

JENS ALLMER

CONTACT DETAILS

Assoc. Prof. Dr. Jens Allmer
Bioinformatics Laboratory
Department of Molecular Biology and Genetics
Izmir Institute of Technology
Gulbahce Koyu Campus
35430, Urla, Izmir, Turkey
Phone: +90-232-750-7310
GMS: +90-537 739 47 81
Fax: +90-232-750-7303
Email: jensallmer@iyte.edu.tr

Bionia Incorporated c/o Jens Allmer
IZTEKGEB, A8 Binasi
35430 Urla, Izmir, Turkey
Email: jensallmer@bionia.biz

EDUCATION

Doçent (similar to Habilitation), Biology, 23.09.2011
Turkish Inter-University Council (ÜAK)

Doktor rerum naturalium, Biology, 29.06.2006
University of Münster, Germany
Dissertation advisor: Prof. Dr. Michael Hippler
Dissertation title: *Development of algorithms for peptide identification from mass spectrometric data in genomic databases.*

Diplom, Zoology and Microbiology, 26.06.2002
University of Münster, Germany
Thesis advisor: Prof. Dr. Rüdiger J. Paul
Thesis Title: *Multiparametric, experimental analysis of the systemic oxygen transport cascade in Daphniids.*

Vordiplom, Biology, 25.03.1996
University of Münster, Germany

EMPLOYMENT

Founder and Chairman, Dec 2013 – present

Bionia Incorporated, IZTEKGEB, Urla, Izmir, Turkey

Leading a team of researchers and employees to establish a prototype service for *de novo* sequencing of MS/MS spectra. Acquisition of funding and customers.

Associate Professor, Oct 2011 – present

Izmir Institute of Technology, Department of Molecular Biology and Genetics, Izmir, Turkey

Teaching Bioinformatics, responsible for lecturing, student affairs, supervision of practical application, and grading for this topic. Data analysis in regards to Proteomics experiments involving mass spectrometric analysis.

Visiting Professor, Jul 2015 – Aug 2015

Knowledge Management in Bioinformatics, Institute of Computer Science, Humboldt-University, Berlin, Germany

Developing a scientific workflow within the Cuneiform and Hiway environment in the lab of Prof. Dr. Ulf Leser.

Visiting Professor, Jun 2013 – Sep 2013

Algorithmic Bioinformatics, Informatics Institute, Freie University, Berlin, Germany

Developing a *de novo* sequencing algorithm using the OpenMS framework in the lab of Prof. Dr. Knut Reinert.

Assistant Professor, Sep 2008 – Sep 2011

Izmir Institute of Technology, Department of Molecular Biology and Genetics, Izmir, Turkey

Teaching Bioinformatics, responsible for lecturing, student affairs, supervision of practical application, and grading for this topic. Data analysis in regards to Proteomics experiments involving mass spectrometric analysis.

Instructor, Feb 2007 – Aug 2008

Izmir University of Economics, Faculty of Computer Sciences, Izmir, Turkey

Teaching advanced programming, introduction to databases, computers and your future, software engineering and bioinformatics among other courses. Responsible for lecturing, student affairs, supervision of practical application, and grading for these classes.

Post Doc, Aug 2006 – Feb 2007

Westfälische Wilhelms University, Prof. Dr. Michael Hippler, Münster, Germany

Establishment of an annotation pipeline with database backend. Creation of high throughput software suite to fully automate processing of MS/MS data. Preparation of graduate level class for MS/MS and computational analysis.

Research Assistant, Jan 2006 – Jul 2006

Westfälische Wilhelms University, Prof. Dr. Michael Hippler, Münster, Germany

Transfer of the established relational database to a server based implementation with access control. Adaptation of GPF to the parallel environments, available in Münster.

Visiting Research Scholar, Jan 2004 – Dec 2005

University of Pennsylvania, Prof. Dr. Michael Hippler, Philadelphia, PA, USA

Development and establishment of a high-throughput proteomics pipeline. Design and implementation of a relational database. Prepared presentations for teaching proteomics with focus on mass spectrometry and subsequent computational processing for graduate level classes.

Research Assistant, Oct 2002 – Dec 2003

Schiller University, Prof. Dr. Michael Hippler, Jena, Germany

Development of an algorithm to identify peptides, split by an intron on the genomic level, from mass spectrometric data. Supervised and tested undergraduates in practical course work.

Research Assistant, Aug 2001 – May 2002

Westfälische Wilhelms University, Prof. Dr. Rüdiger J. Paul, Münster, Germany

Development of a computer program to acquire spectra from a CCD camera and to model the spectra to hemoglobin oxidation state. Analysis of *Daphnia pulex* via the newly established method and further noninvasive techniques.

Research Assistant, Jan 1998 – Jun 1998

Westfälische Wilhelms University, Prof. Dr. Christian Klämbt, Münster, Germany

Photography of *Drosophila melanogaster* larvae sections in various unordered developmental stages. Sorting, ordering, and assembling of the recorded sections. Production of short movies for display.

GRANTS

1. **Allmer J**, Has C, Thiel K, and Reinert K (to be evaluated by April 2016) Development of Reproducible High-Performance Bioinformatics Workflows Using SeqAn and KNIME to Facilitate the Detection of Host-Parasite MicroRNA Inter-Regulation (applied to 2+2 TÜBITAK-BMBF; **~1.000.000€**).
2. **Allmer J**, Genç Ş, Gültekin V, Hofestädt R, and Wingender E (to be evaluated by April 2016) Establishment of a Reproducible High Performance Workflow System, Integrating Proteomics and NGS Analysis Exemplified with the Elucidation of the CDC7 Inhibition Mechanism in Glioblastoma (applied to 2+2 TÜBITAK-BMBF; **~850.000€**).
3. **Allmer J** (2015) IBM Global Entrepreneur Program for Cloud Startups (**\$12000 + Education**).
4. **Allmer J** (2014-2017) A Datawarehouse For The Analysis Of Micro-RNA Metabolic Network Control [Mikro-RNA Metabolik Ağ Kontrol Analizi İçin Veri Ambarı], The Scientific and Technological Research Council of Turkey (*TÜBITAK*), 113E326 (**300.000 TL + Travel; ~113000€**).
5. **Allmer J** (2014-2017) Novel Human Proteins, Detection and Validation of Alternative Open Reading Frames [Alternatif Açık Okuma Çerçevesi'ne ait yeni insan proteinlerinin tespiti ve

