

Curriculum vitae

Grzegorz Marcin Koczyk

Born: 24/10/1978 (Poznań, Poland)

Laboratory of Biometry, Institute of Plant Genetics, Polish Academy of Sciences,
Strzeszyńska 34, 60-479, Poznań, Poland

e-mail: gkoc@igr.poznan.pl

Education:

- 2002-2007 Ph.D. student (Institute of Plant Genetics and Adam Mickiewicz University, Poznań, Poland); thesis' title: „Functional annotation of genes using profile methods of sequence analysis”
- 2001-2002 M.Sc. Molecular Biology (Adam Mickiewicz University, Poznań, Poland); thesis' title: „Computational aspects of phylogenetic analysis: In search of paralogs”
- 1997-2002 Molecular Biology student (Adam Mickiewicz University, Poznań, Poland); Individual Study Course (2000-2002) incorporating elements of Computational Science at Poznań Technical University (including: programming languages and compilers, object-oriented desing and programming, database management systems, mathematics)

Professional activities and work experiences:

- 2010-2013 head of applied research grant NCBiR/LIDER 19/113/L-1/09/NCBiR/2010 “Modelling, prediction and verification of fungal ability to accumulate toxins”
- 2008-... researcher at Institute of Plant Genetics, Laboratory of Biometry (adjunct)
- 2008-... coauthor and maintainer of DHcL webserver for analysis of protein domain hierarchy and underlying closed loop structure (<http://sitron.bccs.uib.no/dhcl>)
- 2006-... author and maintainer of LigProf webserver for prediction of small molecule binding sites on proteins (<http://cropnet.pl/ligprof>)
- 2004-2007 conducted parts of Bioinformatics (biological information databases, analysis of DNA and protein sequences) courses for PhD students at the Faculty of Biology (Adam Mickiewicz University) and the Institute of Plant Genetics (Poznań, Poland)
- 2004-2006 researcher at the BioInfoBank Institute (<http://bioinfo.pl>) working on protein function prediction using sequence profiles, as part of the EU projects: DATAGENOM (LSHB-CT-2003-503017) and GENEFUN (LSHG-CT-2004-503567)
- 2003-... maintainer of the web server and databases of the Polish „Genomics and transgenesis of crop plants” Network (<http://cropnet.pl>)

List of publications:

1. Błaszczyk L, Popiel D, Chełkowski J, Koczyk G, Samuels GJ, Sobieralski K, Siwulski M (2011) "Species diversity of *Trichoderma* in Poland" *J Appl Genet.*; 52(2):233-43.
2. Stępień L, Koczyk G, Waśkiewicz A. (2011) "FUM cluster divergence in fumonisins-producing *Fusarium* species" *Fungal Biol.*; 115(2):112-23.
3. Kaczmarek M, Koczyk G, Ziolkowski PA, Babula-Skowronska D, Sadowski J (2009) „Comparative analysis of the *Brassica oleracea* genetic map and the *Arabidopsis thaliana* genome" *Genome*; 52(7):620-33
4. Ziolkowski PA, Koczyk G, Galganski L, Sadowski J (2009) Genome sequence comparison of Col and Ler lines reveals the dynamic nature of *Arabidopsis* chromosomes. *Nucleic Acids Res.*; 37(10):3189-201
5. Koczyk G, Berezovsky IN (2008) „Domain Hierarchy and closed Loops (DHcL): a server for exploring hierarchy of protein domain structure." *Nucleic Acids Res.*; 36(Web Server issue):W239-45
6. Wyrwicz LS, Koczyk G, Rychlewski L (2008) „ Homologues of HSV-1 nuclear egress factor UL34 are potential phosphoinositide-binding proteins." *Acta Biochim Pol.*;55(1):207-13
7. Stępień Ł, Popiel D, Koczyk G, Chełkowski J. (2008) „Wheat-infecting *Fusarium* species in Poland – their chemotypes and frequencies revealed by PCR assay." *J Appl Genet.*; 49(4): 433-41
8. Masojc B, Medrek K, Debniak T, Lubinski J, Wyrwicz LS, Koczyk G, Hoffmann M, Rychlewski L. (2007) „ARLTS1 Trp149Stop mutation and the risk of ovarian cancer" *Cancer Res.*; 67(9):4533
9. Wyrwicz LS, Koczyk G, Rychlewski L, Plewczynski D (2007) „ProteinSplit: splitting of multidomain proteins using prediction of ordered and disordered regions in protein sequences for virtual structural genomics" *J Phys: Condens. Matter* 19:285222 (8pp); doi:10.1088/0953-8984/19/28/285222
10. Koczyk G, Wyrwicz LS, Rychlewski L. (2007) „LigProf: a simple tool for in silico prediction of ligand-binding sites" *J Mol Model.*; 13(3):445-55
11. Stępień Ł, Mohler V, Bocianowski J, Koczyk G (2007) „Assessing genetic diversity of Polish wheat" *Genet. Resour. Crop Ev.*; doi:10.1007/s10722-006-9140-2
12. von Grotthuss M, Koczyk G, Pas J, Wyrwicz LS, Rychlewski L (2004)

„Ligand.Info small molecule Meta-Database” Comb Chem High Throughput Screen.; 7(8):757-61

13. Koczyk G, Chełkowski J (2003) „An assessment of the resistance gene analogues of *Oryza sativa* ssp. *japonica*: their presence and structure” Cell Mol Biol Lett.; 8(4):963-72

14. Chełkowski J, Koczyk G. (2003) „Resistance gene analogues of *Arabidopsis thaliana*: recognition by structure” J Appl Genet.;44(3):311-21

15. Komosiński M, Koczyk G, Kubiak M (2001) „On Estimating Similarity of Artificial and Real Organisms” Theory in Biosciences; 120(3-4):271-286

Skill highlights:

- excellent, working experience with designing algorithms, implementing and maintaining tools for analysis of protein structures and protein/DNA sequences (e.g.: <http://cropnet.pl/ligprof>, <http://sitron.bccs.uib.no/dhcl>)
- good, working experience with the following programming languages (Python, C/C++, Perl, R),
- databases (SQLite, MySQL, PostgreSQL) and libraries/utilities (Boost, Mygthy, Django, NumPy, SciPy, BioPython, GraphViz, Rpy, Matplotlib, 4Suite)
- moderate familiarity and experience with the following programming languages (Java, JavaScript)
- moderate experience authoring webpages (HTML, CSS, JavaScript)
- experience administrating a web-server (Linux, Apache, ModPython) and cluster computers (scheduling environment: Torque/Maui)
- good, working experience with the following toolsets and programs for analysis of sequences and structures (NCBI-BLAST, WU-BLAST, BLASTZ, CLUSTALW, MUSCLE, HMMer, WISE, MEME/MAST, MODELLER, Jacal, PHYLIP, PyMol, EMBOSS) and familiarity with their underlying algorithmic bases
- moderate experience teaching the above (see Professional activities)
- background in molecular biology (in particular: biochemistry, molecular biology of plants) as well as computational science (probability and statistics, object-oriented design and unit testing, database managements systems)
- languages: English (fluent), Polish (fluent), French (basic)