



UNIVERSITY OF CYPRUS

DEPARTMENT OF BIOLOGICAL SCIENCES

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CURRICULUM VITAE

**Dr. Vasilis J. Promponas, Ph.D**

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NICOSIA, MAY 30, 2017



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## SHORT BIOGRAPHICAL SKETCH

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### Personal information

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Name	Vasilis J. Promponas
Current position	Assistant Profesor in Bioinformatics (tenure-track) Department of Biological Sciences, University of Cyprus Head, Bioinformatics Research Laboratory
email	vprobon@ucy.ac.cy; vasilis.promponas@gmail.com
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### Professional experience

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2012–	Assistant Professor in Bioinformatics, University of Cyprus
2005–	Head, Bioinformatics Research Laboratory University of Cyprus
2005–2012	Lecturer in Bioinformatics, Department of Biological Sciences, University of Cyprus
2004–2005	Postdoctorate Research Fellow, PYTHAGORAS I grant Department of Cell Biology and Biophysics, Faculty of Biology, University of Athens, Greece

### Education

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1997–2004	PhD in Biological Sciences, University of Athens, Greece. Thesis title: “Prediction of protein function from aminoacid sequence”. Thesis advisor: Prof. Stavros J. Hamodrakas. Note: National Service Aug 2001–May 2003, see below.
1991–1996	BSc in Physics, University of Athens, Greece. Diploma Thesis title: “Structural and Modeling studies of possible inhibitors of the enzyme Dihydrofolate Reductase (DHFR)”. Thesis advisor: Prof. Stavros J. Hamodrakas.

### Research interests

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Our research in computational biology and bioinformatics is mainly oriented towards the interpretation of large scale genomic and biological data in order to reveal the principles governing the molecular basis of life. Along these lines, we develop/utilize computational methods (empirical, statistical and machine learning) that exploit any available type of biological information (e.g. macromolecular sequences and structures, biomedical literature) towards understanding biological systems, ranging from macromolecules and macromolecular complexes, to phenotypes.

More specifically, we are interested into devising algorithms, methods, databases and computer systems related to

1. protein sequence analysis and structural bioinformatics,
2. computational comparative genomics,
3. analysis, prediction and modelling of membrane protein structure, and
4. biomedical text mining

## Further training

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2009	MicrobeGR Workshop: Molecular Approaches to Unravel the Hidden Microbial World, Department of Environmental and Natural Resources Management of the University of Ioannina, Agrinion, Greece
2008	EMBO workshop on Microbial diversity and metagenomics: science, technology, applications & regulatory affairs, Porto Carras Resort, Chalkidiki, Greece
2007	EMBO workshop on New Methods in Membrane Protein Research, Stockholm Center for Biomembrane Research
2007	EMBRACE workshop in membrane bioinformatics, Stockholm Center for Biomembrane Research
2005	Biosapiens workshop on Membrane Proteins, CMBI-Nijmegen
2004	EMBO course on Microarray Technology: Genome-Proteome-Function, EMBL-Heidelberg
2004	Onassis Foundation Lecture Series in Biology: “Genomics, Bioinformatics and Beyond”, IMBB-Crete
2003	Onassis Foundation Lecture Series in Biology: “Signal Peptides and Cell Trafficking”, IMBB-Crete
1998	EBI Visitors program fellowship - 3 months with the Computational Genomics Group (Prof. Christos Ouzounis)

## Honors/Fellowships/Awards

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2012	Honorary certificate for “distinguished contributions as a leading reviewer” for the journal <i>Bioinformatics</i> , Oxford University Press.
2004	Travel fellowship: Onassis Foundation Lecture Series in Biology: “Genomics, Bioinformatics and Beyond”, IMBB-Crete
2003	Travel fellowship: Onassis Foundation Lecture Series in Biology: “Signal Peptides and Cell Trafficking”, IMBB-Crete
1998	EBI Visitors program fellowship - 3 months with the Computational Genomics Group (Prof. Christos Ouzounis)

## Other

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Aug 2001– May 2003	National service Military Service (Greek Army, 21 months) - Reserve Officer of Artillery. Received the basic training as a Fire Control Officer, and special training in Artillery Telecommunications.
1999-2000	Analyst/Programmer in the Research and Development Department of Unisoft SA (Greece). Task: development, maintenance, debugging and customer’s technical support for a Commercial Management and Production Management Database software package.

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**Publications in peer-reviewed journals (P)**

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36. † Samara P., Miriagou V., Zachariadis M., Mavrofrydi O., **Promponas V.J.**, Dedos S., Papazafiri P., Voelter W., Kalbacher H., Tsitsilonis O. A fragment of the alarmin prothymosin  $\alpha$  as a novel biomarker in murine models of bacteria-induced sepsis. (2017) *Oncotarget*. In press.
35. † Kyriakou D., Stavrou E., Demosthenous P., Angelidou G., San Luis B.-J., Boone C., **Promponas V.J.**, Kirmizis A. Functional characterisation of long intergenic non-coding RNAs through genetic interaction profiling in *Saccharomyces cerevisiae*. (2016) *BMC Biology* 14 (1):106.
34. † Jacomin A.C., Samavedam S., **Promponas V.**, Nezis I.P. iLIR database: A web resource for LIR motif-containing proteins in eukaryotes (2016) *Autophagy* 12(10):1945-1953.
33. † Klionski D.J., [...] **Promponas V.J.**, [...] , Zughaier S.M. Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition) (2016) *Autophagy* 12(1):1-222.
32. † **Promponas VJ**, Katsani KR, Blencowe BJ, Ouzounis CA Sequence evidence for common ancestry of eukaryotic endomembrane coatomers (2016) *Sci. Rep* 6:22311.
31. † Baichoo S., Botha G., Jaufferally-Fakim Y., Mungloo-Dilmohamud Z., Lundin D., Mulder N., **Promponas V.J.**, Ouzounis C.A. H3ABioNet computational metagenomics workshop in Mauritius: training to analyse microbial diversity for Africa (2015) *Standards in Genome Sciences* 10:115.
30. † **Promponas V.J.\***, Iliopoulos I.\* , Ouzounis C.A.\* Annotation inconsistencies beyond sequence similarity-based function prediction?phylogeny and genome structure. (2015) *Standards in Genome Sciences* 10:108.
29. † Kirmitzoglou I, **Promponas VJ** LCR-eXXXplorer: a web platform to search, visualize and share data for low complexity regions in protein sequences (2015) *Bioinformatics* 31(13), 2208-2210.
28. † Kannas CC, Kalvari I, Lambrinidis G, Neophytou CM, Savva CG, Kirmitzoglou I, Antoniou Z, Achilleos KG, Scherf D, Pitta CA, Nicolaou CA, Mikros E, **Promponas VJ**, Gerhauser C, Mehta RG, Constantinou AI, Pattichis CS. LiSIs: An Online Scientific Workflow System for Virtual Screening. (2015) *Combinatorial Chemistry & High Throughput Screening* 18 (3), 281-295.
27. † Papanikolaou N, Pavlopoulos GA, Pafilis E, Theodosiou T, Schneider R, Satagopam VP, Ouzounis CA, Eliopoulos AG, **Promponas VJ**, Iliopoulos I. BioTextQuest+: a knowledge integration platform for literature mining and concept discovery. (2014) *Bioinformatics*, 30(22):3249-56.
26. † Katsani K.R., Irimia M., Karapiperis C., Scouras Z.G., Blencowe B.J., **Promponas V.J.**, Ouzounis C.A. Functional genomics evidence unearths new moonlighting roles of outer ring coat nucleoproteins. (2014) *Scientific Reports*, 4:4655.
25. † Kalvari I., Tsompanis S., Mulakkal N.C., Osgood R., Johansen T., Nezis I.P.\* , **Promponas V.J.\*** iLIR: A web resource for prediction of Atg8-family interacting proteins. (2014) *Autophagy*, 10(5):913-925.
24. † Chrysos G., Sotiriades E., Rousopoulos C., Pramataris K., Papaefstathiou I., Dollas A., Papadopoulos A., Kirmitzoglou I., **Promponas V.J.**, Theocharides T., Petihakis G., Lagnel J. Reconfiguring the bioinformatics computational spectrum: Challenges and opportunities of fpga-based bioinformatics acceleration platforms. (2014) *IEEE Design and Test*, 31(1):62-73.
23. † **Promponas V.J.\***, Ouzounis C.A.\* and Iliopoulos I\* . Experimental evidence validating the computational inference of functional associations from gene fusion events: a critical survey. (2014) *Briefings in Bioinformatics*, 15(3):443-454.
22. † Samara P., Kalbacher H., Ioannou K., Radu D.L., Livaniou E., **Promponas V.J.**, Voelter W., Tsitsilonis O. Development of an ELISA for the quantification of the C-terminal decapeptide prothymosin  $\alpha$ (100-109) in sera of mice infected with bacteria. (2013) *Journal of Immunological Methods*, 395(1-2):54-62.

