (2020 IF: 3.488)

Invited Seminars

10 Feb '22 *Identification of ice-like structures in rigid classical water models at room condition*
Università degli Studi di Modena e Reggio Emilia, Modena (IT)

18 Oct '19 *Exploration of multiple ligand binding pathways*
Forschungszentrum Jülich, Jülich (DE)

14 May '19 *Exploration of multiple binding pathways*
KIT, Karlsruhe (DE)

30 Oct '18 *Ligand unbinding from the M_2 muscarinic receptor: uncovering molecular recognition exploiting dimensionality reduction and enhanced sampling*
Forschungszentrum Jülich, Jülich (DE)

22 Feb '18 *Biased molecular simulations of non-equilibrium protein dynamics*
Forschungszentrum Jülich, Jülich (DE)

30 Jan '18 *Biased molecular simulations of non-equilibrium protein dynamics*
Università della Svizzera Italiana, Lugano (CH)

Short Invited Scientific Visits

11-15 Sep '17 UNC, Chapel Hill (NC-USA). Prof. Nikolay Dokholyan

20-24 Feb '17 SISSA, Trieste (IT). Prof. Alessandro Laio

Long Invited Scientific Visits

2018-2019 ETHZ/USI, Lugano (CH). Prof. Michele Parrinello - 8 months in total (multiple visits)
During my stay in Prof. Parrinello's group I applied advanced computational chemistry techniques, such as metadynamics, to large biomolecular system to unveil the thermodynamics and kinetics of ligand binding phenomena (ref. 12 and 17) in close collaboration with my group in Jülich. Later, I designed and developed a new technique, called Volume-based metadynamics (ref. 13), devoted to study in an efficient way the possible binding/unbinding pathways in a host/guest system.

Workshop, Courses and Summer Schools

5-16 Apr '21 **ACS Spring Meeting**, Online conference.
Invited talk in the symposium "Kinetics of Macromolecular Systems: Methods and Applications": *"Accuracy of* in silico *Kinetics Calculations Using Infrequent Metadynamics: the Case of M2/iperoxo Unbinding"*

26-27 Nov '19 **German workshop on structural predictions of membrane proteins. From ion channels to G-protein coupled receptors**, Jülich (DE).
Invited talk *"Ligand unbinding from the M_2 muscarinic receptor: uncovering molecular recognition exploiting dimensionality reduction and enhanced sampling"*

24-27 Jul '19 **CECAM Workshop: Open Source Software for Enhanced Sampling Simulations**, Lugano (CH).
Contributed talk *"Exploration of multiple binding pathways"*

5-7 Jun '19 **Mainz Materials Simulation Days 2019**, Mainz (DE).
Contributed talk: *"Exploration of multiple binding pathways"*

4-6 Feb '19 **CECAM Workshop: Multiscale Modeling from Macromolecules to Cell: Opportunities and Challenges of Biomolecular Simulations**, Lausanne (CH).
Participation with the poster *"Uncovering molecular recognition of a ligand binding to the M_2 muscarinic receptor"*

15-18 Oct '18 **Human Brain Project Summit 2018**, Maastricht (NL).
Participation with the poster *"Modelling and simulation in SP6: Recent advances in methods development at the molecular level"*

7-10 Feb '18 **5th Workshop "Physics of biomolecules: structure, dynamics, and function"**, Brixen (IT).

3-7 Jul '17 **Advances in complex systems**, Como (IT)

5-16 Dic '16 **Winter School on Quantitative Systems Biology**, ICTP - Trieste (IT).
Participation with the poster *"Automated scan and scoring of epitope grafting position candidates"*

12-13 Sep '16 **Enabling Software for High Scalable INTEL Architecture**, CINECA - Milan (IT).

3-6 Feb '16 **4th Workshop "Physics of biomolecules: structure, dynamics, and function"**, Brixen (IT).

24 Sep '15 **2nd Workshop "Condensed Matter Highlights"**, Milan (IT).
Contributed talk: *"Path-independent free energy evaluation of amino acid mutations"*

26-30 Jan '15 **XIX School of Pure and Applied Biophysics**, Venice (IT).

15 Jan '15 **2nd Workshop of the Complex Systems Group @ UNIMI**, Milan (IT).
Contributed talk: *"The Role of Surface Energetics in the Formation of Protein-Antibody Interactions"*

15-19 Sep '14 **CECAM Summer School: Atomistic Monte Carlo Simulations of Bio-molecular Systems**, Forschungzentrum Jülich (DE).

9-28 Jul '12 **CECAM Summer School: Summer School on Atomistic Simulation Techniques for material science, nanotechnology and biophysics**, SISSA - Trieste (IT).

5-7 Oct '11 **GPU Programming with CUDA**, CINECA - Milan (IT).

Reviewing activity

Journals
- Scientific Reports
- Journal of Chemical Information and Modeling
- The Canadian Journal of Chemical Engineering
- Proteins: Structure, Function, and Bioinformatics
- Journal of Chemical Theory and Computation

Grants
- ERC Advanced Grant
- Reviewer for EUTOPIA-SIF Fellowship

Habilitations

25/01/22 to 25/01/31 Italian national habilitation (ASN) to associate professor in applied physics, physics teaching and history of physics (SC 02/D1, SSD: FIS/07). Habilitation ID: 39973.

Bibliometric Indexes

Last updated: April 25, 2022

- Google Scholar
  Number of citations: 538; h-index: 11
- Scopus
  Number of citations: 432; h-index: 9
- Web of Science
  Number of citations: 429; h-index: 9