Curriculum vitae

Personal Information

Name and surname: Janez Konc
Date and place of birth: 23.9.1978, Ljubljana
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G: Google Scholar Profile

Education

2008	Ph.D. Pharmacy, University of Ljubljana, Slovenia
2004	B.S. Pharmacy, University of Ljubljana, Slovenia
2000 – 2004	Undergraduate study, Faculty of Computer and Information Science, University of Ljubljana, Slovenia, 2 years completed

Positions

2016	Associate Professor, Bioinformatics, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska, Slovenia
2011	Assistant Professor, Medicinal Chemistry, Faculty of Pharmacy, University of Ljubljana, Slovenia
2006	Teaching Assistant, Medicinal Chemistry, Faculty of Pharmacy, University of Ljubljana, Slovenia

Affiliations

2016–present	Senior Research Associate, Department of Molecular Modeling, National Institute of Chemistry, Ljubljana, Slovenia
2016–present	Senior Research Associate (10%), Department of Applied Natural Sciences, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska
2015–present	Research Associate (10%), Faculty of Chemistry and Chemical Engineering, University of Maribor
2011	Research Associate, Department for Molecular Modeling, National Institute of Chemistry, Ljubljana, Slovenia
2015–2016	Research Associate (10%), Department of Applied Natural Sciences, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska
2008 – 2011	Postdoctoral Associate, Laboratory for Molecular Modeling, National Institute of Chemistry, Ljubljana, Slovenia
2004 – 2008	Young Researcher, Laboratory for Molecular Modeling, National Institute of Chemistry, Ljubljana, Slovenia

Project Leadership

2017–present Project Leader of 3-year research project L7-8269 titled *"New approaches for better biopharmaceuticals"* funded by Slovenian Research Agency

2014 Project Leader of Industrial project with Lek - Sandoz company titled *"In silico profiling of biological drug under development"*

2010 – 2012 Project Leader, 2-year Basic Postdoctoral Project Z1-3666: "Algorithms development for protein binding sites prediction" funded by Slovenian Research Agency

Mentorship

Samo Lešnik Graduate student (young researcher), Faculty of Pharmacy, University of Ljubljana (2017)

Mitja Ogrizek Graduate student, Faculty of Medicine, University of Ljubljana (2016)

Urška Zirnstein Undergraduate student, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska (2015)

Marko Breznik Undergraduate student, Faculty of Chemistry and Chemical Technology, University of Maribor (2017)

Blaž Škrlj Undergraduate student, Faculty of Biotechnology, University of Ljubljana (2016)

Tanja Štular Undergraduate student, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska (2015)

Špela Pikl Undergraduate student, Faculty of Biotechnology, University of Ljubljana (2015)

Samo Lešnik Undergraduate student, Faculty of Pharmacy, University of Ljubljana (2013)

Žiga Strmšek Undergraduate student, Faculty of Biotechnology, University of Ljubljana (2013)

Tomo Česnik Undergraduate student, Faculty of Computer and Information Science, University of Ljubljana (2011)

Professional Activities

2013 Member of a Committee for Assessment of Doctoral Thesis, Faculty of Pharmacy, University of Ljubljana, Slovenia

2012 Member of a Committee for Assessment of Doctoral Thesis, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska, Slovenia

2012 Member of a Committee for Assessment of Candidate for Academic Title, Faculty of Pharmacy, University of Ljubljana, Slovenia

2011 Member of a Committee for Assessment of Doctoral Thesis, Faculty of Pharmacy, University of Ljubljana, Slovenia

Honors and Awards

2013-2014 Fulbright award for research at the National Institutes of Health, Bethesda, MD, USA

2009 Selected as one of the top 15% of reviewers for ACS journal J. Chem. Inf. Model. in year 2009

2004	Krka award for bachelor's degree research thesis awarded by the Krka pharmaceutical company

Fellowships

2013-2014	Fulbright award for research at the National Institutes of Health, Bethesda, MD, USA
2010	ECCB10 Fellowship for Participation in the “9th European Conference on Computational Biology”, Belgium
2010	ERASysBio Fellowship for Participation in the Summer School on “Data Management for Systems Biology III”, Spain
2010	ISMB Fellowship for Participation in the “Intelligent Systems for Molecular Biology Conference”, USA
2009 – 2010	Post-doctoral Fellowship in the Laboratory of Theory of Biopolymers, Faculty of Chemistry, University of Warsaw
2009	Jozef Mianowski Research Fellowship, Foundation for Polish Science, Warsaw, Poland

Skills

- Highly proficient in C++
- Experienced with Javascsript, Python, PHP, Perl, HTML5
- Proficient with Linux platform, Bash scripting
- Experienced with CHARMM, PyMol, OpenMM, etc.
- Languages: English, Polish, Slovenian, German (passive)

Research Interests

1) Development of heuristic and exact algorithms for NP hard problems in bioinformatics (http://insilab.org/maxclique)
2) Development of algorithms for detecting structurally similar binding sites in proteins using protein graph theory
3) Development of a freely accessible web server ProBiS (http://probis.cmm.ki.si) for the detection of protein binding sites
4) Development of a freely accessible web server ENZO (http://enzo.cmm.ki.si) for the study of enzyme kinetics
5) Development of ProBiS-CHARMMing web server (http://probis.nih.gov) for prediction of ligands and their binding energies

Recent Research Activity

I develop new algorithms for the detection of structurally similar protein binding sites, which are based on the fact that protein surface structures are conserved in binding sites regions. These algorithms search for local similarities in physical-chemical properties in different protein surface structures independently of sequence or fold. The proteins are modeled as protein graphs, i.e., rigid 3D objects, consisting of vertices and edges. The newly developed algorithms are used for prediction of protein binding sites on known structures of proteins from the RCSB protein bank;

particularly, I focus on pharmaceutically interesting proteins, which could become targets for the next generation of pharmaceuticals.