21. † Papadopoulos A, **Promponas V.J.\***, and Theocharides T\*. FPGA-based hardware acceleration for local complexity analysis of massive genomic data. (2013) *Integration, the VLSI Journal*, 46(3):230-239.
20. † Psomopoulos F.E., Siarkou V.I., Papanikolaou N., Iliopoulos I., Tsaftaris A.S., **Promponas V.J.** , Ouzounis C.A. The Chlamydiales Pangenome Revisited: Structural Stability and Functional Coherence. (2012) *Genes*, 3(2):291-319.
19. † Ouzounis C.A., **Promponas V.J.** and Iliopoulos I. The quest for an upper limit in systems biology. (2012) *Journal of Biological Research*, 18: 353-358.
18. † Theodosiou A. and **Promponas V.J.\***. LaTcOm: a web server for visualizing rare codon clusters in coding sequences. (2012) *Bioinformatics* 28(4):591-592.
17. † Fokianos K. and **Promponas V.J.**. Biological Applications of Time Series Frequency Domain Clustering. (2012) *Journal of Time Series Analysis* 33 (5): 744-756 (Invited paper).
16. † Kountouris P., Agathocleous M., **Promponas V.J.**, Christodoulou G., Hadjicostas S., Vassiliades V., Christodoulou C. A comparative study on filtering protein secondary structure prediction. (2012) *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9 (3), 731-739.
15. † Papanikolaou N., Pafilis E., Nikolaou S., Ouzounis C.A., Iliopoulos I.\* , **Promponas V.J.\***. BioTextQuest: A Web-based Biomedical Text Mining Suite for Concept Discovery. (2011) *Bioinformatics*, 27(23):3327-8.
14. † Kirschel A.N.G., Cody M.L., Harlow Z.T., **Promponas V.J.**, Vallejo E.E., Taylor C.E. Territorial dynamics of Mexican Antthrushes (*Formicarius moniliger*) revealed by individual recognition of their songs. (2011) *Ibis*, 153(2), 255-268.
13. † Ioannou A., Fokianos K., and **Promponas V.J.\***. Spectral Density Ratio Based Clustering Methods for the Binary Segmentation of Protein Sequences: a Comparative Study. (2010) *BioSystems*, 100, 132-143.
12. † Papanikolaou N., Trachana K., Theodosiou T., **Promponas V.J.\***, and Iliopoulos I\*. Gene socialization: gene order, GC content and gene silencing in *Salmonella*. (2009) *BMC Genomics*, 10:597.
11. † Savvides A., **Promponas V.J.**, and Fokianos K. Clustering of biological time series by cepstral coefficients based distances. (2008) *Pattern Recognition*, 41, 2398-2412.
10. Bagos P.G., Liakopoulos T.D., **Promponas V.J.\***, and Hamodrakas S.J. Prediction of  $\beta$ -barrel Outer Membrane Proteins. (2005) *Proceedings of the Indian National Academy of Sciences - Part B (Biological Sciences)*, 71:1.
9. Papasaikas P.K., Bagos P.G., Litou Z.I., **Promponas V.J.**, Hamodrakas S.J. PRED-GPCR: GPCR recognition and family classification server. (2004) *Nucleic Acids Research*, W380-382.
8. Vernikos G., Gkogkas C., **Promponas V.J.**, Hamodrakas S.J. GeneViTo: Visualizing gene-product functional and structural features in genomic datasets. (2003) *BMC Bioinformatics*, 4:53.
7. Iliopoulos I., Tsoka S., Andrade M.A., Enright A.J., Carroll M., Pouillet P., **Promponas V.J.** , Liakopoulos T., Palaios G., Pasquier C., Hamodrakas S., Tamames J., Yagnik A.T., Tramontano A., Devos D., Blaschke C., Valencia A., Brett D., Martin D., Leroy C., Rigoutsos I., Sander C., Ouzounis C.A. Evaluation of annotation strategies using an entire genome sequence. (2003) *Bioinformatics*, 19(6), 717-726. [Featured as a "Must read" article at the F1000 Biology]
6. Pasquier C., **Promponas V.J.** , Hamodrakas S.J. PRED-CLASS: cascading neural networks for generalized protein classification and genome-wide applications. (2001) *Proteins: Structure Function, and Genetics*, 44(3), 361-369.
5. **Promponas V.J.**, Enright A.J., Tsoka S., Kreil D., Leroy C., Hamodrakas S.J., Sander C., Ouzounis C.A. CAST: an iterative algorithm for the Complexity Analysis of Sequence Tracts. (2000) *Bioinformatics*, 16(10), 915-922.
4. Tsoka S., **Promponas V.** and Ouzounis C. Reproducibility in genome sequence annotation: The *Plasmodium falciparum* chromosome 2 case. (1999) *FEBS Letters*, 451, 354-355.
3. **Promponas V.J.**, Palaios G., Pasquier C.M., Hamodrakas J.S., Hamodrakas S.J. CoPreTHi: A Web tool which combines transmembrane protein segment prediction methods. (1999) *In Silico Biology*, 01(0014).

2. Pasquier C.M., **Promponas V.J.**, Palaios G., Hamodrakas J.S., and Hamodrakas S.J. A novel method for predicting transmembrane segments in proteins based on a statistical analysis of the SwissProt database: the PRED-TMR algorithm. (1999) *Protein Engineering*, 12(5), 381-385.
1. Pasquier C.M., **Promponas V.J.**, Varvayannis N.J., Hamodrakas S.J. A Web server to locate periodicities in a sequence. (1998) *Bioinformatics*, 14(8), 749-750.

