Miguel A. Soler

(updated April 17, 2023)

Personal Data

Place and Date of Birth:	Murcia, Spain | 11 November 1982
Nationality	Spanish
Languages	Spanish, mother tongue
	English, fluent
	Italian, fluent
	Portuguese, fluent
	German, basic
Address:	Università di Udine
	Via delle Scienze 206, 33100 - Udine, Italy.
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Education

Jun 2010 Ph.D. in Theoretical and Computational Chemistry,
University of Murcia, Spain
Thesis: "Study of the Vibrational Relaxation of N-methylacetamide in water solution"
Supervisors: Profs. Alberto Requena and Adolfo Bastida
Mark: Sobresaliente *CUM LAUDE* (highest honor)

Sept 2005 Degree in Chemistry, University of Murcia, Spain
Thesis: "Estudio Computacional del Comportamiento Electrófilo de Sales de 3-Metil-2metiltio-1,3,4-Tiadiazolio"
Supervisor: Arturo Espinosa
Mark: 8.65/10 | GPA: 3.65/4

Further Training

27–28 Jan 2014 Short Winter School on Nano- and Biotechnology.
University of Trieste, Italy.

7 May 2011 Workshop RESMOL of Molecular Reactivity and Solvation.
University of Córdoba, Argentina.

7–12 Jul 2008 Summer School of Mixed Quantum-Classical Dynamics: Foundations and Application to Photo-Biological Questions.
University of Vienna, Austria.

3–29 Sept 2007 Intensive Course in the European Master in Theorical Chemistry and Computational Modelling.
Universidad Autónoma de Madrid, Spain. Mark: Very Good.

5–22 Sept 2004 Research stay in the group of Prof. Pere M. Deyà.
Universitat de les Illes Balears, Spain.

Work Experience

Current - January 2022
Term-contract Researcher (RTDa)
at University of Udine, Udine, Italy
Professional assignment: *Characterising the reactivity of compounds in ionic liquids and deep eutectic solvents*

December 2021 - September 2018
Term-contract Researcher (Co.Co.Co)
at IIT, Genoa, Italy
Professional assignment: *research and methodological development related to the study and modulation of the biomolecular interaction in atomistic simulations*

August 2018 - July 2017
Term-contract Researcher (Co.Co.Co)
at SISSA, Trieste, Italy
Professional assignment: *Design of peptides for the molecular recognition of drugs by using molecular dynamics simulations, enhanced sampling simulations, data mining and clustering.* Funded by Associazione Italiana per la Ricerca sul Cancro (AIRC) 5xMILLE: Application of Advanced Nanotechnology in the Development of Cancer Diagnostics Tools (RIF. 12214, P.I: G. Toffoli, Col: A. Laio).

June 2017 - July 2016
Postdoctoral Researcher (assegnista, L. 240/2010)
at SISSA, Trieste, Italy
Project: *Design of peptides via molecular simulations and data mining,* funded by Associazione Italiana per la Ricerca sul Cancro (AIRC) 5xMILLE: Application of Advanced Nanotechnology in the Development of Cancer Diagnostics Tools (RIF. 12214, P.I: G. Toffoli, Col: A. Laio).

June 2016 - Jan 2014
Postdoctoral Researcher (assegnista, L. 240/2010)
at University of Udine, Italy
Project: *Structural design of nanodevices based on assembled peptides,* funded by 7FP, Ideas, ERC Advanced Grant: Molecular Nanotechnology For Life Science Application: QUantitative Interactomics for Diagnostics, Proteomics and QUantitative Oncology, (Quidroquo) (proposal n. 269025, 2011-2016 PI: G. Scoles).

Dec 2013 - Oct 2011
Postdoctoral Researcher
at University of Lisbon, Portugal
Project: *Insights into folding kinetics and designability of knotted proteins from lattice models,* funded by Fundação para a Ciência e a Tecnologia (PTDC/QUI-QUI/112358/2009, P.I: P. Faisca).

Sept 2011 - April 2011
Postdoctoral Visitor
at University of Quilmes, Argentina
CONICET Research Fellowship: *Theoretical and Computational Study of the Energy Transfer in Conjugated Polymers.*

March 2011 - July 2010
Research Collaborator
at University of Murcia, Spain
supported by the University of Murcia under the program "Postdoctoral Grants for Research Continuity".

