

Lukasz P. Kozłowski

Work Address

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Research Interests

- development of bioinformatics tools and databases for proteins and RNAs
- proteomics
- intrinsic protein disorder and its function in biological systems
- theoretical studies of protein and RNA folding, dynamics
- next-generation sequencing (NGS) data analysis
- single nucleotide polymorphism (SNP) influence on human diseases
- structural bioinformatics and structural biology
- advanced machine learning (deep learning, ANN, SVM, genetic algorithms, numeric optimization)
- protein structure modeling
- protein and RNA sequence analysis

Projects

- 🔗 **Proteome-pI - Proteome Isoelectric Point Database** (an independent project, sole author, published in *Nucleic Acid Research*; the database contains the data for >21 million of sequences from 5,029 proteomes calculated by 18 methods)
- 🔗 **IPC – Isoelectric Point Calculator** (~ 200 visitors per day - [stats](#), an independent project, sole author, published in *Biology Direct*)
- 🔗 **MetaDisorder** – prediction of intrinsic disorder in proteins (in 2008 I developed the best program according [CASP8](#) beating over 20 other programs for protein disorder prediction in blind test, see [here](#), a group 153, the publication cited >100 times, *Highly Cited Paper*)
- 🔗 **GeneSilico fold recognition server** the development and the maintenance; in over 5 years I integrated there >100 bioinformatics tools related to the protein structure prediction; currently the platform uses 1.7TB of disc space for the programs and another 2TB for biological databases e.g., PDB, nr – most updated weekly; run in parallel on three blade servers connected through >40 GB MySQL database (over 3500 registered users)
- 🔗 **GDFuzz3D** – protein contact map to 3D structure retrieval service
- 🔗 Human pre-mRNA 3'-end processing machinery database
- 🔗 Shannon Entropy Calculator (~100 visitors per day - [stats](#))

Technical skills

Problem solving

- analysis of complex data using advanced statistics & machine learning (e.g. deep learning, artificial neural networks, support vector machines, genetic algorithms, numeric optimization)

Software development

- *programming languages*: PYTHON, JavaScript, PHP, R, C++, C, shell
- *databases*: MySQL, PostgreSQL
- *OS*: UNIX (Linux, FreeBSD), Windows

Scientific packages





- in-depth knowledge of bioinformatics programs (e.g. BLAST, HHSearch, ClustalW, MAFFT, UCSD Chimera, VMD, Modeller, MEME, CD-HIT, ABYSS, Ray, Velvet and few hundred others; I have written uncountable number of the wrappers, parsers and pipelines using most of the bioinformatic software related to proteins, RNAs and NGS)

Languages

- Polish (native), English (CAE, fluent spoken and written), German (basic)

Educational Background

Ph.D. (2013, *biochemistry, cum laude*), BSc (2007, *informatics*), MSc (2006, *genetics*), BSc (2004, *biology*)














- 2008 – 2013 **Ph.D. (biochemistry, bioinformatics, *cum laude*)** Institute of Biochemistry and Biophysics of the Polish Academy of Science, **Thesis title:** *Integrated bioinformatics platform for protein analysis. Prediction of protein domain and intrinsic protein disorder* 
- 2005 – 2007 **Bachelor's degree:** Jan Kochanowski University of Humanities and Sciences, Institute of Physics, Division of Computer Science, **Thesis title:** *Determining amino acid composition in proteins using genetic algorithm* 
- 2004 – 2006 **Master's degree:** Jan Kochanowski University of Humanities and Sciences, Institute of Biology, Department of Biochemistry and Genetics, **Thesis title:** *Phylogenetic analysis of the linker histones in vertebrates* 
- 2001 – 2004 **Bachelor's degree:** Jan Kochanowski University of Humanities and Sciences, Institute of Biology, Department of Biochemistry and Genetics, **Thesis title:** *The diversity of linker histones in vertebrates* 