## Publications in peer-reviewed conferences/edited volumes (V)

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11. † Agathocleous M., Christodoulou C., **Promponas V.J.**, Kountouris P., Vassiliades V. Training Bidirectional Recurrent Neural Network Architectures with the Scaled Conjugate Gradient Algorithm. (2016) In: *Artificial Neural Networks and Machine Learning – ICANN 2016: 25th International Conference on Artificial Neural Networks*, Barcelona, Spain, September 6-9, 2016, Proceedings, Part I. pp 123-131.
10. † Pavlopoulos G.A., **Promponas V.J.**, Ouzounis CA, Iliopoulos I. Biological information extraction and co-occurrence analysis. (2014) *Methods in Molecular Biology* 1159:77-92.
9. † Papadopoulos A., Kirmitzoglou I., **Promponas V.J.**, Theocharides T. GPU technology as a platform for accelerating local complexity analysis of protein sequences. (2013) *Proceedings of the Annual International Conference of the IEEE Engineering in Medicine and Biology Society, EMBS*, pp. 2684-2687.
8. † Kannas C.C., Achilleos K.G., Antoniou Z., Nicolaou C.A., Pattichis C.S., Kalvari I., Kirmitzoglou I., **Promponas V.J.** A Workflow System for Virtual Screening in Cancer Chemoprevention. (2012) In *IEEE 12th International Conference on Bioinformatics and BioEngineering, BIBE 2012*, pp. 439-446.
7. † Achilleos K.G., Kannas C.C., Nicolaou C.A., Pattichis C.S., **Promponas V.J.** Open Source Workflow Systems in Life Sciences Informatics. (2012) In *IEEE 12th International Conference on Bioinformatics and BioEngineering, BIBE 2012*, pp. 552-558.
6. † Tamana S, Kirmitzoglou I, **Promponas VJ\*** Sequence Features of Compositionally Biased Regions in Three Dimensional Protein Structures. (2012) In *IEEE 12th International Conference on Bioinformatics and BioEngineering, BIBE 2012*, pp. 270-275.
5. † Chrysos G, Sotiriades E, Rousopoulos C, Dollas A, Papadopoulos A, Kirmitzoglou I, **Promponas VJ** , Theocharides T, Petihakis G, Lagnel J, Vavylis P, Kotoulas G. Opportunities from the Use of FPGAs as Platforms for Bioinformatics Algorithms. (2012) In *IEEE 12th International Conference on Bioinformatics and BioEngineering, BIBE 2012*, pp. 559-565.
4. † Papadopoulos A, **Promponas V.J.** , Theocharides T. Towards systolic hardware acceleration for local complexity analysis of massive genomic data. (2012) In *Proceedings of the ACM Great Lakes Symposium on VLSI, GLSVLSI*, pp. 339-344.
3. † Nikolaou N, Sampaziotis P, Aplikioti M, Drakos A, Kirmitzoglou I, Argyrou M, Papamarkos N, **Promponas VJ\***. VeSTIS: A Versatile Semi-Automatic Taxon Identification System from Digital Images. In Nimis P. L., Vignes Lebbe R. (eds.), *Tools for Identifying Biodiversity: Progress and Problems*- pp. 231-236. ISBN 978-88-8303-295-0. EUT, 2010.
2. † Agathocleous M, Christodoulou G, **Promponas V**, Christodoulou C, Vassiliades V, and Antoniou A. Protein Secondary Structure Prediction with Bidirectional Recurrent Neural Nets: Can Weight Updating for Each Residue Enhance Performance? In H. Papadopoulos, A. S. Andreou and M. Bramer (eds.), *Artificial Intelligence Applications and Innovations (AIAI) 2010*, IFIP International Federation for Information Processing AICT, 339, 128-137, 2010.
1. † **Promponas VJ\***. A simple clustering approach for pathogenic strain identification based on local and global amino acid compositional signatures from genomic sequences: the *Escherichia* genus case. In *Proceedings of the 9th International Conference on Information Technology and Applications in Biomedicine, ITAB 2009*.

## (Guest) Editorials (E)

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5. † Kyriacou E.C., **Promponas V.J.**, Maglogiannis I., Schizas C.N., Pattichis C.S. Editorial: Intelligent Biomedical Systems (2014) *International Journal on Artificial Intelligence Tools*, 23(3):1402003\_1-1402003\_4.
4. † Tsiknakis M., **Promponas V.J.**, Graf N., Wang M.D., Wong S.T.C., Bourbakis N., Pattichis C.S. Guest editorial: Computational solutions to large-scale data management and analysis in translational and personalized medicine (2014) *IEEE Journal of Biomedical and Health Informatics*, 18(3):720-721.
3. † Hamodrakas, S.J., Iliopoulos, I., Ouzounis, C.A., Bagos, P.G., **Promponas V.J.** Meeting report: The seventh conference of the hellenic society for computational biology and bioinformatics (2013) *Computational and Structural Biotechnology Journal*, 6 (7), art. no. e201303006.
2. † Bourbakis N., Pattichis C.S., Schneider R., Kyriacou E.C., Andrade M., **Promponas V.J.**, Schizas C.N. Welcome address (2012) *IEEE 12th International Conference on BioInformatics and BioEngineering, BIBE 2012*, art. no. 6399639, pp. vii-ix.
1. † Spyrou G.M., **Promponas V.J.**, Micheli-Tzanakou E., Vasilakos A. Guest editorial: Special issue Classifying the classifiers in bioinformatics research (2010) *International Journal of Computational Intelligence in BioInformatics and Systems Biology*, 1(3):209-212.

## Papers submitted/in preparation (I)

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6. † Ntertili M., Kirmitzoglou I., **Promponas V.J.\***, Kouvelis V. \*, Typas M.\* MitoFun: A Curated Resource of Complete Fungal Mitochondrial Genomes (Submitted).
5. † Tamana S, Kirmitzoglou I., **Promponas V.J.\***, Standard operating procedure for computing compositionally biased pan-genomes (In preparation).
4. † Kirmitzoglou I., Ioannides A.-N., Papadopoulos A, Theocharides T, Ouzounis C.A., **Promponas V.J.\***, Novel software and hardware tools for fast detection of compositionally biased regions in amino acid sequences (In preparation).
3. † Kirmitzoglou I., **Promponas V.J.\***, Identifying pathogenic strains of *Escherichia* based on local and global amino acid compositional genome signatures (In preparation).
2. † Theodosiou A., **Promponas V.J.\***, A functional and structural view of Rare Codon Clusters in the *Escherichia coli* genome (In preparation).
1. † Gkotsi E-F., **Promponas V.J.\***, Sequence signatures of nitrilase specificity using hidden Markov models (In preparation).

## Book translations

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Contribution to the Greek translation of the book:

“Bioinformatics: A Practical Guide to the Analysis of Genes & Proteins, 2nd edition”

by Andreas D. Baxevasis, and B.F. Ouellete, ISBN: 960-394-222-7, Parisianou Publishers, Athens, 2004.



