

Kristian Vlahoviček**Curriculum Vitae****Contact address**

Prof. Kristian Vlahoviček, PhD
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Date of birth 27. September, 1971.

Place of birth Zagreb, Croatia

Foreign languages

English, Italian, German

Education

2000, PhD Biochemistry Bioinformatics	Chemistry Division, Faculty of Science, University of Zagreb	"Prediction of structural and physicochemical properties of DNA with special regard to curvature and bendability"
1995, BSc Molecular Biology	Biology Division, Faculty of Science, University of Zagreb	"CORRECT, a program for absorption correction and its application to the hydrochlorothiazide-hexamethylenetetramine adduct"

Research interests

Codon usage in prokaryotic metagenomes (www.bioinfo.hr/inca)
 Expression data integration (www.bioinfo.hr/madnet)
 Application of machine learning methods to high throughput –omics data
 Evolution of metazoan genome
 Genome-wide prediction of DNA properties

Appointments

2011- Zagreb, Croatia	Full professor, Bioinformatics group head, Faculty of science, University of Zagreb
2009- Oslo, Norway	Adjunct Associate Professor, Institute for Informatics, University of Oslo
2006-2011 Zagreb, Croatia	Associate professor, Bioinformatics group head, Faculty of science, University of Zagreb
2004-2006 ICGEB Trieste, Italy	Staff Research Scientist, Protein Structure and Bioinformatics Head: Prof. Sándor Pongor
2002-2006 Zagreb, Croatia	Assistant professor, Bioinformatics group head, Faculty of science, University of Zagreb
2001-2004 ICGEB Trieste, Italy	Scientific computing coordinator, Protein Structure and Bioinformatics Head: Prof. Sándor Pongor
1996-2000 ICGEB Trieste, Italy	Research Fellowship, Protein Structure and Function Group Head: Prof. Sándor Pongor
1996-2000 Zagreb, Croatia	Research and Teaching assistant, Chemistry Division, University of Zagreb Head: Prof. Boris Kamenar

Grants

2006-	ICGEB collaborative research project, PI
2006-	EMBO Young Investigator Programme installation grant, PI

Kristian Vlahoviček		Curriculum Vitae
2006-	FP6 CCompSoLLS, collaborator	
2006-	Croatian ministry of science 119-0982913-1211, PI	
2005-2006	Croatian ministry of science 0119161, PI	
2004	Croatian IT grant 090/2004, PI	
Teaching		
Undergraduate course lecturer at the Division of Biology, Faculty of Science, Zagreb University <i>4406 Bioinformatics</i> <i>4408 Computer lab</i>		
Coordinator and teacher (*) at the Masters level Computational biology module, Division of Biology, Faculty of Science, Zagreb University <i>Algorithms and programming*</i> ; <i>Statistics and Machine Learning*</i> ; <i>Mathematical Methods in Biology</i> ; <i>Genomics</i> ; <i>Structural Computational Biophysics</i>		
Graduate course lecturer at the Division of Biology, Faculty of Science, Zagreb University <i>Computational biology</i>		
Course organizer and main lecturer, Introduction to Bioinformatics 2004, 2005, 2007, 2009, 2011 Zagreb, Croatia		
Teaching assistant, Chemistry lab, Division of Chemistry, 2000		
Course assistant (1996-2000) and lecturer (2001-2005) at the ICGEB course: Bioinformatics, computer methods in molecular biology, Trieste, Italy		
Mentoring		
Doctoral students	Vedran Franke (2011-, Zagreb University, Croatia) Maša Roller (2010-, Zagreb University, Croatia) Sofia Pinto (2007-, Zagreb University, Croatia) Vedran Lucić (2006-, Zagreb University, Croatia) Tina Kokan (2006-, Zagreb University, Croatia) Rosa Karlić (2006-, co-supervision with dr. Martin Vingron, MPI Berlin, Germany) Fran Supek (2005-2011, co-supervision with Dr. Šmuc, Rudjer Bošković Institute, Croatia) Mile Šikić (2005-2008, co-supervision with Prof. Jeren, Faculty of Electrical Engineering, Zagreb Univ, Croatia)	
Memberships		
2006-	Matrix Croatica	
2004-	Croatian Biological Society 1885	
2001-	International Society for Computational Biology (ISCB)	
2000-	Croatian Society for Theoretical and Mathematical Biology	
1997-	Croatian Society for Biochemistry and Molecular Biology (FEBS affiliate)	
1996-	Croatian Crystallographic Association	
Awards and honours		
Annual Science Award, Republic of Croatia (2011)		
Annual Science Award, Croatian Academy of Sciences and Arts (2009)		
Activities and Service		
<i>Bioinformatics, BMC Bioinformatics, BMC Structural Biology, DNA research, Extremophiles, Genome Biology, Nucleic Acids Research, PLoS One</i> Manuscript reviewer		
Journal DATABASE (Oxford univ press) - Member of the editorial board (2008-) Journal BMC Structural Biology (BioMed Central) – Associate editor (2009-)		
ERC Programme, EC FP7 Programme, Estonian National Funding Agency, Hungarian National Funding Agency, Croatian National Funding Agencies Evaluator		
University of Zagreb, e-learning Committee President (2010-)		
Faculty of Science, University of Zagreb		