Employment

- 2015 – 2017 Postdoctoral Researcher, Max Planck Institute for Biophysical Chemistry, **Germany**
- 2013 – 2015 Postdoctoral Researcher, The International Institute of Molecular and Cell Biology, **Poland**
- 2010 – 2011 Self-employed sole trader (E-commerce, I wrote a dedicated platform for automatic online transaction processing, the electronic funds transfers, an inventory management and accounting under MySQL database), **Poland**
- 2008 – 2013 Ph.D. Student, The International Institute of Molecular and Cell Biology, **Poland**
- 2007 – 2008 Research assistant, Bioinformatician, The International Institute of Molecular and Cell Biology, **Poland**
- 2006 – 2007 Research assistant, Genetics, The Jan Kochanowski Swietokrzyski University in Kielce, **Poland**

Publications


-   **Kozłowski LP*** *Proteome-pI - Proteome Isoelectric Point Database* **Nucleic Acids Res.** 2017, 45 (D1): D1112-D1116 doi: 10.1093/nar/gkw978
-   **Kozłowski LP*** *IPC - Isoelectric point calculator.* **Biology Direct** 2016, 11:55. doi:10.1186/s13062-016-0159-9
-  Pawłowski M, **Kozłowski L**, Kloczkowski A. *MQAPsingle: A quasi single-model approach for estimation of the quality of individual protein structure models.* **Proteins** 2016, 84(8):1021-8, doi: 10.1002/prot.24787
-   Plotka M, Kaczorowska AK, Morzywolek A, Makowska J, **Kozłowski LP**, et al. *Biochemical Characterization and Validation of a Catalytic Site of a Highly Thermostable Ts2631 Endolysin from the Thermus scotoductus Phage vB_Tsc2631.* **PLoS One** 2015, 10(9):e0137374, doi: 10.1371/journal.pone.0137374
-   Pietal MJ, Bujnicki JM, **Kozłowski LP** *GDFuzz3D: a method for protein 3D structure reconstruction from contact maps, based on a non-Euclidean distance function.* **Bioinformatics** 2015, 31(21), 3499-3505, doi: 10.1093/bioinformatics/btv390
-   Główny D, Pianka D, Sulej AA, **Kozłowski LP**, et al. *Sequence-specific cleavage of dsRNA by Mini-III RNase.* **Nucleic Acids Res.** 2015, 43(5):2864-73, doi: 10.1093/nar/gkv00
-   Sierocka I, **Kozłowski LP**, Bujnicki JM, Jarmolowski A, Szweykowska-Kulinska Z *Female-specific gene expression in dioecious liverwort Pellia endiviifolia is developmentally regulated and connected to archegonia production.* **BMC Plant Biol.** 2014, 14:168, doi: 10.1186/1471-2229-14-168
-   Plotka M, Kaczorowska AK, Stefanska A, Morzywolek A, Fridjonsson O, Dunin-Horkawicz S, **Kozłowski L**, et al. *Discovery and characterization of a novel highly thermostable endolysin from Thermus scotoductus MAT2119 bacteriophage Ph2119 that shows amino-acid sequence similarity to eukaryotic peptidoglycan recognition proteins (PGRPs).* **Appl Env Microbiol** 2013 80(3):886-95, doi: 10.1128/AEM.03074-13
-  Tuszyńska I, Matelska D, Magnus M, Chojnowski G, Kasprzak JM, **Kozłowski LP**, et al. *Computational modeling of protein-RNA complex structures.* **Methods** 2013, 65(3):310-9, doi: 10.1016/j.ymeth.2013.09.014 (review)