## Conference presentations and abstracts (C)

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### Invited talks

1. † **Promponas VJ** “Searching for Compositional Extremes: Open problems and challenges” COST NGP-NET Low Complexity Workshop, 28-29/11/2016, Institute of Molecular Biology, Mainz, Germany.
2. † **Promponas VJ** “Low complexity regions in IDPs” COST NGP-NET Winter School on computational methods for non-globular proteins, 15-19/02/2016, Bressanone/Brixen, Italy.
3. † **Promponas VJ** “Studying local compositional bias in protein sequences: novel tools and methods and biological applications” 1st NGP-NET Symposium on Non-Globular Proteins, 06-09/10/2015, Porto, Portugal.
4. † **Promponas VJ** “In silico tools and resources for identifying novel selective autophagy-associated proteins”, Symposium on “Applications of Bioinformatics in Molecular Biology” 20-21/11/2014, Medical School, University of Crete, Greece.
5. † **Promponas VJ** “Sequence analysis-driven identification of selective autophagy receptors”, Research Symposium in Biological Sciences, 04/12/2013, University of Cyprus, Nicosia, Cyprus.
6. † **Promponas VJ** “Sequence analysis-driven identification of novel selective autophagy receptors in *Drosophila melanogaster*”, 3rd Protein Summer School, University of Athens, 29/06/2013.
7. † **Promponas VJ** “Genome evolution and large-scale protein function prediction”, MSc EES Seminar Series – LMU Munich, 24/06/2013.
8. † **Promponas VJ** “Predicting structural, functional and phenotypic properties using (amino acid) sequences”, Computer Science and Engineering Department, European University of Cyprus, Nicosia, 12/03/2013.
9. † **Promponas VJ** “Predicting protein structure, function and interactions from amino acid sequences and next generation sequencing data”, 6th International Summer School on Emerging Technologies in Biomedicine, Patras, 1-6 July 2012.
10. † **Promponas VJ** “Using (amino acid) sequences for multi-level predictions of structural, functional and phenotypic properties”, School of Biology, Aristotle University of Thessaloniki, Thessaloniki, May 11, 2012..
11. † **Promponas VJ** “Computing Some Secrets of Life”, LinkSCEEM HPC User Meeting, Cyprus Institute, Nicosia, 9/2/2012.
12. † **Promponas VJ** “Computational methods for predicting protein structure and function from (amino acid) sequences”, Bioinformatics Masters Program, University of Bologna, 30/3/2012.
13. † **Promponas VJ** “Computational methods for predicting protein structure and function from amino acid sequences: a personal narrative”, Biophysics Workshop, University of Cyprus, 30/1/2012.
14. † **Promponas VJ** “Biological Sequence Analysis: Tools for Comparative Genomics”, HSCBB11 Satellite Workshop on “Advanced Bioinformatics Tools and Applications”, Patras, 6-7 October 2011.
15. † **Promponas VJ** et al. “Computing local and global descriptors for inferring gene/genomic functional features in prokaryotes”, 27-30/9/2011, 15th Evolutionary Biology Meeting, Marseilles, France.
16. † **Promponas VJ** “From protein sequence to structure and function”, 15/04/2011, in 1st Course in Next Generation Sequencing for Rare and Common Genetic Disorders, Cyprus Institute of Neurology and Genetics, Nicosia, Cyprus.
17. † **Promponas VJ**, “An archaeal stomatin homolog structure provides insights into folding and structural organization of human podocin in health and disease” EuroKUP COST Meeting, Pissouri, 06-07/11/2010.
18. † **Promponas VJ**, “Biomolecular databases and sequence analysis tools”, HSCBB10 Workshop, 17/10/2010, Thraki Palace-Alexandroupolis, Greece.
19. † **Promponas VJ**. “Sequence database search with compositionally biased amino acid sequences”, Second Workshop of the ERCIM Working Group on Computing and Statistics 29-31 October 2009, Grand Resort Hotel, Limassol, Cyprus.
20. † **Promponas VJ**. “Computing Some Secrets of Life: Computational Biology and Bioinformatics Research in the BRL@UCY.AC.CY”. LinkSCEEM Meeting: High Performance Computing Applications in Life Sciences. 05/11/2009, Larnaca, Cyprus.
21. † **Promponas VJ**. “Bridging Computational Biology, Bioinformatics and Biodiversity Informatics”, HSCBB-ELIXIR meeting, 30-31/03/2009, National Hellenic Research Foundation, Athens, Greece.
22. † **Promponas VJ**. “Computational Biology and Bioinformatics Research at BRL@UCY.AC.CY”, 12/12/2008, National Hellenic Research Foundation, Athens.
23. **Promponas VJ**. “Biologically Inspired Computation: Selected Bioinformatics Applications”, at the ‘Biologically Inspired Computation’ Workshop, Aristotle University of Thessaloniki, 19/12/2003.

### Oral Presentations

24. †**Promponas VJ\***, Georgiades K, Tamanas S, Christofi T, Apidianakis Y “A comparative and functional genomics approach for elucidating virulence determinants in *Pseudomonas*” In the Hellenic Bioinformatics 09/HBio-2016: Bioinformatics as a growth engine for Greece ,19-21/11/2016, CERTH, Thessalonica, Greece.

25. †**Promponas VJ\*** “GRANATUM: a social collaborative working space semantically interlinking biomedical researchers, knowledge and data for the design and execution of in-silico models and experiments in cancer chemoprevention.” Technology Track, ISMB/ECCB13, Berlin.
26. †**Promponas VJ**, Iliopoulos I, Ouzounis CA “We still haz a job: genome annotashuns”, Automated Function Prediction SIG 2013, ISMB/ECCB13, Berlin.
27. †Papadopoulos A, **Promponas VJ\***, Theocharides T. “FPGA-accelerated CAST for low-complexity region detection in amino acid sequences”, 2011, In the 6th Conference of the Hellenic Society for Computational Biology, Patras.
28. †Theodosiou A, **Promponas VJ\***. “LaTcOm: Visualizing rare codon clusters in mRNA sequences”, 2011, In the 6th Conference of the Hellenic Society for Computational Biology, Patras.
29. †Nikolaou N, Sampaziotis P, Aplikioti M, Drakos A, Kirmitzoglou I, Argyrou M, Papamarkos N, **Promponas VJ\***. “VeSTIS: A Versatile Semi-Automatic Taxon Identification System from Digital Images”, 2010, In BioIdentify Conference, Tools for identifying biodiversity: progress and problems, National Muséum of Natural History, Paris.
30. †Nikolaou N, Sampaziotis P, Aplikioti M, Drakos A, Kirmitzoglou I, Argyrou M, Papamarkos N, **Promponas VJ\***. “An Open Source system for semi-automatic species identification from digital images”, 2010, In the 5th Conference of the Hellenic Society for Computational Biology, Thraki Palace Hotel, Alexandroupolis.
31. †**Promponas VJ** and Hamodrakas SJ. “Structural analysis and an instance-based learning approach for the prediction of tightly interacting, successive in sequence, transmembrane  $\alpha$ -helices in polytopic transmembrane proteins”, 2009, In the 4th Conference of the Hellenic Society for Computational Biology, NHRF, Athens.
32. †**Promponas VJ**. “Browsing the proceedings of the HSCBB08 conference”, 2008, In the 1st National MikroBioKosmos Society Conference. MikroBioKosmos: Our Unexplored National Wealth, National Center of Scientific Research “Demokritos”, Athens.
33. †Kirmitzoglou I, Mitilinaiou E, **Promponas VJ**. “Local compositional extremes in protein sequences: definitions, algorithms and biological relevance”, 2008, In the 3rd Conference of the Hellenic Society for Computational Biology, CERTH, Thessaloniki, Greece.
34. **Promponas VJ**, Rodakis, GC, and Hamodrakas SJ. “A comprehensive study on the performance of progressive multiple sequence alignment methods based on reference alignment sets and phylogenetic criteria”, 2005, In the Proceedings of the 27th Annual Meeting of the Hellenic Society for Biological Sciences, Nafplio.
35. **Promponas VJ**, and Hamodrakas SJ. “Biologically Inspired Computations: Principles, Methods and Bioinformatics Applications”, 2004, In the Proceedings of the 26th Annual Meeting of the Hellenic Society for Biological Sciences, Volos.
36. **Promponas VJ**, and Hamodrakas SJ. “Machine Learning Computational Techniques for protein Fold Class prediction solely from aminoacid sequence”, 2003, In the Proceedings of the 25th Annual Meeting of the Hellenic Society for Biological Sciences, Mytelene.
37. **Promponas VJ**, Pasquier C, and Hamodrakas SJ. “PRED-CLASS: Bioinformatics software for the classification of protein sequences: Genome-wide applications”, 2001, In the Proceedings of the 23rd Annual Meeting of the Hellenic Society for Biological Sciences, Chios.
38. Pasquier C, **Promponas VJ**, Palaos GA, Hamodrakas JS, and Hamodrakas SJ. “PRED-TMR2: An hierarchical neural network to classify proteins as transmembrane and a novel method to predict transmembrane segments”, 1999, In the Proceedings of the 21st Annual Meeting of the Hellenic Society for Biological Sciences, Syros.
39. **Promponas VJ**, Palaos G, Pasquier, CM, Hamodrakas JS, and Hamodrakas SJ. “CoPreTHi: A program to combine the results of transmembrane protein segment prediction methods, freely available through the Internet”, 1998, In the Proceedings of the 20th Annual Meeting of the Hellenic Society for Biological Sciences, Samos.