- doğrulanması], The Scientific and Technological Research Council of Turkey (*TÜBİTAK*), 114Z177 (**337.000 TL; ~127000€**).
6. Frary A, **Allmer J**, Yalçın T, and Doğanlar S (2014-2017) Investigating tolerance to abiotic stress and boron accumulation in *Puccinellia* via comparative proteomics [Abiyotik Strese Toleransın Anlaşılması: Karşılaştırılmalı Proteomik ile *Puccinellia*'da Bor Birikimi Analizleri], *TÜBİTAK*, 113Z930 (**360.000 TL + Travel; ~135000€**).
 7. **Allmer J** (2014) Support for the 3rd International Workshop on Translational Bioinformatics and Health Informatics, The Scientific and Technological Research Council of Turkey (*TÜBİTAK*), 1929B021400101 (**40.000 TL; ~15000€**).
 8. **Allmer J** (2014) Creating a Ground-Truth Benchmark Dataset for Fine-Tuning Peptide MS/MS Spectrum Scoring Functions, *PRIME-XS 230 (Travel + MS measurements)*.
 9. Has C, Gültekin V, and **Allmer J** (2013-2014) ProteoGaia: de novo dizilemede yeni bir yaklaşım [ProteoGaia: A Novel Approach to de novo Sequencing], Technology and Innovation Funding Directorate (*TEYDEB*), 2130354 (**100.000 TL; ~38000€**).
 10. **Allmer J** (2013-2015) Employing human blood plasma mass spectrometric data for accurate gene annotation, Research Project [Bilimsel Araştırma Projesi], *IzTech*, 2013IYTE30 (**20.000 TL; ~8000€**).
 11. **Allmer J** (2011-2012) RAY: A Profile-based Approach for Homology Matching of Tandem-MS Spectra to Sequence Databases [MS Homolog Özellğe Dayalı Veritabanı Aramalarının Kapsamının Genişletilmesi], Short Term R&D Funding Program [Hizli Destek], *TÜBİTAK*, 111E139 (**25.000 TL; ~9000€**).
 12. **Allmer J** (2009-2010) Accuracy Assessment of Label-Free Protein Quantitation using MS/MS, Research Project [Bilimsel Araştırma Projesi], *IzTech*, 2009IYTE30 (**7000 TL; ~3000€**).
 13. **Allmer J** (2008) PTMPredictor, Research Project, *CPU Turkey (Software + Machinery +Travel)*.

AWARDS

EMBO, Short Term Fellowship, 2013

DAAD, Research Stays for University Academics and Scientists, 2013 (declined).

Turkish Academy of Sciences (*TÜBA*), Outstanding Young Researcher Award (*GEBİP*), 2010.

PATENTS

Hippler M and **Allmer J** Method to identify peptides from mass spectrometric data in genomic databases. Patent number DE 103 41 595 A1, German Patent Office, 2004, patent pending

Hippler M and **Allmer J** Method to identify peptides from mass spectrometric data in genomic databases. Patent number DE 10 2004 018 655 A1, German Patent Office, 2005, patent pending

PUBLICATIONS

1. Tüfekçi KU, Erkan EP, **Allmer J**, Carman KB, Bayram E, Topçu Y, Kurul SH, Genç Ş, and Yis U Antiviral microRNA expression signatures are altered in subacute sclerosing panencephalitis, *PLOS One* (submitted).
2. Has C, Singer J, Reinert K, and **Allmer J** Lelantos: Fast Proteogenomic Peptide Mapping *Bioinformatics* (under revision).
3. Bağcı C, and **Allmer J** (2016) One Step Forward, Two Steps Back; Xeno-MicroRNAs Reported in Breast Milk are Artifacts, *PLOS One*, doi: 10.1371/journal.pone.0145065.
4. Yousef M, **Allmer J**, and Khalifa W (2016) Feature Selection for MicroRNA Target Prediction, *Proceedings of the 9th International Joint Conference on Biomedical Engineering Systems and Technologies*, BIOINFORMATICS(3): 216-225.
5. Yousef M, **Allmer J**, and Khalifa W (2016) Accurate Plant MicroRNA Prediction Can Be Achieved Using Sequence Motif Features, *Journal of Intelligent Learning Systems and Applications*, 8(1):9-22, doi: 10.4236/jilsa.2016.81002.
6. Yousef M, **Allmer J**, and Khalifa W (2015) Sequence Motif-Based One-Class Classifiers Can Achieve Comparable Accuracy to Two-Class Learners for Plant microRNA Detection, *Journal of Biomedical Science and Engineering*, 8(10):684-694, doi: 10.4236/jbise.2015.810065.
7. Alural B, Özderem A, **Allmer J**, Genç K, and Genç Ş (2015) Lithium protects against paraquat neurotoxicity by NRF2 activation and miR-34a inhibition in SH-SY5Y cells, *Frontiers Neuroscience* 9:209, doi: 10.3389/fncel.2015.00209.
8. Uncu A, Gültekin, V, **Allmer J**, Frary A, and Doğanlar S (2015) Genomic SSR Markers Reveal Patterns of Genetic Relatedness and Diversity in Sesame, *The Plant Genome*, doi: 10.3835/plantgenome2014.11.0087.
9. Saçar MD, Bağcı C, and **Allmer J** (2014) Computational Prediction of MicroRNAs from *Toxoplasma gondii* Potentially Regulating the Hosts' Gene Expression, *Genomics, Proteomics & Bioinformatics*, 12(5):228-238, doi:10.1016/j.gpb.2014.09.002.
10. Alural B, Duran GA, Tüfekçi KU, **Allmer J**, Önköl Z, Tunali D, Genç K, and Genç Ş (2014) EPO Mediates Neurotrophic, Neuroprotective, Anti-Oxidant and Anti-Apoptotic Effects via Downregulation of miR-451 and miR-885-5p in SH-SY5Y Neuron-Like Cells, *Frontiers Immunology*, 5:475-482, doi: 10.3389/fimmu.2014.00475.
11. Yousef M, Trinh HV, and **Allmer J** (2014) Intersection of MicroRNA and Gene Regulatory Networks and their Implication in Cancer, *Current Pharmaceutical Biotechnology*, 15(5): 445-454, doi: 10.2174/1389201015666140519120855.
12. Hamzeiy H, Yousef M, and **Allmer J** (2014) Computational Methods for miRNA Target Prediction, *Methods in Molecular Biology*, 1107:207-221, doi: 10.1007/978-1-62703-748-8_12.
13. Saçar MD and **Allmer J** (2014) Machine Learning methods for miRNA Gene prediction, *Methods in Molecular Biology*, 1107:177-187, doi: 10.1007/978-1-62703-748-8_10.