Kristian Vlahoviček

Curriculum Vitae

Head, Division of Biology (2008-)

Unity through Knowledge Fund, Croatian National Scientific Funding Programme (www.ukf.hr)
Steering Committee Member (2008-)

Croatian Society for Theoretical and Mathematical Biology
President (2007-2010)

CBM (Consorzio Biomedico Molecolare), Italy
Member of the 'Core Bioinformatics Facility' coordination group (2005-2006)

ICGEB Trieste, Italy
Member of the information technology and infrastructure committee (2002)

EMBNet (European molecular biology network)
Secretary for Research and Development committee (2002-2006)

Elettra Synchrotron, Trieste, Italy
Beamline control software consultant for the ESCA microscopy beamline (2001)

Faculty of science, University of Zagreb
Computer and network system administrator at the Division of chemistry (2000-2003)

Hobbies

Photography; Squash; Role-playing games; World Wide Web, Computer animations

Publications

- Pinto, S., **Vlahoviček, K.**, and Buratti, E. (2011) PRO-MINE: A bioinformatics repository and analytical tool for TARDBP mutations, *Hum Mutat* **32**, E1948-1958.
- Supek, F., Škunca, N., Repar, J., **Vlahoviček, K.**, and Šmuc, T. (2010) Translational selection is ubiquitous in prokaryotes, *PLoS Genet* **6**, e1001004.
- Šegota, I., Glažar, P., and **Vlahoviček, K.** (2010) MADNet: A Web Server for Contextual Analysis and Visualization of High-Throughput Experiments, In *Systems biology for signaling networks* (Choi, S., Ed.) 1st ed., pp 877-888, Springer, New York.
- Pucić, M., Pinto, S., Novokmet, M., Knežević, A., Gornik, O., Polašek, O., **Vlahoviček, K.**, Wang, W., Rudd, P. M., Wright, A. F., Campbell, H., Rudan, I., and Lauc, G. (2010) Common aberrations from the normal human plasma N-glycan profile, *Glycobiology* **20**, 970-975.
- Karlič, R., Chung, H. R., Lasserre, J., **Vlahoviček, K.**, and Vingron, M. (2010) Histone modification levels are predictive for gene expression, *Proc Natl Acad Sci U S A* **107**, 2926-2931.
- Harcet, M., Roller, M., Četković, H., Perina, D., Wiens, M., Muller, W. E., and **Vlahoviček, K.** (2010) Demosponge EST sequencing reveals a complex genetic toolkit of the simplest metazoans, *Mol Biol Evol* **27**, 2747-2756.
- Perina D, Harcet M, Mikoč A, **Vlahoviček K**, Muller WEG, Četković H (2009) Highly Expressed Genes in Marine Sponge *Suberites domuncula* Prefer C- and G-Ending Codons. *Food Technol Biotechnol* **47**: 269-274