June 2010 - Jan 2006
Ph.D. Fellow
at University of Murcia, Spain
granted by the Spanish National Fellowship "Formación de Profesorado Universitario (FPU)".

Grants and Honors

Dec 2017	Spanish Accreditation as "Profesor Ayudante Doctor" *(equivalent to RTDb position, according to DM 662/2016)* ANECA (Agencia Nacional de Evaluación de la Calidad y Acreditación)
Apr 2016	Research Mobility Grant n.19938/IV/15 (Fundación Seneca, 3000€) University of Murcia, Spain.
Apr 2011	Postdoctoral Mobility Fellowship (CONICET, Argentina)
	University of Quilmes, Buenos Aires, Argentina
Dec 2010	Postdoctoral Grant for Research Continuity (2400€) University of Murcia, Spain
Apr 2006	Ph.D. Fellowship (FPU, Spanish National Fellowship) University of Murcia, Spain
Oct 2004	Research Undergraduate Scholarship (2341€) University of Murcia, Spain

Teaching Activities

Feb–Jun 2023 Feb–Jun 2022	Assistant Professor - Physics for IOT devices, Degree in Internet of Things, Big Data, Machine Learning, University of Udine, Italy (10+16 hours).
Sep 2022– Jan 2023	Professor - Principles of Physics, Degree in Building and Land Use Techniques, University of Udine, Italy (48 hours)
Feb–Jun 2022	Assistant Professor - Physics with Laboratory, Degrees in Agricultural Sciences and in Food Science & Technology, University of Udine, Italy (15+15 hours)
Feb–Jun 2009	Assistant Professor - Experiments in Advanced Physical Chemistry, Chemistry Degree, University of Murcia, Spain (30 hours)
Feb–Jun 2009	Assistant Professor - Experiments in Physical and Analitical Chemistry, Chemical Engineering Degree, University of Murcia, Spain (15 hours)
Feb–Jun 2009	Assistant Professor - Chemistry, Physics Degree, University of Murcia, Spain (15 hours)

Commissions of Trust

2018 -	**Peer Review** for JACS Au (ACS), Frontiers Molecular Biosciences (Frontiers), PeerJ (PeerJ), Entropy, International Journal of Molecular Sciences, Molecules, Biomolecules, Micromachines (MDPI).
2022 -	**Review Editor** for Frontiers Molecular Biosciences (Frontiers) in the Biological Modeling and Simulation area.

Research Interests

My current background in chemical physics, computational chemistry and biophysics applied to different molecular systems offers me the unique opportunity to cover a wide range of problems and applications, in basic science, medicine or industry. My PhD thesis in Murcia (Spain) focused on the multiscale simulation of the vibrational relaxation of peptides in liquid solvents, exploring a wide range of simulations techniques, such as molecular dynamics, hybrid quantum/classical perturbative treatments and hybrid quantum/classical simulations. These skills were polished during my stay in Argentina in a joint project with A.Roitberg (AMBER, Gainesville, USA) and S.Tretiak (Los Alamos, USA) to study the mechanisms of energy transfer in dendrimers. Motivated by expanding my knowledge in biological systems and additional computational approaches I moved to Lisbon (Portugal) to work as postdoc in the protein folding field. There, I developed coarse grained models to study how proteins with physical knots are able to fold into their native structure. At the beginning of 2014, I came to Italy to work, first in the Scoles' group in Udine and subsequently in the Laio's group in SISSA (Trieste), in a multidisciplinary approach for the design of peptides as probes for the molecular recognition of proteins and drugs. This period was fundamental for improving my background in statistical physics, and for learning more advanced computational techniques, such as enhanced sampling molecular dynamics, clustering or high performance computing simulations. Moreover, I had the opportunity of collaborating with researchers of many different fields (medical doctors, molecular biologists, or experimental physics), as well as participating in the development of a software for the design of peptides and antibody fragments as binders (PARCE). Currently, I am carrying on new projects, always in the field of protein biophysics for medical applications, in which my expertise in this intriguing triangular relationship in protein among dynamics-structure-function that regulates their biological role is often exploited.

