

Łukasz P. Kozłowski

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<http://bioinformatics.mlhpc.org>
<http://www.solidscientometrics.com>

Research Interests

- computational biology (bioinformatics, structural biology, proteomics, genomics, intrinsic protein disorder, next-generation sequencing, single nucleotide polymorphism)
- big data & machine learning (deep learning, SVM, genetic algorithms, numeric optimization, HPC)
- bibliometrics, scientometrics

Projects

-  **pSSdb - the database of predicted secondary structure of (almost) all proteins.** Covers databases such as [UniProt](#), [NCBI nr](#), [PDB](#), [BFD](#), [Mgnify](#), [JGI IMG](#), [GMGC AlphaFold database](#) and [ESMatlas](#) sequences. Contains secondary structure predictions from up to eight methods for over 7 billion protein sequences and >90k proteomes. HPC resources used: 20M CPUh, 1M GPUh at TOP500 machines ([Ares](#), [Athena](#), [LUMI](#)). Contribution: 100% Status: operational since 2024
-  **Proteome-pI 2.0 - Proteome Isoelectric Point Database** (pI for over 61 million sequences from 20,115 proteomes calculated by 21 methods). Contribution: 100% Status: *operational since 2021*
-  **Unicorn Papers** – a list with top $\frac{1}{10,000}$ (permyriad, "for every ten thousand") cited papers from PUBMED. Contribution: 100% Status: *operational since 2021*
-  **IPC 2.0** – prediction of isoelectric point and pKa dissociation constants using deep learning and SVR. Contribution: 100% Status: *operational since 2020*
-  **fCite – a fractional citation tool to quantify an individual's scientific research output** (divide the citations by the number of authors; the metrics are calculated based on 770 million citations and references, 38 million publications and 2.5 million ORCID profiles). Contribution: 100%. Status: *operational since 2018*
-  **IPC – Isoelectric Point Calculator** (cited >150 times in Web of Science, >200k visitors since 2016, [the stats](#)). Contribution: 100% Status: *operational since 2016*
-  **Proteome-pI - Proteome Isoelectric Point Database** (pI for over 21 million sequences from 5,029 proteomes calculated by 18 methods, cited >100 times in Web of Science). Contribution: 100% Status: *operational since 2016*
-  **MetaDisorder** – prediction of intrinsic disorder in proteins (in 2008-2010 the best program according [CASP8](#) defeating >20 programs for protein disorder prediction in a blind test, see [here](#), a group 153, the publication cited >200 times Web of Science). Contribution: ~80% Status: *operational since 2010*
-  **GeneSilico fold recognition server** – the development and the maintenance; in ten years I integrated there >100 bioinformatics tools (1.7TB for the programs, 2TB for biological databases; >40 GB MySQL database). Contribution: ~50% Status: retired (*management from 2008 to 2017*)
-  **CompaRNA** – benchmarking of RNA structure prediction methods. Contribution: ~15% Status: *operational since 2010*
-  **GDFuzz3D** – protein contact map to 3D structure retrieval service. Contribution: ~35% Status: *operational since 2015*
-  **mRNA3db** - Human pre-mRNA 3'-end processing machinery database. Contribution: ~80% Status: *operational since 2013*
-  **Shannon Entropy Calculator** (~100 visitors per day – [the stats](#)). Contribution: 100% Status: *operational since 2012*

Technical skills

Problem solving: analysis of big data using advanced statistics & machine learning (e.g. deep learning, support vector machines, genetic algorithms, numeric optimization)

Computational:

programming languages: PYTHON, JavaScript, PHP, R, C++, C, shell

databases: MySQL, PostgreSQL high performance computing (HPC): [Ares](#), [Athena](#), [LUMI](#)

Scientific packages: in-depth knowledge of bioinformatics programs (e.g. BLAST, HHSearch, ClustalW, UCSD Chimera, Modeller, MEME, CD-HIT, ABYSS, Ray, Velvet and many others);

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

Educational Background

Habilitation (2022, biological sciences), **Ph.D.** (2013, biochemistry),
BSc (2007, informatics), **MSc** (2006, genetics), **BSc** (2004, biology)