-   Puton T, **Kozłowski L**, Rother KM, Bujnicki JM *CompaRNA: a server for continuous benchmarking of automated methods for RNA secondary structure prediction*. **Nucleic Acids Res.** **2013**, 41(7):4307-23, doi: 10.1093/nar/gkt101 **Highly accessed**
-   **Kozłowski LP**, Bujnicki JM *MetaDisorder: a meta-server for the prediction of intrinsic disorder in proteins*. **BMC Bioinformatics** **2012**, 13:111, doi: 10.1186/1471-2105-13-111 **Highly accessed**  **Highly Cited Paper**
-  Al-Haggar M, Madej-Pilarczyk A, **Kozłowski L**, et al. *A novel homozygous p.Arg527Leu LMNA mutation in two unrelated Egyptian families causes overlapping mandibuloacral dysplasia and progeria syndrome*. **Eur J Human Genet** **2012**, 20 (11), 1134-1140, doi: 10.1038/ejhg.2012.77
-   Puton T, **Kozłowski L**[&], Tuszynska I, Rother K, Bujnicki JM *Computational methods for prediction of protein-RNA interactions*. **J Struct Biol** **2012**, 179 (3), 261-268 doi:10.1016/j.jsb.2011.10.001 (review) **Highly accessed**
-   Nakagome S, Mano S, **Kozłowski L**, Bujnicki JM, Shibata H, Fukumaki Y, Kidd JR, Kidd KK, Kawamura S, Oota H *Crohn's disease risk alleles on the NOD2 locus have been maintained by natural selection on standing variation*. **Mol Biol Evol.** **2012** Jun;29(6):1569-85, doi: 10.1093/molbev/mss006
-  **Kozłowski L**, Orłowski J, Bujnicki JM *Structure prediction of alternatively spliced proteins* in "Alternative pre-mRNA Splicing: Theory and Protocols" Editors: Stefan Stamm, Christopher Smith, Reinhard Luehrmann, Wiley-Blackwell, **2012**, 582-591 (**book chapter**)
-  Majorek K, **Kozłowski L**, Jakalski M, Bujnicki JM *First steps of protein structure prediction* in *Prediction of Protein Structures, Functions and Interactions* Editors: Bujnicki; Wiley&Sons, **2008**, 2, 39–62, (**book chapter**)
-  Pałyga J, **Kozłowski L** *Structure and function of molecular chaperone HSP90*. *Sowriemiennyj Naucznyj Wiestnik Ser. Biologija Chimija* **2007**, 15(23), 46-65 (review)

* single authorship publications & shared first authorship  Highly Cited Paper (Top 1% in WoS)
 the main paper  supplementary data



Other

- Referee in Scientific Journals  Nucleic Acid Res. (13), Bioinformatics (4), BMC Bioinformatics (1), PeerJ (2), Knowledge-Based Systems (4), Acta Biochimica Pol. (1), IJMS (1) and few others (>30 reviews)
- Membership in Societies International Society for Computational Biology (ISCB, 2009-)
 Society for Bioinformatics in Northern Europe (SocBiN, 2017-)
 Polish Bioinformatics Society (PTBI, 2008-)
 Polish Biochemical Society (PTBioch, 2015-)
- Member of expert panel in the National Centre of Research and Development (NCRD, pol. *NCBiR*), Poland

Conferences

- 2017 ISMB/ECCB 2017, Prague, **Czech Republic**, Jul 21-25 (poster)
- 2016 13th Horizons in Molecular Biology Symposium, Gottingen, **Germany**, Sep 12-15
- 2016 FRET 2, International Discussion Meeting on Förster Resonance Energy Transfer, Gottingen, **Germany**, Apr 3-6
- 2016 DAGStat2016, 4th Joint Statistical Meeting, Gottingen, **Germany**, Mar 14-18
- 2015 RECOMB 2015 (19th Annual International Conference on Research in Computational Molecular Biology) Warsaw, **Poland**, Apr 12-15 ([poster](#)),
- 2014 BIO 2014 (1st Congress of the Polish Biochemistry, Cell Biology, Biophysics and Bioinformatics), Warsaw, **Poland**, Sep 9-12 ([poster](#))
- 2014 ECCB'14 – European Conference on Computational Biology, Strasburg, **France**, Sep 7-10 ([poster](#)),
- 2013 RNA 3' ends: Mechanism and biological function in eukaryotic genomes, Oxford, **UK**, Sep 25-29 ([poster](#))
- 2013 SocBiN Bioinformatics/BIT13, Torun, **Poland**, Jun 26-29 ([poster](#))
- 2013 Cancer genetics for medical community, Warsaw, **Poland**, Jun 17 (poster)
- 2012 CASP10, Gaeta, **Italy**, Dec 9-12 ([poster](#))
- 2012 BIT12, Torun, **Poland**, Sep 27-29 (lecture & poster)
- 2012 PTBI12, **Poland**, May 25-27 ([lecture](#) & [poster](#))