14. **Allmer J** (2014) Computational and Bioinformatics Methods for miRNA Gene Prediction, *Methods in Molecular Biology*, 1107:157-175, doi: 10.1007/978-1-62703-748-8_9.
15. Çelik I, Gültekin V, **Allmer J**, Doğanlar S, and Frary A (2014) Development of Genomic Simple Sequence Repeat Markers in Opium Poppy by Next-Generation Sequencing, *Molecular Breeding*, 34(2): 323-334, doi: 10.1111/pbr.12059.
16. Saçar MD and **Allmer J** (2013) Current Limitations for Computational Analysis of miRNAs in Cancer, *Pakistan Journal of Clinical and Biomedical Research*, 1(2): 3-5.
17. Saçar MD and **Allmer J** (2013) Data Mining for MicroRNA Gene Prediction: On the Impact of Class Imbalance and Feature Number for MicroRNA Gene Prediction, *IEEE Xplorer*, doi: 10.1109/HIBIT.2013.6661685.
18. Has C, Kundakci CU, Altay A, and **Allmer J** (2013) Ranking Tandem Mass Spectra: and the Impact of Database Size and Scoring Function on Peptide Spectrum Matches, *IEEE Xplorer*, doi: 10.1109/HIBIT.2013.6661686.
19. **Allmer J** (2013) Predicting the C-Terminal Amino Acid of a Peptide from MS/MS Data, *Journal of Integrative OMICS*, 3(2): 112-119, doi:10.5584/jiomics.v2013i2013.137.
20. Şelale H, Çelik I, Gültekin V, **Allmer J**, Doğanlar S, and Frary A (2013) Development of EST-SSR Markers for Diversity and Breeding Studies in Opium Poppy, *Plant Breeding*, 132(3):344–351, doi:10.1111/pbr.12059.
21. Saçar MD, Hamzeiy H and **Allmer J** (2013) Can MiRBase Provide Positive Data for Machine Learning for the Detection of MiRNA Hairpins? *Journal of Integrative Bioinformatics*, 10(2):215-226, doi:10.2390/biecoll-jib-2013-215.
22. Saçar MD and **Allmer J** (2013) Comparison of Four Ab Initio MicroRNA Prediction Tools, 4th *International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2013*, Barcelona, Spain, doi:10.5220/0004248201900195.
23. **Allmer J** (2012) A Call for Benchmark Data in Mass Spectrometry-Based Proteomics, *Journal of Integrative OMICS*, 2(2): 1-5, doi: 10.5584/jiomics.v2012i2012.113.
24. **Allmer J** and Yousef M (2012) Computational Methods for ab initio Detection of MicroRNAs, *Frontiers in Genetics*, 3:209, doi: 10.3389/fgene.2012.00209.
25. Takan S and **Allmer J** (2012) De Novo Markup Language, a Standard to Represent De Novo Sequencing Results from MS/MS Data, *IEEE Xplorer*, doi:10.1109/HIBIT.2012.6209038.
26. Bağcı C and **Allmer J** (2012) Removing Contaminations from Genomic Sequences Based on Vector Reference Libraries, *IEEE Xplorer*, doi: 10.1109/HIBIT.2012.6209053.
27. **Allmer J** (2011) Algorithms for the De Novo Sequencing of Peptides from Tandem Mass Spectra, *Expert Reviews of Proteomics*, 8(5), 645-657, doi: 10.1586/epr.11.54.
28. **Allmer J** (2010) Existing bioinformatics tools for the quantitation of post translational modifications, *Amino Acids*, 42(1), 129-138, doi: 10.1007/s00726-010-0614-3.
29. **Allmer J** (2010) Label Free Quantitation in Mass Spectrometry based Proteomics, *ProteomeIstanbul, International Proteomics Workshop*, Theoretical Proceeding, pp. 112-134, Istanbul, Turkey.

30. **Allmer J** (2010) Guide to Practical Quantitation of Mass Spectrometric Results, ProteomeIstanbul, *International Proteomics Workshop, Practical Proceeding*, pp. 53-61, Istanbul, Turkey.
31. **Allmer J** (2010) Relative protein quantitation with post translational modifications in Mass spectrometry based proteomics, *IEEE Xplorer*, doi: 10.1109/HIBIT.2010.5478886.
32. Çakır MV and **Allmer J** (2010) Systematic Computational Analysis of Potential RNAi Regulation in *Toxoplasma gondii*, *IEEE Xplorer*, doi: 10.1109/HIBIT.2010.5478909.
33. **Allmer J** (2009) Label-free quantitation, an extension to 2DB. *Amino Acids*, 38(4), 1075-1087, doi: 10.1007/s00726-009-0317-9.
34. **Allmer J**, Kuhlert S and Hippler M (2009) 2DB News: Security and Functional Enhancements, 4th *International Symposium on Health Informatics and Bioinformatics*, Ankara, Turkey.
35. **Allmer J**, Kuhlert S, and Hippler M (2008) 2DB: a Proteomics database for storage, analysis, presentation, and retrieval of information from mass spectrometric experiments. *Bioinformatics*, 9,302-313, doi: 10.1186/1471-2105-9-302.
36. Naumann B, Busch A, **Allmer J**, Ostendorf E, Zeller M, Kirchhoff H and Hippler M (2007) Comparative quantitative proteomics to investigate the remodelling of bioenergetic pathways under iron-deficiency in *Chlamydomonas reinhardtii*. *Proteomics*, 7 (21): 3964-3979, doi: 10.1002/pmic.200700407.
37. Merchant S, Prochnik S, Vallon O, Harris EH, Karpowicz SJ, et al. (2007) The evolution of key animal and plant functions is revealed by analysis of the *Chlamydomonas* genome, *Science*, 318 (5848), 245-251, doi: 10.1126/science.1143609.
38. **Allmer J**, Naumann B, Markert C, Zhang M, and Hippler M (2006) Mass spectrometric genomic data mining: Novel insights into bioenergetic pathways in *Chlamydomonas reinhardtii*, *Proteomics*, 6, 23, 6207-6220, doi: 10.1002/pmic.200600208.
39. **Allmer J**, Markert C, Stauber EJ, and Hippler M (2004) A new approach that allows identification of intron-split peptides from mass spectrometric data in genomic databases. *FEBS letters*, 562, 202-206, doi: 10.1016/S0014-5793(04)00212-1.