- 2022 **Habilitation (biological sciences)** Institute of Biochemistry and Biophysics of the Polish Academy of Science (Warsaw), **Thesis title:** Prediction of isoelectric point and pK_a dissociation constants of proteins, peptides, and amino acids
- 2013 **Ph.D. (biochemistry, bioinformatics, cum laude)** Institute of Biochemistry and Biophysics of the Polish Academy of Science (Warsaw), **Thesis title:** Integrated bioinformatics platform for protein analysis. Prediction of protein domain and intrinsic protein disorder
- 2007 **Bachelor's degree:** Jan Kochanowski University (Kielce), Institute of Physics, Division Computer Science, **Thesis title:** Determining amino acid composition in proteins using genetic algorithm
- 2006 **Master's degree:** Jan Kochanowski University (Kielce), Institute of Biology, Department of Biochemistry and Genetics, **Thesis title:** Phylogenetic analysis of the linker histones in vertebrates
- 2004 **Bachelor's degree:** Jan Kochanowski University (Kielce), Institute of Biology, Department of Biochemistry and Genetics, **Thesis title:** The diversity of linker histones in vertebrates

Employment

- 2018 – Assistant Professor (University of Warsaw, Institute of Informatics), **Poland**
- 2018 – Chairman, CEO and Owner ([Solid Scientometrics Sp. z o.o.](#)), **Poland**



- 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 trader (E-commerce), **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, Jan Kochanowski University in Kielce, **Poland**

Publications & Preprints

- 6 Wons E, ..., **Kozłowski LP**, ..., et al. A transcription factor from the cryptic Escherichia coli Rac prophage controls both phage and host operons. **Nucleic Acids Res.** **2025**, 53 (5), 1-21
- 6 Gucwa, K, ..., **Kozłowski LP**, ..., et al. Lethal perturbation of an Escherichia coli regulatory network is triggered by a restriction-modification system's regulator and can be mitigated by excision of the cryptic prophage Rac. **Nucleic Acids Res.** **2024**, 52 (6), 2942-2960
- 6 Szadkowska M, ..., **Kozłowski LP**, ..., et al. Molecular characterization of PhiKo endolysin of Thermus thermophilus HB27 bacteriophage phiKo and its cryptic lytic peptide RAP-29. **Front. Microbiol.** **2023** 14:1303794
- 6 Dorawa, ..., **Kozłowski LP**, ..., et al. Molecular Characterization of a DNA Polymerase from Thermus thermophilus MAT72 Phage vB_Tt72: A Novel Type-A Family Enzyme with Strong Proofreading Activity. **Int. J. Mol. Sci.** **2022**, 23, 7945
- 6 **Kozłowski LP*** ✉ Proteome-pI 2.0: Proteome Isoelectric Point Database Update. **Nucleic Acids Res.** **2022**, 50 (D1), D1535–D1540
- 6 Morzywolek, ..., **Kozłowski LP**, ..., et al. Novel lytic enzyme of prophage origin from Clostridium botulinum E3 strain Alaska E43 with bactericidal activity against clostridial cells. **Int. J. Mol. Sci** **2021**
- Aevansson, ..., **Kozłowski LP**, ..., et al. Going to extremes - a metagenomic journey into the dark matter of life. **FEMS Microbiol. Lett** **2021** (review)
- 6 **Kozłowski LP*** ✉ IPC 2.0 – prediction of isoelectric point and pKa dissociation constants. **Nucleic Acids Res.** **2021**, 49 (W1): W285–W292.
- Erijman A, **Kozłowski L**, et al. A High-Throughput Screen for Transcription Activation Domains Reveals Their Sequence Features and Permits Prediction by Deep Learning. **Molecular Cell** **2020**; 78, 1–13
- 6 **Kozłowski LP*** ✉ fCite: a fractional citation tool to quantify an individual's scientific research output. **bioRxiv** 771485; 2019; doi: 10.1101/771485 (**preprint**) **Highly accessed**
- 6 Plotka M, ..., **Kozłowski LP**, ..., et al. Structure and function of the Ts2631 endolysin of Thermus scotoductus phage vB_Tsc2631 with unique N-terminal extension used for peptidoglycan binding. **Sci Rep.** **2019**, 9(1):1261
- 6 **Kozłowski LP*** ✉ Proteome-pI - Proteome Isoelectric Point Database. **Nucleic Acids Res.** **2017**, 45 (D1): D1112-D1116
- 6 **Kozłowski LP*** ✉ IPC - Isoelectric point calculator. **Biology Direct** **2016**, 11:55 **Highly accessed** Highly Cited Paper
- 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