Participation in Research Projects

2021-2025	Investigator Grant (IG), AIRC (IT), 409000 €, as COLLABORATOR. Project: COMPUTATIONAL DESIGN OF THERAGNOSTIC NANOBODIES: TARGETING MISSENSE MUTANTS IN METASTATIC BREAST CANCER CELLS
2019-2020	ARDF Annual Open Grant (US), $39,980 US, as **co-PI**. Project: IN SILICO DESIGN OF CUSTOMISED HIGH-AFFINITY ANTIBODY FRAGMENTS
2007-2010	Project CTQ2007-66528/BQU, Ministerio de Educación y Ciencia (Spain) 60500 €, as COLLABORATOR. Project: RELAJACIÓN Y REDISTRIBUCIÓN INTRAMOLECULAR DE ENERGÍA VIBRACIONAL EN MOLÉCULAS CON ENLACES DE TIPO PEPTÍDICO

Main HPC Projects

Oct 2022 - Aug 2023	ISCRA Class B funding project, as COLLABORATOR 552,000 stand. hours on Marconi100, CINECA, Italy.
Oct 2021 - Jan 2023	ISCRA Class B funding project, as COLLABORATOR 558,000 stand. hours on Marconi100, CINECA, Italy.
Jun 2020 - Dec 2020	PRACE COVID-19 Fast Track Call, as **PI** 416,667 stand. hours on ARCHER (EPCC, United Kingdom)
Apr 2020 - Apr 2021	ISCRA Class B funding project, as COLLABORATOR 576,000 stand. hours on Marconi100, CINECA, Italy.
Oct 2019 - Oct 2020	PRACE Tier0 Call 19, as COLLABORATOR 4,925,000 stand. hours on Galileo & Marconi100, CINECA, Italy.
Aug 2019 - Oct 2020	ISCRA Class B funding project, as COLLABORATOR 401,342 stand. hours on Galileo, CINECA, Italy.
Apr 2019 - Dec 2020	ISCRA Class C funding project, as **PI** 33,600 stand. hours on Marconi A2, CINECA, Italy.
Feb 2018 - May 2019	ISCRA Class B funding project, as COLLABORATOR 640,000 stand. hours on Marconi A1 & A2, CINECA, Italy.
Mar 2017 - Sept 2017	PRACE Preparatory Access Projects - cut off 27, as **PI** 50,000 stand. hours on Marconi A1 & A2, CINECA, Italy.
Aug 2015 - Jun 2016	ISCRA Class C funding project, as COLLABORATOR 100,800 stand. hours on Galileo, CINECA, Italy
Jun 2014 - Mar 2015	ISCRA Class C funding project, as **PI** 40,000 stand. hours on Eurora, CINECA, Italy

Publication Lists

Corresponding author is marked as (*)

WOS Citation Metrics: h-index=16, 626 citations.
Google Scholar Citation Metrics: h-index=18, 803 citations.

1. A. Bastida*, J. Zúñiga, B. Miguel, **M. A. Soler***
Description of conformational ensembles of disordered proteins by residue-local probabilities,
Phys. Chem. Chem. Phys. 25, 10512-10524 (2023)

2. **M. A. Soler**, O. Ozkilinc, Y. Hunashal, P. Giannozzi, G. Esposito, F. Fogolari*
Molecular electrostatics and pKa shifts calculations with the Generalized Born model. A tutorial through examples with Bluues2,
Comput. Phys. Commun. 287, 108716 (2023)

3. **M. A. Soler**, N. Minovski, W. Rocchia, S. Fortuna*
Replica-exchange optimization of antibody fragments,
Comput. Biol. Chem. Volume 103, 107819 (2023)

4. B. Medagli*, **M. A. Soler**, R. De Zorzi, S. Fortuna*
Antibody Affinity Maturation Using Computational Methods: From an Initial Hit to Small-Scale Expression of Optimized Binders. In: K. Tsumoto, D. Kuroda, (eds) Computer-Aided Antibody Design,
Methods Mol. Biol. 2552, 333-359 (2023)

5. E. Calì, S. J. Lin, C. Rocca, Y. Sahin, A. Al Shamsi, S. El Chehadeh, M. Chaabouni, K. Mankad, E. Galanaki, S. Efthymiou, and **others**.
A homozygous MED11 C-terminal variant causes a lethal neurodegenerative disease,
Genet. Med. 24 (10), 2194-2203 (2022).