BOOKS

1. Yousef M and **Allmer J**, eds. (2014) miRNomics: MicroRNA Biology and Computational Analysis, *Humana Press*, ISBN: 978-1-62703-747-1.
2. **Allmer J**, ed. (2014) Proceedings of the 3rd International Workshop on Translational Bioinformatics and Health Informatics, Izmir, Turkey.
3. **Allmer J**, ed. (2012) Sequence Alignment in Bioinformatics [Biyoinformatikte Dizi Kiyaslamasi], *Nobel Publishing*, Ankara, Turkey, ISBN: 978-605-133-297-0.
4. **Allmer J**, ed. (2011) 6th International Symposium on Health Informatics and Bioinformatics, Izmir, Turkey, ISBN: 978-1-4507-7534-2

BOOK CHAPTERS

1. Saçar D, Bağcı C, and **Allmer J** (2016) Differential Expression of *T. gondii* MicroRNAs in Murine and Human Hosts, in Non-coding RNAs and Inter-Kingdom Communication (ed. Francisco Javier Lombardo Enguita), Springer (accepted).
2. **Allmer J** (2012) Pattern Matching [Motif Eşleşmesi], in Sequence Alignment in Bioinformatics [Biyoinformatikte Dizi Kıyaslaması] (ed. **Allmer J**), pp. 11-34, *Nobel Publishing*, Ankara, Turkey.
3. **Allmer J** (2010) Computational approaches in microRNA analysis and storage [microRNA Analizi ve Saklanması Hesaplamaya Dayalı Yaklaşımlar], in MicroRNAs and the Nerve System [MikroRNA ve Sinir Sistemi] (eds. Genç Ş and Genç K), 92-125, *TÜBA Publishing*.

PEER REVIEWED ABSTRACTS

1. **Allmer J** (2015) On the State of the Art in Protein Identification and Sequencing using Mass Spectrometry, Keynote, International Congress on Analytical Proteomics, Lisbon, Portugal.
2. Erkan EP, Dinç M, Eren E, Allmer J, Yalçın T, Genç Ş (2015) A Cell Division Cycle 7-related Protein Kinase Inhibitor Suppresses Glioblastoma Cell Growth *in vitro*, XII European Meeting on Glial Cells in Health and Disease, Bilbao, Spain <http://glia2015.abstract-management.de/planner/?action=abstractDetails&abstract=54>.
3. Has C, Mungan MD, Çiftçi C, and **Allmer J** (2015) Database Normalization is Crucial for Reliable Protein Identification in Mass Spectrometry-based Proteomics, 14th International Conference on Amino Acids, Peptides and Proteins (ICAAPP14), Vienna, Austria.
4. Has C, Mungan MD, Çiftçi C, and **Allmer J** (2015) Preparing Sequence Databases for Application in Proteogenomics, 14th International Conference on Amino Acids, Peptides and Proteins (ICAAPP14), Vienna, Austria.
5. Göktay M, Ayvaz M, un-Hua Liu C, Smith W, Zhang HB, and **Allmer J** (2015) Application of Next Generation Sequencing for Differential Gene Expression Analysis of four Cotton Cultivars, 6th International German/Turkish/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany.
6. Bağcı C and **Allmer J** (2015) How to Avoid Pitfalls in Next Generation Sequencing Data Analysis, 6th International German/Turkish/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany.
7. Suluyayla R, Saçar MD, and **Allmer J** (2015) Analysis of Features Describing pre-microRNAs, 6th International German/Turkish/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany.
8. Bağcı C and **Allmer J** (2015) Next Generation Sequencing's Sensitivity is both Boon and Bane, 2nd International Congress on Biosensors, Gediz University, Izmir, Turkey.
9. Bağcı C and **Allmer J** (2015) How to Avoid Pitfalls in Next Generation Sequencing Data Analysis, 2nd International Congress on Biosensors, Gediz University, Izmir, Turkey.