-   6 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
-   6 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
-   6 Głow 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
-   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
-   6 Plotka M, ..., **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
-  Tuszynska 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 (review)
-   6 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
-   6 **Kozłowski LP**, Bujnicki JM *MetaDisorder: a meta-server for the prediction of intrinsic disorder in proteins*. **BMC Bioinformatics** **2012**, 13:111  
-  6 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
-  6 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 (review)
-   Nakagome S, Mano S, **Kozłowski L**, et al. *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
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-  **Kozłowski Ł**, Orłowski J, Bujnicki JM "Structure prediction of alternatively spliced proteins" in "Alternative pre-mRNA Splicing: Theory and Protocols" Editors: Stamm S, Smith Ch, Luehrmann R, Wiley-Blackwell, **2012**, 582-591. doi: 10.1002/9783527636778 (book chapter)
-  Majorek K, **Kozłowski Ł**, Jakalski M, Bujnicki JM "First steps of protein structure prediction" in "Prediction of Protein Structures, Functions and Interactions" Editors: Bujnicki JM; Wiley&Sons, **2008**, 2, 39–62. doi: 10.1002/9780470741894.ch2 (book chapter)

 the main paper
 supplementary data

* single authorship publications
 & shared first authorship
 6 Free / Open Access (OA) article

 corresponding author
 Highly Cited Paper (Top 1% in WoS)

Scientometric data













Other

Referee in Journals



Nucleic Acid Res. (23), Bioinformatics (16), International Journal of Molecular Sciences (22), Knowledge-Based Systems (5), Food Technology and Biotechnology (4), Scientometrics (4), PeerJ (2), Chemical Reviews (2), J Prot Res., Scientific Rep., Viruses, and few others (>100 reviews in total)

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-)
 Open Bioinformatics Foundation (OBF, 2025-)

Member of an expert panel in the National Center of Research and Development (NCRD, pol. *NCBiR*), Poland (the evaluation of R&D projects with total valuation over \$100M). Occasionally, the assessment for other institutions such as Polish National Agency for Academic Exchange (NAWA), Polish Agency for Enterprise Development (PARP), Register of Expert Peer Reviewers for Italian Scientific Evaluation (REPRISE), e-COST (European Cooperation in Science and Technology), Fonds de la Recherche Scientifique (F.R.S.–FNRS).

 The National Centre
for Research and Development

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IN SCIENCE & TECHNOLOGY

Conferences

- 2025 **NVIDIA GTC AI Conference and Expo March**,
 2024 **ISMB (poster)**, **NVIDIA GTC AI Conference and Expo March, SCP24**
 2023 **NVIDIA GTC Spring 2023 Conference**
 2022 **MLCB 2022, APFED-22** (Advances in Protein Folding, Evolution and Design), **SCP22** (Single-Cell Proteomics Conference), **UK BioBank Scientific Conference**, **CMSB 2022** (Computational Methods in Systems Biology)
 2021 **MLCB 2021** (Machine Learning in Computational Biology), **HUPO ReCONNECT 2021** (Human Proteome Organization Congress), **UK BioBank Scientific Conference**, **ML in PL 2021** (Machine Learning in Poland; [poster](#)), **CSDS 2021** (Conference on Statistics and Data Science), **STI2021** (Conference on Science, Technology and Innovation Indicators), **RECOMB (poster)**, **ISMB/ECCB (poster & talk)**, **SCFE21, ICCS** (International Conference on Computational Science), **AI in Healthcare**
 2020 **ECCB, ISMB (poster & talk)**, **RECOMB, SCFE20** (Supercomputer Frontiers 2020)
 2019 **ISMB/ECCB (poster & talk)**
 2017 **ISMB/ECCB (poster)**
 2016 **13th Horizons in Molecular Biology Symposium, FRET 2** (International Discussion Meeting on Förster Resonance Energy Transfer), **DAGStat2016** (4th Joint Statistical Meeting)
 2015 **RECOMB** (19th Annual International Conference on Research in Computational Molecular Biology; [poster](#)),
 2014 **BIO 2014** (1st Congress of the Polish Biochemistry, Cell Biology, Biophysics & Bioinform; [poster](#)), **ECCB (poster)**
 2013 **RNA 3' ends: Mechanism and biological function in eukaryotic genomes (poster)**, **SocBiN Bioinformatics/ BIT13 (poster)**, **Cancer genetics for medical community (poster)**
 2012 **CASP10 (poster)**, **BIT12 (lecture & poster)**, **PTBI12 (lecture & poster)**
 2011 **MultiPole Approach to Structural Biology (poster)**, **PTBI11 (lecture & poster)**, **BIT11 (lecture & poster)**
 2010 **CASP9 (poster)**, **EURASNET** (Frontiers in Structural Biology of RNAs and RNPs; poster), **BIT10 (lecture & poster)**
 2009 **PTBI09 (lecture & poster)**, **ISMB/ECCB** (Intelligent Systems for Molecular Biology/ European Conference on Computational Biology; poster), **BIT09** (Bioinformatics in Toruń; lecture & poster)
 2008 **CASP8** (Critical Assessment of Techniques for Protein Structure Prediction; [poster](#) & invited lecture), **PTBI08** (1st Annual Meeting of Polish Bioinformatics Society; lecture & poster), **SocBin Bioinformatics** (lecture & [poster](#))