#### Poster Presentations in International Conferences

40. †Georgatos F, Christian N, Hoste K, Laczny C, Loizou T, Jurkowski W, Panteli A, Schneider R, Tsouloupas G, Timmerman J, **Promponas VJ**. “Facilitating Computational Biology and Bioinformatics on HPC Systems Using EasyBuild” Benelux Bioinformatics Conference 2013, 9-10/12/2013, Brussels, Belgium.
41. †Tsompanis S, Kalvari I, Mulakkal NC, Nezis I, **Promponas VJ**. “Sequence analysis-driven identification and experimental validation of novel selective autophagy receptors in *Drosophila melanogaster*”, 21st International Conference on Intelligent Systems for Molecular Biology and 12th European Conference on Computational Biology, Berlin, Germany, 21-23/07/2013.
42. †Kirmitzoglou I, Kalvari I, Kannas C, Achilleos K, Antoniou Z, Nicolaou C, Neophytou C, Savva C, Scherf D, Gerhauser C, Constantinou A, Pattichis C, **Promponas VJ**. “GRANATUM-LiSIs: Making complex in silico predictive models accessible to wet biologists”, 21st International Conference on Intelligent Systems for Molecular Biology and 12th European Conference on Computational Biology, Berlin, Germany, 21-23/07/2013.
43. †Kalvari I, Lamprinidis G, Kirmitzoglou I, Kannas C, Achilleos K, Antoniou Z, Nicolaou C, Neophytou C, Savva C, Scherf D, Gerhauser C, Mikros E, Constantinou A, Pattichis C, **Promponas VJ**. “GRANATUM-LiSIs: Making complex in silico predictive models accessible to wet biologists”, 21st International Conference on Intelligent Systems for Molecular Biology and 12th European Conference on Computational Biology, Berlin, Germany, 21-23/07/2013.
44. † **Promponas VJ**, Kirmitzoglou I, “Identifying pathogenic strains of Escherichia based on local and global amino acid compositional genome signatures” , 21st International Conference on Intelligent Systems for Molecular Biology and 12th European Conference on Computational Biology, Berlin, Germany, 21-23/07/2013.

45. †Tamana S, Kirmitzoglou I, and **Promponas VJ**. “Accessibility of Compositionally Biased Regions in PDB structures”. 19th International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Vienna, Austria, 17-19/07/2011.
46. †Xenophontos M, Theodosiou A, Kirmitzoglou I, and **Promponas VJ**. “Evaluation of transmembrane helix (TMH) packing prediction methods on successive in sequence TMHs”. 19th International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Vienna, Austria, 17-19/07/2011.
47. †Theodosiou A, and **Promponas VJ**. “LaTcOm: A web server for visualizing rare codon clusters”. 19th International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Vienna, Austria, 17-19/07/2011.
48. †Ouzounis CA, Hamdrakas SJ, Iliopoulos I, Bagos PG, and **Promponas VJ**. “The Hellenic Society for Computational Biology and Bioinformatics”. 19th International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Vienna, Austria, 17-19/07/2011.
49. †Kountouris P, Agathocleous M, **Promponas VJ**, Christodoulou G, Hadjicostas S, Vassiliades V, and Christodoulou C. “A comparative study on filtering protein secondary structure prediction”. 19th International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Vienna, Austria, 17-19/07/2011.
50. †Kirmitzoglou I and **Promponas VJ**. “On the quality of established datasets for benchmarking sequence database search and low-complexity handling tools: the ASTRAL compendium test case”. 17th International Conference on Intelligent Systems for Molecular Biology and 8th European Conference on Computational Biology, Stockholm, Sweden, 27/06-02/07/2009.
51. †**Promponas VJ** and Mytilineou E. “Comparative analysis of local compositional complexity in plant encoded proteins”. 17th International Conference on Intelligent Systems for Molecular Biology and 8th European Conference on Computational Biology, Stockholm, Sweden, 27/06-02/07/2009.
52. †Kirmitzoglou I and **Promponas VJ**. “Effects of different masking strategies on protein sequence database searches with BLASTP”. 15th International Conference on Intelligent Systems for Molecular Biology and 6th European Conference on Computational Biology, Vienna, Austria, 21-25/07/2007.
53. †Tsirigos C., Bagos P, **Promponas VJ** Hamdrakas SJ. “Enhancing Transmembrane  $\beta$ -Barrel Topology Prediction by Information Encoded in Multiple Sequence Alignments”. 5th European Conference on Computational Biology, Eilat, Israel, 21-24/01/2007.
54. †**Promponas VJ**, Papanikolaou N, Iliopoulos I. “Conservation of genomic neighbourhood is related to the rate by which intraparalogous proteins evolve in two bacterial species”. 14th International Conference on Intelligent Systems for Molecular Biology, Fortaleza, Brazil, 06-10/08/2006.
55. †**Promponas VJ**, Limitsiou O. “Computational identification and analysis of paralogous gene families encoding  $\alpha$ -helical transmembrane proteins in two complete bacterial genomes”, In silico analysis of proteins - celebrating the 20th anniversary of Swiss-Prot 20, Fortaleza, Brazil, 30/07-04/08/2006.