10. Has C, Mungan MD, Çiftçi C, and **Allmer J** (2015) On the Use of Multiple Databases for DB Search in Mass Spectrometry-Based Proteomics, Proteomics Forum, Congress of the German Society of Proteome Research, Technical University Berlin, Germany.
11. Hamzeiy H and Allmer J (2014) MicroRNA Data Analysis: A Special Focus on Console Applications, WiBioSE Conference, Arandjelovac and Belgrade, Serbia.
12. Suluyayla R, Has C, and **Allmer J** (2014) Novel Methodology for Integration of Results from Searching Multiple Sequence Databases in Mass Spectrometry-Based Proteomics, 4th International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
13. Bağcı C and **Allmer J** (2014) Efficient Removal of Adapter and Plasmid Contaminations from Short Sequence Reads Without the Need of a Database, 4th International German/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
14. Suluyayla R, Has C, and **Allmer J** (2014) OMSSA was discontinued by NCBI; did its performance cause this decision? International Workshop on MS-Based Proteomics, Bioinformatics, and Health Informatics, Izmir, Turkey.
15. Saçar MD and **Allmer J** (2014) An Integrative Data Mining Approach for MicroRNA Detection in Human. 3rd International Workshop on Translational Bioinformatics and Medical Informatics, Izmir, Turkey.
16. Has C, Toprak M, and **Allmer J** (2013) AthenaDB, Data Integration for Protein Secondary Structure Analyses, 4th International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
17. Saçar MD and **Allmer J** (2013) "Comparison of Four Ab Initio MicroRNA Prediction Tools", 4th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2013, p. 66, Barcelona, Spain.
18. Hamzeiy H, Saçar MD, and **Allmer J** (2012) Regulatory Role of MicorRNAs in Breast Cancer and Importance of *In Silico* MicroRNA Discovery, 9th International Winter School for Molecular Biology and Genetics (IÜGEN), Istanbul, Turkey.
19. Has C, Göktay M, Teke E, Tosun C, and **Allmer J** (2012) Using Public Mass Spectrometric Data from Human Plasma Samples to Annotate the Human Genome, BePac 2012 - Two-day symposium of the Belgian Proteomics Association, Gent, Belgium.
20. Has C, Boz S, **Allmer J** (2012) Using Human Blood Plasma Proteomics Data for the Validation of Gene Models, ECCB'12, 11th European Conference on Computational Biology, Basel, Switzerland.
21. Has C, Toprak M, **Allmer J** (2012) PROMETHEUS: Secondary Structural Elements' Profiles of Proteins, ECCB'12, 11th European Conference on Computational Biology, Basel, Switzerland.
22. Has C, Yılmaz Ş, Aytun B, **Allmer J** (2012) COMAS: Ant Colony Optimization a De Novo Sequencing Algorithm, ECCB'12, 11th European Conference on Computational Biology, Workshop: From Mass Spectrometry to Protein Complexes, Basel, Switzerland.
23. Akçimen F, Sayın S, Bakırbaş A, Firatligil B, Has C, and **Allmer J** (2012) Genome Annotation of Sesamum Indicum, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey.

24. Boz S, Has C, and **Allmer J** (2012) Using Proteomics Data for the Validation of Gene Models, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey.
25. Hamzeiy H, Saçar MD, and **Allmer J** (2012) A Closer Look at Features Used in In Silico miRNA Hairpin Fingerprinting and Predicting, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey.
26. Toprak M, Has C, and **Allmer J** (2012) Prometheus Secondary Structural Elements' Profiles of Proteins, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey.
27. Sacar MD, Hamzeiy H, and **Allmer J** (2012) Have Features for miRNA Hairpin Detection been Saturated? 3rd International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
28. Hamzeiy H, Saçar MD, and **Allmer J** (2012) The Predictive Power of Specific Features Used for miRNA Discovery, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey.
29. Yilmaz S and **Allmer J** (2012) RAY: Increasing the Scope of Mass Spectrometry-Homology Based Database Search, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey.
30. Doğanlar S, Gültekin V, **Allmer J**, and Frary A (2012) Development of Genomic Tools for Eggplant, International Symposium on Biotechnology and other Omics in Vegetable Science, Antalya, Turkey.
31. Hamzeiy H, Saçar MD, and **Allmer J** (2011) A Handful of miRNA Fingerprints, Computational Systems Biology, German/Russian Network of Computational Systems Biology, Shaker Verlag, pp. 1-3, ISBN 978-3-8440-0653-7.
32. Şelale H, Çelik I, **Allmer J**, Frary A, and Doğanlar S (2011) Development of EST-SSR markers for opium poppy (*Papaver somniferum*), Plant Genomics European Meeting, Istanbul, Turkey.
33. Çelik I, Gültekin V, **Allmer J**, Doğanlar S, and Frary A (2011) Development of SSR Markers Derived from Genomic Sequence of *Papaver somniferum* L., The International Congress on Bioinformatics and Biomics, Kusadası, Turkey
34. **Allmer J**, (2010) Mass Spectrometry Based Proteomics, 4. Moleküler Biyoloji ve Genetik Araştırma ve Uygulama Platformu, p. 19, Izmir, Turkey
35. Has C and **Allmer J** (2010) An integrative view on protein secondary structure prediction, 5th Int. Symposium on Health Informatics and Bioinformatics, p. 233, Antalya, Turkey.
36. **Allmer J** (2010) De Novo Amino Acid Sequencing in Mass Spectrometry based Proteomics, 9th GEBIP Annual Meeting, Istanbul, Turkey
37. Aytun B and **Allmer J** (2010) Tandem MS Fragment Ion Naming for Enhancement of de novo Sequencing, 5th Int. Symposium on Health Informatics and Bioinformatics, p. 232, Antalya, Turkey.
38. Geçer EC, Batur N, and **Allmer J** (2010) Sequential Process Management System 'KERB', 5th Int. Symposium on Health Informatics and Bioinformatics, p. 224, Antalya, Turkey.
39. **Allmer J** (2009) Enabling the quantitation of post translational modifications, *Amino Acids* 37, S32.

