

## **Dr. Filip Miljković**

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<b>LinkedIn profile</b>	<a href="https://www.linkedin.com/in/fmiljkovic/">https://www.linkedin.com/in/fmiljkovic/</a>
<b>ResearchGate profile</b>	<a href="https://www.researchgate.net/profile/Filip_Miljkovic">https://www.researchgate.net/profile/Filip_Miljkovic</a>
<b>Work experience</b>	<p>February 2020 – Present</p> <p><b>Data Scientist, Computational DMPK &amp; Safety</b></p> <p>AstraZeneca R&amp;D, Gothenburg, Sweden</p> <p>Department of Clinical Pharmacology &amp; Safety Sciences</p>
<b>Education</b>	<p>June 2016 – December 2019</p> <p><b>PhD (Dr. rer. nat.) in Computational Life Sciences</b></p> <p>Rheinische Friedrich-Wilhelms-Universität Bonn, Germany</p> <p>LIMES Program Unit Chemical Biology and Medicinal Chemistry</p> <p>Department of Life Science Informatics, b-it</p> <p>Grade: 0.7 (<i>Magna cum laude</i>)</p> <p>Thesis: Chemoinformatics-Driven Approaches for Kinase Drug Discovery</p> <p>Supervisor: Prof. Jürgen Bajorath</p> <p>October 2009 – September 2014</p> <p><b>Master degree in Pharmacy (Integrated studies)</b></p> <p>University of Niš, Serbia</p> <p>Faculty of Medicine</p> <p>Department of Pharmacy</p> <p>Grade: 9.58/10.00</p> <p>Thesis: An Overview of Dipeptidyl Peptidase-IV Inhibitors.</p> <p>Supervisor: Prof. Andrija Šmelcerović</p>
<b>International experience</b>	<p>July 2013 – August 2013</p> <p><b>IPSF Student Exchange Programme</b></p> <p>Medical University of Gdańsk, Poland</p> <p>Department of Analytical Chemistry</p>

Description: Quality consistency evaluation of *Melissa officinalis* L. samples using HPLC fingerprints.

Supervisor: Agnieszka Viapiana, PhD

**Technical skills**

Data extraction/curation (KNIME, RDKit and OpenEye Chemistry Toolkit), SAR analysis, Network analysis (Cytoscape, Gephi, NetworkX Python package), 2D and 3D ligand similarity, Structure- and Ligand-based virtual screening, Molecular modeling suites (MOE), Docking (MOE Dock, AutoDock, PLANTS, DockTite for covalent docking), Protein-ligand interaction fingerprints, Machine learning (SVM, RF, DNN; scikit-learn, TensorFlow).

**Computer skills**

Windows, Office suite, Chemoffice, Python (advanced knowledge), Bash (basic knowledge), R (basic knowledge), SQL (basic knowledge).

**Language skills**

Serbian (native speaker)

English (professional knowledge): TOEFL (109/120)

German (good knowledge)

**Teaching**

**Master's Program in Pharmacy at the Medical faculty, University of Niš, Serbia**

“General Chemistry with Stoichiometry”, October 2010 – January 2011.

“Organic Chemistry”, March 2011 – June 2011.

**Master's Program in Life Science Informatics at the University of Bonn, Germany**

“Introduction to Chemistry”, September 2016 – October 2016.

“Structural Bioinformatics”, October 2016 – January 2018.

“Molecular Modeling and Drug Design”, April 2017 – February 2019.

“Programming Lab I” (Python), April 2019 – June 2019.

“Introduction to Machine Learning Tutorial”, April 2019 – June 2019.

Supervision of Master Thesis, Mariana González-Medina, 2019.

**Visiting Students Coming from Collaborative Projects between  
University of Bonn, Germany and Kyoto University, Japan or  
Waseda University, Japan**

“Structural Bioinformatics and Molecular Modeling”, October 2017 –  
December 2019.