Workshops & Training

- 2024 Poland End to End LLM workshop (March 5-7)
 2023 HPC Comprehensive General LUMI Course (November 3-6)
 2021 Key Innovations ERC Workshop
 2017, 2021 Central Anti-Corruption Bureau's (CBA) training (three modules: [Corruption in public administration](#), [Corruption in bussines](#) and [Social consequences of corruption](#))
 2014 Advanced RNA-Seq and ChIP-Seq Data Analysis Course
 2013 Automated and Reproducible Analysis of NGS data (ARANGS13) Course
 2011 EMBO Young Scientists Forum
 2010 Workshop on Interdisciplinary Grant Application; HealthProt workshop; Grid Computing and Bioinformatics (PL-GRID); Workshop on Scientific Communication; EMBO workshop: RNA and RNA-processing enzymes, School of Molecular Medicine; Cambridge PYTHON's Innovation Academy

Grants

- 2019-2021 National Science Centre (PL, OPUS 2018/29/B/NZ2/01403) – **principal investigator** (~150k Euro) [🔗](#)
 2016-2020 Virus-X: Viral Metagenomics for Innovation Value (EU, Horizon2020, grant no. 685778) – contractor [🔗](#)
 2013-2014 Polish Ministry of Science and Higher Education (PL, IUVENTUS PLUS, 0301/IP1/2013/72) – **principal investigator** (~35k Euro)
 2012-2014 Exgenome Molecular Enzymes (EU, FP7, grant no. 286556) – contractor [🔗](#)
 2011-2015 European Research Council (EU, ERC StG Grant RNA+P=123, grant no. 26135) – contractor [🔗](#)
 2009-2012 Health-Prot: Proteins in Health and Disease (EU, FP7, grant no. 229676) – contractor [🔗](#)
 2008-2013 Polish Ministry of Science and Higher Education (PL, grant no. NN301 190139) – **the main contractor**, so called “promotor’s grant” funding PhD training (~10k Euro)

Fellowships & Awards

- 2023 Individual award of the Rector of the University of Warsaw for scientific achievements
 2015-2017 Max Planck Institute Fellowship
 2008 Masovian Fellowship for Ph.D. Students

Teaching

- 2024/2025 Data analysis and visualization (*Lecture & Labs [x2]*), Architecture of large projects in bioinformatics (*Lecture & Labs [x2]*), Introduction to computational biology (*Labs [x1]*)
 2023/2024 Data analysis and visualization (*Lecture & Labs [x2]*), Architecture of large projects in bioinformatics (*Lecture & Labs [x1]*), Introduction to computer science (*Labs [x2]*)
 2022/2023 Data analysis and visualization (*Lecture & Labs [x2]*), Architecture of large projects in bioinformatics (*Lecture & Labs [x1]*), Introduction to computer science (*Labs [x2]*)

2021/2022 Introduction to computer science (*Labs [x1]*), Data analysis and visualization (*Lecture & Labs [x2]*),
 Architecture of large projects in bioinformatics (*Lecture & Labs [x1]*), Web applications (*Labs [x1]*)
 2020/2021 Data analysis and visualization (*Lecture & Labs [x3]*), Architecture of large projects in bioinformatics
 (*Lecture & Labs [x1]*)
 2019/2020 Data analysis and visualization (*Lecture & Labs [x2]*)
 2018/2019 Web applications (*Labs [x1]*), Probability theory and statistics (*Classes [x1]* & *Labs [x1]*), Statistical data
 analysis 2 (*Labs [x1]*), Introduction to computer science (*Labs [x1]*)

Classes - whiteboard exercises (old school way); *Labs* – in front of the computer; [x1], [x2], ... – number of groups (each 30h);
 210 h per semester, Teaching activities conducted at University of Warsaw

Varia

2022-2025 evaluator in Interdisciplinary Doctoral School, University of Warsaw
 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](#))
 2011 co-organization of “MultiPole Approach to Structural Biology”, Warsaw, **Poland**, Nov 16-19 ([badge](#))

In free time active Wikipedian



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

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