40. **Allmer J** (2009) Label-free quantitation with 2DB, *Amino Acids* 37, S123.
41. Batur N and **Allmer J** (2009) Database Management System Independence by Amending 2DB with a Database Access Layer, 4th International Symposium on Health Informatics and Bioinformatics, Ankara, Turkey.
42. **Allmer J** (2009) Systematic computational analysis of RNAi regulation in *Toxoplasma gondii*, 4th International Symposium on Health Informatics and Bioinformatics, Ankara, Turkey.
43. Kirmacı E, İnce T, and **Allmer J** (2008) PTM Predictor, Güncel, Gömsis, CPU Turkey, Istanbul, Turkey.
44. **Allmer J** (2008) Efficient String Matching, 3rd International Symposium on Health Informatics and Bioinformatics, Istanbul, Turkey.
45. Kuhlger, S. and **Allmer J** (2007) 2DB: a publication grade proteomics database poster presentation, 2nd International Symposium on Health Informatics and Bioinformatics, Belek, Turkey.
46. Hippler M, Busch A, **Allmer J**, Ostendorf E, Zeller M, Kirchhoff H, and Naumann B (2007) Comparative quantitative proteomics to investigate the remodelling of bioenergetic pathways under iron-deficiency in *Chlamydomonas reinhardtii*, *Photosynthesis research*, 91(2-3): 290-290, PS2226.
47. Naumann B, **Allmer J**, Zhang M, and Hippler M (2006) Comparative quantitative proteomics to investigate the remodeling of bioenergetic pathways in response to iron deprivation in *Chlamydomonas reinhardtii*. 13th International Symposium on Iron Nutrition and Interactions in Plants, Montpellier, France.
48. **Allmer J**, Markert C, Stauber EJ, and Hippler M (2004) A new approach that allows identification of intron-split peptides from mass spectrometric data in genomics databases. Proc. 13th International Congress on Photosynthesis, p. 20, Montréal, Québec, Canada.
49. **Allmer J**, Markert C, Meyer H, and Hippler M (2004) Digging into the thylakoid proteome of *Chlamydomonas* by optimizing the search of mass spectrometric data in genomic databases. Proc. 13th International Congress on Photosynthesis, pp. 57-58, Montréal, Québec, Canada.
50. **Allmer J**, Markert C, Stauber EJ, and Hippler M (2004) A new approach that allows identification of intron-split peptides from mass spectrometric data in genomic databases. 11th International Conference on the Cell and Molecular Biology of *Chlamydomonas*, Kobe, Japan.
51. **Allmer J**, Seidl MD, Pirow R, and Paul RJ (2002) Physiological responses of Hb-poor and Hb-rich *Daphnia pulex* to sudden hypoxia. International Symposium on Animal Physiology, p1, Alexisbad, Germany.

INVITED TALKS

1. **Allmer J** (2015) On the State of the Art in Protein Identification and Sequencing using Mass Spectrometry, Keynote, International Congress on Analytical Proteomics, Lisbon, Portugal.

2. Has C, Mungan MD, Çiftçi C, and **Allmer J** (2015) Database Normalization is Crucial for Reliable Protein Identification in Mass Spectrometry-based Proteomics, International Conference on Amino Acids, Peptides and Proteins (ICAAPP14), Vienna, Austria
3. Göktay M, Ayvaz M, un-Hua Liu C, Smith W, Zhang HB, and **Allmer J** (2015) Application of Next Generation Sequencing for Differential Gene Expression Analysis of four Cotton Cultivars, International German/Turkish/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany.
4. Bağcı C and **Allmer J** (2015) How to Avoid Pitfalls in Next Generation Sequencing Data Analysis, International German/Turkish/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany.
5. Suluyayla R, Saçar MD, and **Allmer J** (2015) Analysis of Features Describing pre-microRNAs, International German/Turkish/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany.
6. Bağcı C and **Allmer J** (2015) Next Generation Sequencing's Sensitivity is both Boon and Bane, 2nd International Congress on Biosensors, Gediz University, Izmir, Turkey.
7. Bağcı C and **Allmer J** (2015) How to Avoid Pitfalls in Next Generation Sequencing Data Analysis, 2nd International Congress on Biosensors, Gediz University, Izmir, Turkey.
8. Saçar MD, Bağcı C, and **Allmer J** (2014) Toxoplasma Gondii may Regulate its Host Cell via Leaking of MicroRNAs, International Workshop on MicroRNA cancer biomarkers and next generation sequencing techniques, 2014, Izmir, Turkey.
9. Suluyayla R, Has C, and **Allmer J** (2014) Novel Methodology for Integration of Results from Searching Multiple Sequence Databases in Mass Spectrometry-Based Proteomics, 4th International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
10. Bağcı C and **Allmer J** (2014) Efficient Removal of Adapter and Plasmid Contaminations from Short Sequence Reads Without the Need of a Database, 4th International German/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
11. **Allmer J** (2013) BioInfOmics; or from Genomics via Transcriptomics and Proteomics to ProteoGenomics, Boğaziçi University, Istanbul, Turkey.
12. Sacar MD, Hamzeiy H, and **Allmer J** (2012) Have Features for miRNA Hairpin Detection been Saturated?, 3rd International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
13. **Allmer J** (2012) A Bioinformatics View on Sequence Similarity and Homology, 3rd International German/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.
14. Hamzeiy H, Saçar MD and **Allmer J** (2011) MiRNA Hairpin Prediction Accuracy, Concordia University, Montreal, Canada.
15. Hamzeiy H, Saçar MD and **Allmer J** (2011) A Handful of miRNA Fingerprints, 2nd International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany.

16. **Allmer J** (2011) Bioinformatics in Turkey, Informatics Institute 15th Anniversary Celebration, Middle East Technical University, Ankara, Turkey.
17. **Allmer J** (2011) Computationally Establishing miRNA Regulatory Networks from Seed Genes, VIII. International Molecular Biology and Genetics Student Winter School, Istanbul University, Istanbul, Turkey.
18. **Allmer J** (2010) Mass Spectrometry Based Proteomics, 4th Moleküler Biyoloji ve Genetik Araştırma ve Uygulama Platformu, Izmir, Turkey.
19. **Allmer J** (2010) Label Free Quantitation in Mass Spectrometry based Proteomics, ProteomeIstanbul, International Proteomics Workshop, Istanbul, Turkey.
20. **Allmer J** (2010) Guide to Practical Quantitation of Mass Spectrometric Results, ProteomeIstanbul, International Proteomics Workshop, Istanbul, Turkey
21. **Allmer J** (2007) Enhanced Gene Annotation by Mass Spectrometry and Proteomics, Dokuz Eylül University, Izmir, Turkey.
22. **Allmer J** (2006) High throughput mass spectrometric analysis of the thylakoid proteome of *Chlamydomonas reinhardtii* coupled to computational data mining, invited talk, Westfälische Wilhelms University, Münster, Germany.
23. **Allmer J** (2006) From Problem to Solution: Software Development to Enhance and Facilitate Analysis of Mass Spectrometric Data, Izmir University of Economics, Izmir, Turkey.
24. **Allmer J** (2006) GenomicPeptideFinder: enhanced protein identification and gene annotation from MS/MS data, Ernst Moritz Arndt University, Greifswald, Germany.
25. **Allmer J** (2006) Development of algorithms for peptide identification from mass spectrometric data in genomic databases Middle East Technical University, Ankara, Turkey.