6. P. B. P. S. Reis, G. P. Barletta, L. Gagliardi, S. Fortuna, **M. A. Soler***, W. Rocchia*
Antibody-Antigen Binding Interface Analysis in the Big Data Era,
Front. Mol. Biosci. 9, 945808 (2022)

7. P. Borgia, S. Baldassari, N. Pedemonte, E. Alkhunaizi, G. D'Onofrio, D. Tortora, E. Calì, P. Scudieri, G. Balagura, I. Musante, and **others**.
Genotype-phenotype correlations and disease mechanisms in PEX13-related Zellweger spectrum disorders,
Orphanet J. Rare Dis. 17(1), 286 (2022)

8. R. Ochoa, **M. A. Soler**, I. Gladich, A. Battisti, N. Minovski, A. Rodriguez, S. Fortuna, P. Cossio, A. Laio
Computational Evolution Protocol for Peptide Design. In: T. Simonson (eds) Computational Peptide Science.
Methods Mol. Biol. 2405, 335-359 (2022)

9. N. Scafuri, **M. A. Soler***, A. Spitaleri and W Rocchia*
Enhanced Molecular Dynamics Method to Efficiently Increase the Discrimination Capability of Computational Protein–Protein Docking
J. Chem. Theory Comput. 17, 7271-7280 (2021)

10. C. Cantarutti*, M. C. Vargas, C. J. D. Foumthuim, M. Dumoulin, S. La Manna, D. Marasco, C. Santambrogio, R. Grandori, G. Scoles, **M. A. Soler**, A. Corazza and S. Fortuna*
Insights on Peptides Topology in the Computational Design of Protein Ligands: The Example of Lysozyme Binding Peptides
Phys. Chem. Chem. Phys. 23, 23158-23172 (2021)

11. **M. A. Soler***, B. Medagli, J. Wang, S. Oloketuyi, G. Bajc, H. Huang, S. Fortuna and A. de Marco*
Effect of Humanizing Mutations on the Stability of the Llama Single-Domain Variable Region
Biomolecules 11 (2), 163 (2021)

12. A. F. Adedeji Olulana*, **M. A. Soler**, M. Lotteri, H. Vondracek, L. Casalis, D. Marasco, M. Castronovo and S. Fortuna*
Computational Evolution of Beta-2-Microglobulin Binding Peptides for Nanopatterned Surface Sensors
Int. J. Mol. Sci. 22, 812 (2021)

13. R. Ochoa, **M. A. Soler**, A. Laio and P. Cossio*
PARCE: Protocol for Amino Acid Refinement through Computational Evolution
Comput. Phys. Commun. 260, 107716 (2021)

14. A. Spitaleri, S. R. Zia, P. Di Micco, B. Al-Lazikani, **M. A. Soler*** and W. Rocchia*
Tuning Local Hydration Enables a Deeper Understanding of Protein–Ligand Binding: The PP1-Src Kinase Case
J. Phys. Chem. Lett. 12, 49–58 (2020)

15. J.-A. Huang*, M. Z. Mousavi, G. Giovannini, Y. Zhao, A. Hubarevich, **M. A. Soler**, W. Rocchia, D. Garoli* and F. De Angelis
Multiplexed Discrimination of Single Amino Acid Residues in Polypeptides in a Single SERS Hot Spot
Angew. Chem. Int. Ed. 59, 11423–11431 (2020)

16. V. Salpietro, C. L. Dixon, H. Guo, O. D. Bello, J. Vandrovcova, S. Efthymiou, R. Maroofian, G. Heimer, L. Burglen, S. Valence and **others**
AMPA Receptor GluA2 Subunit Defects Are a Cause of Neurodevelopmental Disorders
Nat. Commun. 10, 1–16 (2019)

17. **M. A. Soler**, B. Medagli, M. S. Semrau, P. Storici, G. Bajc, A. De Marco, A. Laio* and S. Fortuna*
A Consensus Protocol for the in Silico Optimisation of Antibody Fragments
ChemComm 55, 14043–14046 (2019)

18. R. Ochoa, **M.A. Soler**, A. Laio, and P. Cossio
Assessing the capability of in silico mutation protocols for predicting the finite temperature conformation of amino acids
Phys. Chem. Chem. Phys. 20, 25901-25909 (2018)

19. **M.A. Soler***, S. Fortuna*, A. de Marco, and A. Laio
Binding affinity prediction of nanobody-protein complexes by scoring of molecular dynamics trajectories
Phys. Chem. Chem. Phys. 20, 3438-3444 (2018)