#### Poster Presentations in National/Regional Conferences

56. †Agathocleous M, Hadjicostas S, Kountouris P, **Promponas VJ**, Vassiliades V, and Christodoulou C. “Improving protein secondary structure prediction using evolutionary strategies and RBF networks.”, In the 6th Conference of the Hellenic Society for Computational Biology, Patras.
57. †**Promponas VJ**. “Computational Biology and Bioinformatics Research at BRL@UCY.AC.CY”, 2008, In the 1st National MikroBioKosmos Society Conference. MikroBioKosmos: Our Unexplored National Wealth, National Center of Scientific Research Demokritos, Athens.
58. † Kirmitzoglou I, **Promponas VJ**. “Effects of different masking strategies on protein sequence database searches with BLASTP”, 2008, In the 3rd Conference of the Hellenic Society for Computational Biology, CERTH, Thessaloniki, Greece.
59. † Tsakogiannis A, Papanikolaou N, **Promponas VJ**, Ioannis Iliopoulos. “Gene Order Conservation Studies in three Pyrococcus species”, 2008, In the 3rd Conference of the Hellenic Society for Computational Biology, CERTH, Thessaloniki, Greece.
60. † **Promponas VJ**, Bagos PG, Hamdrakas SJ. “Structural neighborhood analysis of successive in sequence transmembrane  $\alpha$ -helices in polytopic  $\alpha$ -helical transmembrane proteins”. 2008, In the proceedings of the 4th Conference of the Hellenic Crystallographic Association, National Hellenic Research Foundation, Athens.
61. † Panousis NJ, Kalantzi A-S, **Promponas VJ**, Hamdrakas SJ. “Computational studies of  $\alpha$ -helices-lipid interactions in  $\alpha$ -helical transmembrane proteins”. 2008, In the proceedings of the 4th Conference of the Hellenic Crystallographic Association, National Hellenic Research Foundation, Athens.
62. † Mytilineou E, Kirmitzoglou I, **Promponas VJ**. “Comparative analysis of compositionally biased regions of two complete plant proteomes”, 2008, In the Proceedings of the 29th Annual Meeting of the Hellenic Society for Biological Sciences, Thessaloniki.
63. † Panousis NJ, **Promponas VJ**, Hamdrakas SJ. “Computational studies of interactions between  $\alpha$ -helices in transmembrane proteins”, 2008, In the Proceedings of the 29th Annual Meeting of the Hellenic Society for Biological Sciences, Thessaloniki.

64. †Kirmitzoglou I and **Promponas VJ**. “Effects of different masking strategies on protein sequence database searches with BLASTP”. 2007, In the Proceedings of the 29th Annual Meeting of the Hellenic Society for Biological Sciences, Kavala.
65. † Limitsiou OK, **Promponas VJ**. “Computational identification and analysis of paralogous gene families encoding for bacterial  $\alpha$ -helical transmembrane proteins”. 2006, In the Proceedings of the 28th Annual Meeting of the Hellenic Society for Biological Sciences, Ioannina.
66. † Tsirigos KD, **Promponas VJ**, Bagos PG, Rodakis GC, Hamodrakas SJ. “Enhancing the performance of protein structure prediction by information encoded in multiple sequence alignments”. 2006, In the Proceedings of the 28th Annual Meeting of the Hellenic Society for Biological Sciences, Ioannina.
67. Gkogkas CG, Tzavaras N, **Promponas VJ**, and Hamodrakas SJ. “Assessment and refinement of ‘*In Silico*’ annotation strategies in complete Genomes: the Chlamydia trachomatis Genome revisited”, 2004, In the Proceedings of the 26th Annual Meeting of the Hellenic Society for Biological Sciences, Volos.
68. Zographos LA, **Promponas VJ**, and Hamodrakas SJ. “A Computational method for pairwise alignment of  $\alpha$ - helical transmembrane protein sequences”, 2004 In the Proceedings of the 26th Annual Meeting of the Hellenic Society for Biological Sciences, Volos.
69. Limitsiou OK, **Promponas VJ**, and Hamodrakas SJ. “Comparative Computational analysis of  $\alpha$ -helical transmembrane proteins from two pathogenic bacteria of the genus Chlamydia”, 2004, In the Proceedings of the 26th Annual Meeting of the Hellenic Society for Biological Sciences, Volos.
70. Vernikos G, Gkogkas C, **Promponas VJ**, and Hamodrakas SJ “GeneRATOR: A software platform for complete Genome-Proteome Sequence feature analysis and visualization”, 2003, In the Proceedings of the 25th Annual Meeting of the Hellenic Society for Biological Sciences, Mytelene.
71. Bashir A, Alexopoulos I, Liakopoulos Th, Bagos P, Ikonomidou V, Katsaloulis P, Litou Z, Papandreou N, Pavlou K, **Promponas VJ**, Hamodrakas JS, and Hamodrakas SJ. “Bioinformatics Postgraduate Programme at the University of Athens: Announcing a new Masters Programme funded by the Hellenic Ministry of Education (EPEAEK II)”, 2003, In the Proceedings of the 25th Annual Meeting of the Hellenic Society for Biological Sciences, Mytelene.
72. Iconomidou VA, Chryssikos G, Troganis A, Paipetis A, **Promponas VJ**, Pavlou K, Iconomidis F, Bravou S, Komporozos K, and Hamodrakas SJ. “Studies of ‘mutant’ peptide-analogues of a part of the central domain of the B-family of silkmoth chorion proteins: induction/inhibition of amyloid-like fibril formation”, 2001, In the Proceedings of the 23rd Annual Meeting of the Hellenic Society for Biological Sciences, Chios.
73. Liakopoulos Th, Harkiolakis N, **Promponas VJ**, Pasquier C, Hamodrakas IS, Papandreou NC, Iconomidou V, Papandreou N, Tzafesta E, Tzafestas S, Eliopoulos E., and Hamodrakas SJ. “DAMBIO: Bioinformatics internet workbench for protein analysis. New modules and application to biological problems”, 2001, In the Proceedings of the 23rd Annual Meeting of the Hellenic Society for Biological Sciences, Chios.
74. Liakopoulos Th, Palaios GA, **Promponas VJ**, Hamodrakas JS Pasquier C, and Hamodrakas SJ. “A workbench for computational analysis of protein sequence and structure on the Internet”, 2000, In the Proceedings of the 22nd Annual Meeting of the Hellenic Society for Biological Sciences, Skiathos.
75. Palaios GA, **Promponas VJ**, Liakopoulos Th, Hamodrakas J, and Hamodrakas SJ. “WINPBM: a biomolecular visualization software package for personal computers”, 1999, In the Proceedings of the 21st Annual Meeting of the Hellenic Society for Biological Sciences, Syros.
76. **Promponas VJ**, Tsoka S, Ouzounis C, and Hamodrakas SJ. “CAST: A computational method for the complexity analysis of protein sequences”, 1999, In the Proceedings of the 21st Annual Meeting of the Hellenic Society for Biological Sciences, Syros
77. Pasquier CM, **Promponas VJ**, Varvayiannis NI, and Hamodrakas SJ. “A Web interface for FT: A tool dedicated to the study of periodicities in sequences”, 1998, In the Proceedings of the 20th Annual Meeting of the Hellenic Society for Biological Sciences, and the 1st Biological Meeting of Balcan Countries, Thessaloniki, Hellas.

#### Other Presentations

78. **Promponas VJ** “Open Access Publishing: a personal narrative”, Open Access to Knowledge – University of Cyprus & Cyprus Association of Librarians – Information Scientists (CALIS), 24/12/2014, Nicosia, Cyprus.
79. **Promponas VJ** “Microbial diversity and metagenomics: Science, Technology and Applications”, Free University – Skali Aglantzias, 21/01/2009, Nicosia, Cyprus.

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## TEACHING

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### University of Cyprus – Department of Biological Sciences

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#### Courses - Current

Since 2012	Instructor: “BIO 230 – Introduction to Computational Biology”, for the undergraduate program of the department (2nd year obligatory course)
Since 2005	Instructor: “BIO 650 – Special Topics in Bioinformatics”, for the graduate programmes of the department
Since 2013	Instructor: “BIO 331 – Computational and Systems Biology”, undergraduate departmental elective
2007-2010, 2012-	Instructor: “BIO 003 – Special Topics in Bioinformatics” (free elective undergraduate course).