- Zampieri S, Filocamo M, Buratti E, Stroppiano M, **Vlahoviček K**, et al. (2009) Molecular and functional analysis of the HEXB gene in Italian patients affected with Sandhoff disease: identification of six novel alleles. *Neurogenetics* **10**: 49-58.
- Šikić M, Tomić S, **Vlahoviček K** (2009) Prediction of protein-protein interaction sites in sequences and 3D structures by random forests. *PLoS Comput Biol* **5**: e100027
- Šegota I, Bartoniček N, **Vlahoviček K** (2008) MADNet: microarray database network web server. *Nucleic Acids Res* **36**: W332-335.
- Mihel J, Šikić M, Tomić S, Jeren B, **Vlahoviček K** (2008) PSAIA - protein structure and interaction analyzer. *BMC Struct Biol* **8**: 21.
- Supek, F. and **Vlahoviček, K.** (2005). "Comparison of codon usage measures and their applicability in prediction of microbial gene expressivity." *BMC Bioinformatics* **6**(1): 182.
- Vlahoviček, K.**, A. Pintar, et al. (2005). "CX, DPX and PRIDE: WWW servers for the analysis and comparison of protein 3D structures." *Nucleic Acids Res* **33** (Web Server issue): W252-4.
- Vlahoviček, K.**, Kajan, L., Agoston, V. and Pongor, S. (2005) The SBASE domain sequence resource, release 12: prediction of protein domain-architecture using support vector machines. *Nucleic Acids Res*, **33** Database Issue, D223-225.
- Gaspari Z, **Vlahoviček K**, Pongor S (2005) Efficient recognition of folds in protein 3D structures by the improved PRIDE algorithm. *Bioinformatics* **21**: 3322-3323
- Miocic, S., Filocamo, M., Dominissini, S., Montalvo, A.L., **Vlahoviček, K.**, Deganuto, M., Mazzotti, R., Cariati, R., Bembì, B. and Pittis, M.G. (2005) Identification and functional characterization of five novel mutant alleles in 58 Italian patients with Gaucher disease type 1. *Hum Mutat*, **25**, 100.
- Supek, F. and **Vlahoviček, K.** (2004) INCA: synonymous codon usage analysis and clustering by means of self-organizing map. *Bioinformatics*, **20**, 2329-2330.
- Abramić, M., Šimaga, S., Osmak, M., Čičin-Šain, L., Vukelić, B., **Vlahoviček, K.** and Dolovčak, L. (2004) Highly reactive cysteine residues are part of the substrate binding site of mammalian dipeptidyl peptidases III. *Int J Biochem Cell Biol*, **36**, 434-446.
- Tosato, V., Gjuracic, K., **Vlahoviček, K.**, Pongor, S., Danchin, A. and Bruschi, C.V. (2003) The DNA secondary structure of the *Bacillus subtilis* genome. *FEMS Microbiol Lett*, **218**, 23-30.
- Veljković, N., Branch, D.R., Metlaš, R., Prljic, J., **Vlahoviček, K.**, Pongor, S. and Veljković, V. (2003) Design of