20. **M.A. Soler***, and S. Fortuna*
Influence of Linker Flexibility on the Binding Affinity of Bidentate Binders
J. Phys. Chem. B. 121(16), 3918-3924 (2017)

21. **M.A. Soler**, A. Rodriguez, A. Russo, A.F. Adedeji, C.J.D. Foumthuim, C. Cantarutti, E. Ambrosetti, L. Casalis, A. Corazza, G. Scoles, D. Marasco, A. Laio, and S. Fortuna*
Computational design of cyclic peptides for the customized oriented immobilization of globular proteins
Phys. Chem. Chem. Phys. 19, 2740-2748 (2017)

22. **M.A. Soler***, J. Zúñiga, A. Requena, and A. Bastida
Understanding the connection between conformational changes of peptides and equilibrium thermal fluctuations
Phys. Chem. Chem. Phys. 19, 3459-3463 (2017)

23. **M.A. Soler***, A. De Marco*, and S. Fortuna*
Molecular dynamics simulations and docking enable to explore the biophysical factors controlling the yields of engineered nanobodies
Scientific Reports 6, 34869 (2016)

24. **M.A. Soler**, A. Rey*, and P.F.N. Faísca*
Steric confinement and enhanced local flexibility assist knotting in simple models of protein folding
Phys. Chem. Chem. Phys. 18 (38), 26391-26403 (2016)

25. A. Bastida*, J. Zúñiga, A. Requena, B. Miguel, M.E. Candela, and **M. A. Soler**
Conformational changes of trialanine in water induced by vibrational relaxation of the amide I mode
J. Phys. Chem. B, 120 (2), pp 348-357 (2016)

26. F. Fogolari*, C.J.D. Foumthuim, S. Fortuna, **M. A. Soler**, A. Corazza, and G. Esposito
Accurate estimation of the entropy of rotation-translation probability distributions
J. Chem. Theory Comput., 12 (1), pp 1-8 (2016)

27. F. Fogolari*, A. Corazza, S. Fortuna, **M. A. Soler**, B. VanSchouwen, G. Brancolini, S. Corni, G. Melacini, and G. Esposito
Distance-based configurational entropy of proteins from molecular dynamics simulations
PLoS ONE 10(7): e0132356. (2015)

28. **M. A. Soler***, A. Nunes and P. Faísca*
Effects of knot type in the folding of topologically complex lattice proteins
J. Chem. Phys. 141, 025101 (2014)

29. **M. A. Soler**, T. Nelson, A. Roitberg, S. Tretiak* and S. Fernández-Alberti*
A signature of nonadiabatic couplings in molecular excited states vibrational modes
J. Phys. Chem. A, 118 (45), 10372-10379 (2014)

30. **M. A. Soler*** and P.F.N. Faísca*
The effects of knots on protein folding properties
PLoS ONE 8(9): e74755 (2013)

31. **M. A. Soler*** and P.F.N. Faísca*
How Difficult Is It to Fold a Knotted Protein? In Silico Insights from Surface-Tethered Folding Experiments
PLoS ONE 7(12): e52343 (2012)

32. **M. A. Soler**, A. Roitberg, T. Nelson, S. Tretiak and S. Fernández-Alberti*
Analysis of state-specific vibrations coupled to the unidirectional energy transfer in conjugated dendrimers

J. Phys. Chem. A, 116, 9802-9810 (2012)

33. A. Bastida*, **M. A. Soler**, J. Zúñiga, A. Requena, A. Kalstein and S. Fernández-Alberti*
Hybrid Quantum/Classical Simulations of the Vibrational Relaxation of the Amide I Mode of N-Methylacetamide in D2O Solution
J. Phys. Chem. B, 116, 2969-2980 (2012)

34. **M. A. Soler**, A. Bastida*, M. H. Farag, J. Zúñiga and A. Requena
A method for analyzing the vibrational energy flow in biomolecules in solution
J. Chem. Phys., 135, 204106 (2011)

35. A. Kalstein, S. Fernández-Alberti, A. Bastida*, **M. A. Soler**, M. H. Farag, J. Zúñiga and A. Requena
Vibrational dynamics of polyatomic molecules in solution: assignment, time evolution and mixing of instantaneous normal modes
Theor. Chem. Acc. 128, 769-782 (2011)