#### Courses - Past

2009-2012	Instructor: “BIO 331 – Principles and Methods in Bioinformatics I”, for the undergraduate program of the department (3rd year obligatory course)
2010-2012	Instructor: “BIO 431 – Principles and Methods in Bioinformatics II”, for the undergraduate program of the department (elective course)
2008-2013	Guest lectures and practicals for the undergraduate courses: “BIO 241, 242 – Experimental methods and techniques I and II”
2008	Coordinator: “BIO 680 – Scientific Methodology in Molecular Biology”, MSc programme in Molecular Biology
2005-2008	Guest lectures for the undergraduate course: “BIO 001 – Introduction to Modern Biological Sciences”
Spring 2007, Fall 2008	Coordinator: “BIO 800-3 – Departmental seminar series”
2007	Lectures for the undergraduate course: “BIO 141 – Research in the Biological Sciences”
Since 2005	Advisor for the graduate courses: “BIO 780/790 – Autonomous study I/II”

#### Supervision

Since Sep 2011	Supervised the Diploma thesis of two incoming Erasmus undergraduate students. Currently supervising one external undergraduate student (Univ. of Athens).
Since Apr 2005	Supervised 2 completed PhD theses (I. Kirmitzoglou – now postdoc in Imperial College London; A. Theodosiou – Laboratory Scientific Officer in Cyprus Institute of Neurology and genetics) three Master’s Thesis students and 6 BSc students at the Department of Biological Sciences, University of Cyprus. Currently supervising three PhD candidates, one MSc and one BSc student.
Since Apr 2005	Member of advising/examining committees for a number PhD, MSc, BSc students of the Department of Biological Sciences (+2 PhDs of the Physics Department, +1 MSc of the Department of Education, + 2 PhD and 8 BSc of the Computer Science Department)

#### Local workshops organised

19/03/2011	Mining The Biomedical Literature: Focus on automated document annotation, knowledge discovery, microRNA research
07/02/2011	Modern techniques for studying biodiversity of aquatic ecosystems
17-18/09/2008	1st Cyprus Practical Workshop on Protein Bioinformatics

2006-2013	Supervised two MSc Theses for the MSc Bioinformatics Programme, in the Department of Cell Biology and Biophysics
2006-2013	Co-Instructor & Co-coordinator: “Microarray Technologies and Applications” for the MSc Bioinformatics Programme, in the Department of Cell Biology and Biophysics
2000-2005	Co-supervised the Diploma Project of 5 under-graduate students, in the Department of Cell Biology and Biophysics.
2003-2005	Active participation in the setting up of the MSc Bioinformatics Programme, in the Department of Cell Biology and Biophysics Instructor for the Postgraduate full semester courses: “Computational Analysis of Biomolecular Sequences” “Programming Languages and Software Tools in Bioinformatics I”, and “Programming Languages and Software Tools in Bioinformatics II”,
2003-2004	Teaching Assistant for the Postgraduate full semester courses of the MSc Bioinformatics Programme: “Bioinformatics: Principles and Methods”, and “Methodology in Research”
1996-2000, 2002-2003	Active participation in setting up computer labs and practicals, as well as Laboratory Assistant for the Undergraduate courses: “Molecular Biophysics”, and “Bioinformatics (Computer Applications In Biology)” in the Department of Cell Biology and Biophysics.

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## ADMINISTRATION & SERVICE

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### Administration (UCY)

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2016-	Member, Senate Computing Infrastructure Committee Duties: Participation in meetings (4-5 each semester). Also member of the subcommittee for approving top level domain .cy names until Nov 2016.
2011-2015	Elected Departmental representative to the Faculty of Pure and Applied Sciences board Duties: Participation in meetings (4-5 each semester).
2009-2011	Member, Senate Public Relations Committee Duties: Participation in meetings (4-5 each semester).
2007-2009	Member, Senate Student Housing Committee Duties: Participation in meetings (4-5 each semester). Participation in subcommittees for selecting students for accommodation in the dorms.
Spring 2007, Fall 2008	Coordinator of Departmental Seminar Series Invited speakers included: Prof. Gunnar von Heijne (Stockholm University, Sweden); Prof. Michael Ashburner (University of Cambridge, UK); Prof. Christos Ouzounis (King's College London, UK); Prof. Charles Dorman (Trinity College Dublin, IE); Prof. Joel Sussman (Weizmann Institute of Science, IL)
2010-2012	Chairperson, Undergraduate Program Committee
2006-2010	Member, Undergraduate Program Committee
2005-2009	Member, Postgraduate Program Committee
2005-2007	Member, Building Committee
Since 2007	Departmental ERASMUS coordinator – public relations contact point
2005-2007	Departmental Computer infrastructure officer
2007	Member of the national committee for University Entry Examination in Biology
2007–2008	Coordination and lecturing for the course offered by the department to forthcoming secondary education teachers (PRY015 – Biological and environmental sciences)
Since 2005	Academic advisor of several undergraduate (since 2007) and graduate students of the department
Since 2005	Member in several committees of the Department for equipment purchases

## Service

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### Editorial duties

2011-2014	Editorial Board Member, Journal of Biological Research Co-Guest Editor: Special Issue in Intelligent Biomedical Systems, International Journal on Artificial Intelligence Tools
2014	Co-Guest Editor: Special Section in Computational Solutions to Large-Scale Data Management and Analysis in Translational and Personalized Medicine, IEEE Journal of Biomedical and Health Informatics
2012-2012	Editorial Board Member, Computational and Structural Biotechnology Journal
2011-2011	Editorial Board Member, Conference Papers in Biology (Hindawi Publishing Corporation)
2011-2011	Academic Editor, PLoS One
2011-2011	Editorial Board Member, ISRN Bioinformatics (Hindawi Publishing Corporation)
2010	Guest editor for the 'International Journal of Computational Intelligence in Bioinformatics and Systems Biology' (Inderscience Publishers); Special issue: 'Classifying the Classifiers: Investigating the Optimum Classification Technique per case in Bioinformatics'
Since 2010	Editorial Board Member, International Journal of BioSciences and Technology