- 2011 MultiPole Approach to Structural Biology, Warsaw, **Poland**, Nov 16-19 (poster)
- 2011 PTBI11, Krakow, **Poland**, Sep 30 - Oct 2, 2011 ([lecture](#) & poster)
- 2011 BIT11, Torun, **Poland**, June 2-4 (lecture & poster)
- 2010 CASP9, Pacific Groove, **USA**, Dec 5-9 (poster)
- 2010 HealthProt workshop, Warsaw, **Poland**, Aug 27-30 (poster)
- 2010 EURASNET, Frontiers in Structural Biology of RNAs and RNPs, Poznan, **Poland**, Aug 16-19 (poster)
- 2010 BIT10, Toruń, **Poland**, June 10-12 (lecture & poster)
- 2009 PTBI09, Poznań, **Poland**, October 2-4 (lecture & poster)
- 2009 ISMB/ECCB (Intelligent Systems for Molecular Biology/ European Conference on Computational Biology) 2009, Stockholm, **Sweden**, Jun 27 – Jul 2 (poster)
- 2009 BIT09 (Bioinformatics in Toruń), Toruń, **Poland**, May 21-23 (lecture & poster)
- 2008 CASP8 (Critical Assessment of Techniques for Protein Structure Prediction), Sardinia, **Italy**, Dec 3-7 ([poster](#) & invited lecture)
- 2008 PTBI08 (1st Annual Meeting of Polish Bioinformatics Society), Jadwisin, **Poland**, Oct 3-5 (lecture & poster)
- 2008 SocBin Bioinformatics 2008, Warsaw, **Poland**, Apr 24-27 (lecture & [poster](#))





Workshops & Training

- 2017 Central Anti-Corruption Bureau's (CBA) online training (three modules: [Corruption in public administration](#), [Corruption in bussines](#) and [Social consequences of corruption](#)), Mar-Apr
- 2014 Advanced RNA-Seq and ChIP-Seq Data Analysis Course, EMBL-EBI, **UK**, May 12-15
- 2013 Automated and Reproducible Analysis of NGS data (ARANGS13) Course, Oeiras, **Portugal**, Oct 21-24
- 2011 EMBO Young Scientists Forum, Warsaw, **Poland**, Jun 30 -Jul 01
- 2010 Workshop on Interdisciplinary Grant Application, Warsaw, **Poland**, Oct 6
- 2010 Workshop, Grid Computing and Bioinformatics, PL-GRID, Toruń, **Poland**, Jun 12
- 2010 Workshop on Scientific Communication, Warsaw, **Poland**, Apr 26-30
- 2010 EMBO workshop: RNA and RNA-processing enzymes. Warsaw, **Poland** Apr 14-16 ([poster](#))
- 2010 School of Molecular Medicine. Warsaw, **Poland**, Apr 12-15
- 2010 CambridgePYTHON's Innovation Academy, Warsaw, **Poland**, Mar 6, 20, 29

Varia

- 2011 co-organization of “MultiPole Approach to Structural Biology”, Warsaw, **Poland**, Nov 16-19
- 2016 organization of the tutorial on protein modeling, within Bioinformatics Course for master students in Gottingen University, Gottingen, **Germany**, Nov 1-2 ([Part 1](#), [Part2](#))

Grants

- 2008-2013 Polish Ministry of Science and Higher Education (grant no. NN301 190139) – the main contractor
- 2009-2012 Health-Prot: Proteins in Health and Disease (EU, FP7, grant no. 229676) – a contractor 
- 2011-2015 European Research Council (ERC StG Grant RNA+P=123, grant no. 26135) – a contractor 
- 2012-2014 Exgenome Molecular Enzymes (EU, FP7, grant no. 286556) – a contractor 
- 2013-2014 Polish Ministry of Science and Higher Education (IUVENTUS PLUS grant no. 0301/IP1/2013/72) – a **PI**
- 2016-2020 Virus-X: Viral Metagenomics for Innovation Value (EU, Horizon2020, grant no. 685778) – contractor 

Fellowships

- 2008 Masovian Fellowship for Ph.D. Students
- 2015-2017 Max Planck Institute Fellowship

In free time active Wikipedian
(> 1,000 edits)



Online version of CV available at: <http://goo.gl/JgTHzC>



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