Other Activities

1. **Allmer J** (2015), Interview by Lutz Steinbrück for the German University Journal (DUZ).
2. **Allmer J** and Hippler M (2006) Interview by Proteomics, for the most influential article of the month, available as podcast (Proteomics, 6, 23, online).

REFEREEING AND PEER REVIEWING

Member of the editorial board for Journal of Integrated Bioinformatics, 2015, continuing

Editor for Journal of Integrated Bioinformatics Tools, 2013, continuing

Associated Editor for the Journal of Integrated Omics, 2012, continuing

TÜBİTAK grant applications referee, 2012-continuing

Reviewer for Molecular Biosystems, ISSN 1742-2051, 2010 continuing

Reviewer for BMC Bioinformatics, ISSN 1471-2105, 2010 continuing

Reviewer for Expert Reviews of Proteomics, ISSN 1478-9450, 2010 continuing

Reviewer for Oxford Journal of Bioinformatics, ISSN 1367-4803, 2009, continuing

Reviewer for Int. Symposium on Health Informatics and Bioinformatics, 2009-2013

OTHER SCIENTIFIC AND ADMINISTRATIVE WORK

Member of program committee, BIOINFORMATICS, Rome, Italy (2016).

Member of organizing committee, Integrative Bioinformatics, Bielefeld, Germany (2016).

Member of the organizing committee, EURO CBBM, Istanbul, Turkey (2016).

Member of program committee, BIOINFORMATICS, Lisbon, Portugal (2015).

Member of the scientific committee, NETTAB and Integrative Bioinformatics, Bari, Italy (2015).

Member of organizing committee, 6th International German/Turkish/Russian Summer School in Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany (2015).

Member of organizing committee, 6th International German/Turkish/Russian Workshop in Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany (2015).

Attended the Symposium "Excellence in Science, Enabling Young Researchers" by the Turkish Academy of Sciences on invitation (2014).

Member of program committee, CELLmicrocosmos neXt workshop, Bielefeld, Germany (2014).

Member of the scientific committee, 3rd International Congress of the Molecular Biology Association of Turkey, Izmir, Turkey (2014).

Member of the organizing committee, International Workshop on Proteomics, Bioinformatics and Health Informatics, Izmir, Turkey (2014).

Workshop organizer and chair, 3rd International Workshop on Translational Bioinformatics and Health Informatics, Izmir, Turkey (2014).

Local organizer for the OPENMS developer workshop, Izmir, Turkey (2014).

Member of program committee, BIOINFORMATICS, Barcelona, Spain (2014).

Attended the workshop on innovations in health sciences and technology transfer, Dokuz Eylül University, Izmir, Turkey (2013)

ERASMUS coordinator, Department of Molecular Biology and Genetics, Izmir Institute of Technology (2009-2012).

ERASMUS coordinator, Department of Biotechnology, Izmir Institute of Technology (2009-2012).

Member of Program Committee, 8th International Symposium on Health Informatics and Bioinformatics, Ankara, Turkey (2013).

Scientific Advisor, and Member of Program Committee, 7th International Symposium on Health Informatics and Bioinformatics, Cappadocia, Turkey (2012).

Workshop Organizer, 7th International Symposium on Health Informatics and Bioinformatics, Cappadocia, Turkey (2012).

Conference Chair, 6th International Symposium on Health Informatics and Bioinformatics, Izmir, Turkey (2011).

Member of Program Committee, 5th International Symposium on Health Informatics and Bioinformatics, Antalya, Turkey (2010).

Member of Organizing Committee, 4th International Symposium on Health Informatics and Bioinformatics, Ankara, Turkey (2009).

PROFESSIONAL AFFILIATIONS

ISCB - International Society for Computational Biology

BID - Turkish Bioinformatics Society

EURO - The Association of European Operational Research Societies

Turkish Society of Medical Informatics

LIST OF COURSES

Academic Year	Semester	Course Name
2015-2016	Spring	CS102 Introduction to Programming
		MBG404 Computational Biology, IYTE
		MBG517 Algorithms in Bioinformatics, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
	Fall	MBG305 Applied Bioinformatics, IYTE
		MBG580 Genomics, IYTE
MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE		
2014-2015	Summer	ERASMUS Course on Proteomics Data Analysis, FUB
	Spring	MBG404 Computational Biology, IYTE
		MBG581 Proteomics Data Analysis, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
	Fall	MBG305 Applied Bioinformatics, IYTE
		MBG517 Algorithms in Bioinformatics, IYTE
MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE		
2013-2014	Spring	MBG580 Genomics, IYTE
		MBG404 Computational Biology, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE

	Fall	MBG305 Applied Bioinformatics, IYTE
		MBG581 Proteomics Data Analysis, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
2012-2013	Summer	ERASMUS Course on Computational Proteomic, BU
	Spring	MBG517 Algorithms in Bioinformatics, IYTE
		MBG581 Proteomics Data Analysis, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
	Fall	MBG305 Applied Bioinformatics, IYTE
		MBG403 Computational Biology, IYTE
MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE		
2011-2012	Spring	MBG517 Algorithms in Bioinformatics, IYTE
		MBG581 Proteomics Data Analysis, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
	Fall	MBG305 Applied Bioinformatics, IYTE
		MBG403 Computational Biology, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
2010-2011	Spring	MBG517 Algorithms in Bioinformatics, IYTE
		MBG305 Applied Bioinformatics, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
	Fall	MBG517 Algorithms in Bioinformatics, IYTE
		MBG305 Applied Bioinformatics, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
2009-2010	Spring	MBG517 Algorithms in Bioinformatics, IYTE
		MBG403 Computational Biology, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
	Fall	MBG305 Applied Bioinformatics, IYTE
		MBG403 Computational Biology, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
2008-2009	Spring	MBG305, Applied Bioinformatics, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
	Fall	MBG426 Computational Biology, IYTE
		MBG500 Thesis Studies, MBG811 Special Topics, MBG911 Special Studies, IYTE
2007-2008	Spring	CS100 Introduction to Computers and Information Systems, IEU
		CS100 Introduction to Computers and Information Systems, IEU
		SE102 Introduction to Software Engineering, IEU
		CS300 Bioinformatics, IEU
	Fall	CS100 Introduction to Computers and Information Systems, IEU
		CS100 Introduction to Computers and Information Systems, IEU
		ISE201 System Analysis and Design, IEU
		ISE311 Data Mining, IEU
		KRS504 Bioinformatics in Genomics and Proteomics, DEU
2006-2007	Summer	IS202 Database Management Systems, IEU
	Spring	Methoden der funktionellen Proteomik, WWU