**Publications**

1. **Miljković, F.**; Rodríguez-Pérez, R.; Bajorath J. Machine Learning Models for Accurate Prediction of Kinase Inhibitors with Different Binding Modes. *J. Med. Chem.* doi: 10.1021/acs.jmedchem.9b00867.
2. **Miljković, F.**; Bajorath, J. Data structures for computational compound promiscuity analysis and exemplary applications to inhibitors of the human kinome. *J. Comput. Aided Mol. Des.* **2020**, *34*, 1-10.
3. González-Medina, M.; **Miljković, F.**; Haase, G. S.; Drueckes, P.; Trappe, J; Laufer, S; Bajorath, J. Promiscuity analysis of a kinase panel screen with designated p38 alpha inhibitors. *Eur. J. Med. Chem.* **2020**, *187*, 112004.
4. Feldmann, C.; **Miljković, F.**; Yonchev, D.; Bajorath, J. Identifying promiscuous compounds with activity against different target classes. *Molecules* **2019**, *24*, e4185.
5. **Miljković, F.**; Bajorath J. Data Structures for Compound Promiscuity Analysis: Cliffs, Pathways, and Hubs Formed by Inhibitors of the Human Kinome. *Future Sci. OA* **2019**, *5*, FSO404.
6. **Miljković, F.**; Vogt, M.; Bajorath, J. Systematic Computational Identification of Promiscuity Cliff Pathways Formed by Inhibitors of the Human Kinome. *J. Comput. Aided Mol. Des.* **2019**, *33*, 559-572.
7. Blaschke, T.; **Miljković, F.**; Bajorath, J. Prediction of Different Classes of Promiscuous and Nonpromiscuous Compounds Using Machine Learning and Nearest Neighbor Analysis. *ACS Omega* **2019**, *4*, 6883-6890.
8. **Miljković, F.**; Bajorath, J. Computational Analysis of Kinase Inhibitors Identifies

- Promiscuity Cliffs across the Human Kinome. *ACS Omega* **2018**, *3*, 17295–17308.
9. **Miljković, F.**; Bajorath, J. Data-Driven Exploration of Selectivity and Off-Target Activities of Designated Chemical Probes. *Mol.* **2018**, *23*, e2434.
  10. **Miljković, F.**; Bajorath, J. Evaluation of Kinase Inhibitor Selectivity Using Cell-Based Profiling Data. *Mol. Inform.* **2018**, *37*, e1800024.
  11. **Miljković, F.**; Bajorath, J. Reconciling Selectivity Trends from a Comprehensive Kinase Inhibitor Profiling Campaign with Known Activity Data. *ACS Omega* **2018**, *3*, 3113–3119.
  12. **Miljković, F.**; Bajorath, J. Exploring Selectivity of Multikinase Inhibitors across the Human Kinome. *ACS Omega* **2018**, *3*, 1147–1153.
  13. **Miljković, F.**; Kunitomo, R.; Bajorath, J. Identifying Relationships between Unrelated Pharmaceutical Target Proteins on the Basis of Shared Active Compounds. *Future Sci. OA* **2017**, *3*, FSO212.
  14. Smelcerovic, A.; **Miljkovic, F.**; Kolarevic, A.; Lazarevic, J.; Djordjevic, A.; Kocic, G.; Anderluh, M. An Overview of Recent Dipeptidyl Peptidase-IV Inhibitors: Linking Their Structure and Physico-Chemical Properties with SAR, Pharmacokinetics and Toxicity. *Curr. Top. Med. Chem.* **2015**, *15*, 2342-2372.
  15. Toropov, A. A.; Veselinović, J. B.; Veselinović, A. M.; **Miljković, F. N.**; Toropova, A. P. QSAR Models for 1,2,4-Benzotriazines as Src Inhibitors Based on Monte Carlo Method. *Med. Chem. Res.* **2015**, *24*, 283-290.
  16. Toropova, A. P.; Toropov, A. A.; Veselinović, J. B.; **Miljković, F. N.**; Veselinović, A. M. QSAR Models for HEPT Derivates as NNRTI Inhibitors Based on Monte Carlo Method. *Eur. J. Med. Chem.* **2014**, *77*, 298-305.

## Conferences

1. “Chemoinformatics Strasbourg Summer School”, 25 June – 29 June 2018, University of Strasbourg, Strasbourg, France. Poster: **Miljković, F.**; Bajorath, J. “Exploring Selectivity of Multi-kinase Inhibitors across the Human Kinome”, awarded as the best poster by public choice.
2. “11<sup>th</sup> International Conference “Physical Chemistry 2012””, 24 September – 28 September 2012, Society of Physical Chemists of Serbia, Belgrade, Serbia. Conference Paper: Nikolić, G.M.; Veselinović, A. M.; Mitić, Ž. J.; **Miljković F. S.** Application of Multivariate Curve Resolution-alternating Least Squares (MCRALS) Method for the Study of Cu(II) Ion Influence on the Pyrogallol Autoxidation in Aqueous Solution. *Proceedings of the 11th International Conference on Fundamental and Applied Aspects of Physical Chemistry* **2012**, *1*, 188-190.

3. "4<sup>th</sup> BBBB International Conference on Pharmaceutical Sciences", 29 September – 1 October 2011, Slovenian Pharmaceutical Society, Bled, Slovenia. Conference Paper: Nikolić, G. M.; Živković, J. V.; Nikolić, M. G; **Miljković, F.** Synergism in the Extraction of Paracetamol from the Aqueous NaCl Solutions by the Diethyl Ether/1-Butanol Binary Solvent Mixtures. *Eur. J. Med. Chem.* **2011**, 44 (S1), 183-184.