36. A. Bastida*, **M. A. Soler**, J. Zúñiga, A. Requena, A. Kalstein and S. Fernández-Alberti
Molecular dynamics simulations and instantaneous normal mode analysis of the vibrational relaxation of the C-H stretching modes of N-methylacetamide-D in liquid deuterated water
J. Phys. Chem. A, 114, 11450-11461 (2010)

37. A. Bastida*, **M. A. Soler**, J. Zúñiga, A. Requena, A. Kalstein and S. Fernández-Alberti
Instantaneous normal modes, resonances. and decay channels in the vibrational relaxation of the amide I mode of N-methylacetamide-D in liquid deuterated water
J. Chem. Phys., 132, 224501 (2010)

38. A. Bastida*, **M. A. Soler**, J. Zúñiga, A. Requena and B. Miguel
Efficient parabolic evaluation of coupling terms in hybrid quantum/classical simulations
Chem. Phys, 358, 57-60 (2009)

39. A. Espinosa*, A. Frontera, R. García, **M. A. Soler** and A. Tárraga*
Electrophilic behavior of 3-methyl-2-methylthio-1,3,4-thiadiazolium salts: a multimodal theorical approach
ARKIVOC, IX, 415-437 (2005)

Conference Contributions

1. Miguel A. Soler.
   In silico design of protein binders for medical applications.
   Integrative Approaches to Protein Folding & Aggregation.
   Oral Presentation.
   Lisbon, Portugal. June 11–12, 2019.

2. Miguel A. Soler, Sara Fortuna, and Alessandro Laio.
   In silico design of binders for the molecular recognition of protein targets.
   Self-Assembly, Recognition, and Applications (SARA) 2017.
   Oral Presentation.
   Lincoln, UK. December 14, 2017.

3. Miguel A. Soler, Sara Fortuna, and Alessandro Laio.
   Computational design of binders for protein molecular recognition.
   5th Annual CCP-BioSim Conference "Frontiers of Biomolecular Simulation".
   Oral Presentation.
   Southampton, UK. September 13–15, 2017.

4. Miguel A. Soler, and Sara Fortuna.
   Computational design of nanobodies for the molecular recognition of protein targets.
   Congress: Self-assembly, Recognition and Applications, Institute of Physics (IOP).
   Oral Presentation.
   Edinburgh, UK. December 9, 2016.

5. Miguel A. Soler, Ario de Marco and Sara Fortuna.
   Computational design of customised nanobodies for biotechnological applications.
   The Physics of Soft and Biological Matter, Institute of Physics (IOP).
   Poster.
   Cambridge, UK. April 6–8, 2016.

6. Miguel A. Soler, Sara Fortuna and Giacinto Scoles.
   Computational design of peptides as probes for the recognition of protein biomarkers.
   10th European Biophysics Congress.
   Dresden, Germany. July 18–22, 2015.
   Poster.
   Published in: **M.A. Soler***, S. Fortuna, G. Scoles. Eur Biophys J, 44 (Suppl 1):S149 (2015).

7. Miguel A. Soler, Sara Fortuna y Giacinto Scoles.
   Computational design of peptides as probes for the recognition of Beta-2-microglobulin.
   EMBO Workshop on Advances in protein-protein interaction analysis and modulation.
   Poster.
   Hyeres, France. September 9–12, 2014.

8. Miguel A. Soler and Patricia F.N. Faísca.
   Understanding the effects of knots on protein folding properties.
   The 27th Annual Symposium of the Protein Society.
   Boston, USA. July 20–23, 2013.
   Poster.
   Published in: **M. A. Soler*** and P.F.N. Faísca*. Protein Science, 22, Issue S1, 96-97 (2013).

9. Miguel A. Soler and Patricia F.N. Faísca.
   How difficult is it to fold a knotted protein? The effect of surface tethering.
   Workshop of Protein Folding: Integrating theory, simulation and experiment.
   Poster.
   Zurich (Switzerland). September 3–6, 2012.

Technical Skills

- Advanced user of the Linux and Windows OSs.
- Advanced knowledge of programming in Fortran, C++ and Bash Scripting.
- Advanced user of Gromacs, HADDOCK, Autodock Vina, FoldX, Pymol, Chimera and VMD programs.
- Advanced user in national/international high performance computing (HPC) resources.
- Italian Course Level B1 (100 hours).
  University of Udine.