Kristian Vlahoviček

Curriculum Vitae

- peptide mimetics of HIV-1 gp120 for prevention and therapy of HIV disease. *J Pept Res*, **62**, 158-166.
21. **Vlahoviček, K.**, Carugo, O. and Pongor, S. (2002) The PRIDE server for protein three-dimensional similarity. *Journal of Applied Crystallography*, **35**, 648-649.
 22. **Vlahoviček, K.**, Kajan, L., Murvai, J., Hegedus, Z. and Pongor, S. (2003) The SBASE domain sequence library, release 10: domain architecture prediction. *Nucleic Acids Res*, **31**, 403-405.
 23. **Vlahoviček, K.**, Kajan, L. and Pongor, S. (2003) DNA analysis servers: plot.it, bend.it, model.it and IS. *Nucleic Acids Res*, **31**, 3686-3687.
 24. **Vlahoviček, K.**, Kajan, L., Szabó, G.J., Tosato, V., Bruschi, C.V. and Pongor, S. (2003) Web servers for the prediction of curvature as well as other characteristics from DNA sequence. In Markoff, A. (ed.), *Analytical Tools for Genes, Genomes and Sequence: The DNA Level*. DNA Press, Eagleville, PA, p. in press.
 25. **Vlahoviček, K.**, Murvai, J., Barta, E. and Pongor, S. (2002) The SBASE protein domain library, release 9.0: an online resource for protein domain identification. *Nucleic Acids Res*, **30**, 273-275.
 26. Murvai, J., **Vlahoviček, K.**, Szepesvari, C. and Pongor, S. (2001) Prediction of protein functional domains from sequences using artificial neural networks. *Genome Res*, **11**, 1410-7.
 27. **Vlahoviček, K.** and Pongor, S. (2001) Modelling DNA structure from sequence. In Pifat, G. (ed.) *Supramolecular Structure and Function*. Kluwer Scientific, Dordrecht/Plenum Press, New York, USA, (in press).
 28. Murvai, J., **Vlahoviček, K.** and Pongor, S. (2001) A memory-based approach to protein sequence similarity searching. In Pifat, G. (ed.) *Supramolecular Structure and Function*. Kluwer Scientific, Dordrecht/Plenum Press, New York, USA, p. (in press).
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 31. **Vlahoviček, K.** (2000) Prediction of structural and physicochemical properties of DNA with special regards to curvature and bendability; Doctoral Thesis. *Division of Chemistry*. University of Zagreb, Zagreb, p. 132.
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 33. Murvai, J., **Vlahoviček, K.**, Barta, E., Cataletto, B. and Pongor, S. (2000) The SBASE protein domain library, release 7.0: a collection of annotated protein sequence segments. *Nucleic Acids Res*, **28**, 260-2.
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 35. **Vlahoviček, K.**, Munteanu, M.G. and Pongor, S. (1999) Elastic models of DNA bending. In Bradbury, E.M. and Pongor, S. (eds.), *Structural biology and functional genomics*. Kluwer Scientific, Amsterdam, pp. 97-114.
 36. Murvai, J., **Vlahoviček, K.**, Barta, E., Szepesvari, C., Acatrinei, C. and Pongor, S. (1999) The SBASE protein domain library, release 6.0: a collection of annotated protein sequence segments. *Nucleic Acids Res*, **27**, 257-9.
 37. Murvai, J., **Vlahoviček, K.**, Barta, E., Parthasarathy, S., Hegyi, H., Pfeiffer, F. and Pongor, S. (1999) The domain-server: direct prediction of protein domain-homologies from BLAST search. *Bioinformatics*, **15**, 343-4.
 38. **Vlahoviček, K.**, Gabrielian, A. and Pongor, S. (1998) Prediction of bendability and curvature in genomic DNA. *J Math Model Sci Comp*, **9**, 53-57.
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 40. Gabrielian, A., **Vlahoviček, K.**, Munteanu, M.G., Gromiha, M.M., Brukner, I., Sanchez, R. and Pongor, S. (1998) Prediction of bendability and curvature in genomic DNA. *Periodicum Biologorum*, **100**, 127-139.
 41. Gabrielian, A., **Vlahoviček, K.**, Munteanu, M.G., Gromiha, M.M., Brukner, I., Sanchez, R. and Pongor, S. (1998) Prediction of bendability and curvature in genomic DNA. In Sarma, R.H. and Sarma, M.H. (eds.), *Structure, Motion, Interaction and Expression of Biological Macromolecules, Proceedings of the Tenth Conversation*. Adenine press, Albany, NY, Vol. 1, pp. 117-132.
 42. Gabrielian, A., **Vlahoviček, K.** and Pongor, S. (1997) Distribution of sequence-dependent curvature in genomic DNA sequences. *FEBS Lett*, **406**, 69-74.
 43. Fabian, P., Murvai, J., Hatsagi, Z., **Vlahoviček, K.**, Hegyi, H. and Pongor, S. (1997) The SBASE protein domain library, release 5.0: a collection of annotated protein sequence segments. *Nucleic Acids Res*, **25**, 240-3.