### Committee Member in National/International Conferences - Meetings

2016	Member, Organizing and Programme Committee, Hellenic Bioinformatics/HBio-2016: Bioinformatics as a growth engine for Greece, 19-21/11/2016, CERTH, Thessalonica, Greece
2013	Member, Organizing Committee and Scientific Program Committee, 8th Conference of the Hellenic Society for Computational Biology and Bioinformatics HSCBB13, 22-24/11/2013, Department of Computer Science & Biomedical Informatics, University of Thessaly, Greece
2012	Program Committee Co-Chair, IEEE 12th International Conference on Bioinformatics and BioEngineering, November 11-13, Larnaca, Cyprus
2012	Member, Organizing Committee and Scientific Program Committee, 7th Conference of the Hellenic Society for Computational Biology and Bioinformatics HSCBB12, 4-6/10/2012, IMBB, Heraclion, Greece
2011	Chairperson, Session: "Evolution of Complex Traits", 27-30/9/2011, 15th Evolutionary Biology Meeting, Marseilles, France
2011	Member, Organizing Committee and Scientific Program Committee, 6th Conference of the Hellenic Society for Computational Biology and Bioinformatics HSCBB11, 7-9/10/2011, University of Patras, Patras, Greece
2011	SIG Moderator at PRACE/LinkSceem High Performance Computing Winter School, Cyprus Institute, 26/01/2011, Nicosia, Cyprus
2010	Member, Organizing Committee, 5th Conference of the Hellenic Society for Computational Biology and Bioinformatics HSCBB10, 17-19/10/2010, Thraki Palace Hotel, Alexandroupolis, Greece
2009	Chair, Bioinformatics and Computational Biology Track, 9th International Conference on Information Technology and Applications in Biomedicine, ITAB 2009, 5-7/11/2009, Larnaca, Cyprus
2009	Chair, Program Committee & Member, Organizing Committee, 4th Conference of the Hellenic Society for Computational Biology and Bioinformatics HSCBB09, 18-20/12/2009, NHRF, Athens, Greece
2009	Member, National Organizing Committee, 19th International Conference of Artificial Neural Networks (ICANN 2009), 14-17 September 2009 in Limassol, Cyprus
2008	Chair, Program Committee & Member, Organizing Committee, 3rd Conference of the Hellenic Society for Computational Biology and Bioinformatics HSCBB08, 30-31/10/2008, CERTH, Thessaloniki, Greece
2008	Organizer of the 1st Practical Workshop on Protein Bioinformatics, 17-18/09/2008, UCY
2008	Member of the European Life-science Infrastructure for Biological Information (ELIXIR) Preparatory Phase WP3 Bioinformatics Communities Working Committee, EBI-EMBL, Hinxton, UK, 9-10/4/2008 and 17-18/11/2008
2008-2009	Chair, executive committee, Hellenic Society for Computational Biology and Bioinformatics
2008	Program Committee Member, IEEE Conference on Bioinformatics and Bioengineering (BIBE 2008)
2007	Co-organizer, Hellenic Bioinformatics & Medical Informatics Meeting, Biomedical Research Foundation Academy of Athens, Athens, Greece, 4-5/10/2007
Since 2003	Member of the International Society for Computational Biology, ISCB.



## Service (cont'd)

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### Reviewer

International Journals	Advances in Bioinformatics, Autophagy, Bioinformatics, Biosystems, BMC Bioinformatics, BMC Genomics, BMC Research Notes, Briefings in Bioinformatics, Cell Cycle, Computer Methods and Programs in Biomedicine, Computers in Biology and Medicine, HIPPOKRATIA journal, Integrative Biology, International Journal of Computer Mathematics, International Journal of Data Mining and Bioinformatics, International Journal of Molecular Sciences, ISRN Bioinformatics, Journal of Biological Research-Thessaloniki, Journal of Systems and Software, Medical Hypotheses, Methods in Ecology and Evolution, Molecular BioSystems, Nucleic Acids Research, PLoS One, PLoS Computational Biology, Proceedings of the Indian Academy of Sciences, Part B (Biological Sciences), Proteins: Structure, Function, and Bioinformatics, Proteomics
International Conferences	BITS14, BIBE2012, BIBE2008
Funding Agencies	EU ESF-COST Expert panel member (Transdomain proposals).
Thesis Examiner/Evaluator	University of Athens (a number of MSc and 2 PhD Theses), MAICh (2 MSc Theses), Technical University of Denmark (1 PhD Thesis)

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## FUNDING & COLLABORATORS

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### Principal Investigator/Coordinator in National (N) / International (I) Research Programs

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2008–2011	(N) CRPF–PENEK (Coordinator) Project Title: “Development of novel computational genomics web services and methods for the analysis of low complexity regions in amino acid sequences.” Budget: 90000 euros
2008–2010	(N) CRPF–HEALTH (Coordinator) Project Title: “Development of an integrated Computer System for Text Mining Biomedical Databases.” Budget: 120000 euros (total) – 84000 BRL
2008–2010	(N) CRPF–AEIFORIA (Coordinator) Project Title: “Development of a prototype computer-aided system for semi-automatically identifying key species of the marine benthic macrofauna of Cyprus.” Budget: 140000 euros (total) – 67000 BRL
2007–2008	(I) CRPF–KYEL/0406/71 (Bilateral cooperation Cyprus–Greece) (Principal Investigator & Coordinator) Project Title: “Development of a novel bioinformatics method for recognizing neighboring in space transmembrane A-helices in polytopic transmembrane proteins by information encoded in their amino acid sequence.” Budget: 36000 euros (total) - 24000 euros BRL
<b>Total funding 2005-</b>	<b>386000 euros (total) - 265000 euros BRL</b>

### Participation in National (N) / International (I) Research Programs

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2017–	(I) EC H2020-WIDESPREAD-04-2017-TeamingPhase1 (Partner) Project title: “Integrated Precision Medicine Technologies Research Centre of Excellence”
2011–2013	(I) EC FP7 ICT-2009.5.3 (Partner) Project title: “GRANATUM: A Social Collaborative Working Space Semantically Interlinking Biomedical Researchers, Knowledge And Data For The Design And Execution Of In-Silico Models And Experiments In Cancer Chemoprevention”
2011–2014	(N) NEA YPODOMH/STRATH/0308/31 (Partner) Project Title: “Cy-Tera: A Multi-Teraflops Computing Facility for Science and Technology in Cyprus”
2008–2011	(N) TPE/CALL ORIZO/0308/05(FR) (Partner) Project Title: “Developing of Novel and Efficient Second-Order Learning and Optimisation Techniques for Protein Structure Prediction” Budget: 85000 euros (total) - 3000 euros BRL
2004–2005	(N) EPEAEK II 2003–PYTHAGORAS (Postdoctoral Fellow – Software Analysis – Development)
2000–2004	(N) INTRAGENOME SA (Project Manager – Software and Database Analysis/Development)
1998–2001	(N) GSRT-PENED-1999 and GSRT-EPETII-EKBAN 1.3.4 (Software Analysis - Development)
1998	(I) TMR-EEC (EBI Visitors programme, 1998) (Software Analysis - Development)
1996–1997	(N) GSRT-PAVE-1996 (Software Analysis - Development)

## Major collaborators (in alphabetical order)

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Chris Christodoulou	Department of Computer Science, University of Cyprus Topic: Artificial neural network systems for protein secondary structure prediction
Andreas Constantinou	Department of Biological Sciences, University of Cyprus Topic: Virtual Screening for Cancer Biology
Kostas Fokianos	Department of Mathematics & Statistics, University of Cyprus Topic: Fourier transform–based methods for sequence analysis; statistical methods in Bioinformatics
Stavros J. Hamodrakas	University of Athens, Greece Topic: Topology and structure prediction of transmembrane proteins
Ioannis Iliopoulos	University of Crete, Greece Topic: Biomedical Literature Mining
Vassilis Kouvelis	University of Athens, Greece Topic: Fungal mitochondrial genomics
Ioannis Nezis	School of Life Sciences, University of Warwick, UK Topic: Delineation of Selective autophagy ( <i>in model eukaryotes</i> )
Christos Ouzounis	BCPL/CPERI/CERTH, Greece Topic: Comparative Genomics; theory and practice of sequence comparison methods
Nikos Papamarkou	Department of Electrical & Computer Engineering, Demokritus University of Thrace Topic: Content–based image retrieval methods for biodiversity informatics
Constantinos Pattichis	Department of Computer Science, University of Cyprus Topic: Scientific Workflows for Virtual Screening
Theocharis Theocharides	Department of Electrical and Computer Engineering, University off Cyprus Topic: Hardware accelerated computational biology and bioinformatics applications
Milton Typas	University of Athens, Greece Topic: Fungal mitochondrial genomics