		CS100 Introduction to Computers and Information Systems, IEU
		CS116 Advanced Programming, IEU
		IS202 Database Management Systems, IEU

WWU: Westfaelische Wilhelms University, Münster, Germany

DEU: Dokuz Eylül University, Izmir, Turkey

IEU: Izmir University of Economics, Izmir, Turkey

IYTE: Izmir Institute of Technology, Izmir, Turkey

BU: Bielefeld University, Bielefeld, Germany

FUB: Freie University, Berlin, Germany

COURSES DESIGNED

Methoden der funktionellen Proteomik, co-designed with Susan Hawat and Michael Hippler, WWU (graduate course)

KRS504 Bioinformatics in Genomics and Proteomics, DEU (mixed undergraduate and graduate course)

CS300 Bioinformatics, IEU (undergraduate course)

MBG305, Applied Bioinformatics, IYTE (undergraduate course)

MBG426, MBG403, MBG404 Computational Biology, IYTE (undergraduate course)

MBG517 Algorithms in Bioinformatics, IYTE (graduate course)

MBG580 Genomics, IYTE (graduate course)

MBG581 Proteomics Data Analysis, IYTE (graduate course)

ERASMUS course Computational Proteomics, BU (mixed undergraduate and graduate)

ERASMUS course Proteomics Data Analysis (mixed undergraduate and graduate)

OTHER COURSES

CS100 Introduction to Computers and Information Systems, IEU (undergraduate course)

CS102 Introduction to Programming, IYTE (undergraduate course)

SE102 Introduction to Software Engineering, IEU (undergraduate course)

CS116 Advanced Programming, IEU (undergraduate course)

IS202 Database Management Systems, IEU (undergraduate course)

ISE201 System Analysis and Design, IEU (undergraduate course)

ISE311 Data Mining, IEU (undergraduate course)

For more information on course content, please visit <http://jens.allmer.de/index.php?dirInd=2>.

ONGOING DOCTORAL THESES

Visam Gültekin (2013 -) Graph-based De Novo Sequence Assembly from Mixed Next Generation Sequencing Data, Department of Molecular Biology and Genetics, IYTE.

Müşerref Duygu Saçar (2013 -) An Integrative Data Mining Approach for Establishing MicroRNA Regulative Networks in Human, Department of Molecular Biology and Genetics, IYTE.

Canan Has, (2012 -) Enhancement and Validation of Current Human Genome Annotation via Novel Proteogenomic Algorithms, Department of Molecular Biology and Genetics, IYTE.

CONCLUDED MASTER THESES

Müşerref Duygu Saçar (2013) An Integrative Data Mining Approach for MicroRNA Detection in Human, Department of Molecular Biology and Genetics, IYTE.

Visam Gültekin, (2013) Quality Assessment of *De Novo* Sequence Assembly Tools, Department of Molecular Biology and Genetics, IYTE.

Savaş Takan (2013) A Common Representation, Standardization, Analysis for *De Novo* Sequencing Results (co-Advisor with Dr. Sıtkı Aytaç, Computer Engineering, IYTE), Department of Computer Engineering, IYTE.

Şule Yılmaz (2012) RAY: A Profile-based Approach for Homology Matching of Tandem-MS Spectra to Sequence Databases (co-Advisor with Dr. Bilge Karaçalı), Department of Biotechnology, IYTE.

Canan Has (2012) Evaluations of Protein Secondary Structure Prediction Algorithms on a New Advanced Benchmark DataSet, Department of Molecular Biology and Genetics, IYTE.

Belgin Aytun (2011) Exploiting Fragment-Ion Complementarity for Peptide De Novo Sequencing From Collision Induced Dissociations Tandem Mass Spectra, Department of Molecular Biology and Genetics, IYTE.

Mehmet Volkan Çakır (2009) Systematic Computational Analysis of Potential RNAi Regulation in *Toxoplasma gondii*, Department of Molecular Biology and Genetics, IYTE.

ONGOING MASTER THESES

Mehmet Direnç Mungan (2014 -) TBA, Department of Biotechnology, IYTE.

Cansu Çiftçi (2014 -), Extending mass spectrometry-based computational proteomics analyses to the cloud (co-Advisor with Dr. Hasan Bulut, Department of Computer Engineering, EGE University), Biotechnology, IYTE.

Caner Bağcı, Biotechnology (2013 -) Automatic, Fast and Accurate Sequence Decontamination (co-Advisor with Dr. Selma Tekir, Department of Computer Engineering, IYTE), Biotechnology, IYTE.

Rabia Suluyayla (2013 -) ProteoMagna: Artificial Intelligence-Based Protein Quantitation for Mass Spectrometric Data, Department of Molecular Biology and Genetics, IYTE.

Mehmet Göktay (2012 -) Characterization of World Spinach Genetic Collection by Using Molecular Markers (co-Advisor with Dr. Sami Doğanlar, Department of Molecular Biology and Genetics, IYTE), Department of Molecular Biology and Genetics, IYTE.

Mustafa Toprak (2012 -) A Detailed Analysis on Infrastructure and Programming Dependencies of Selected Data Mining Algorithms (co-Advisor with Dr. Selma Tekir, Department of Computer Engineering, IYTE), Department of Computer Engineering, IYTE.

INTERNS IN MY LAB

Erkin Acar, Ege University (2015)

Semih Başlar, Izmir Institute of Technology (2015)

Semih Erdoğan, Istanbul University (2014)

Murat Caner Yarımcam, Izmir Institute of Technology (2014)

Mehmet Direnç Mungan, Istanbul University (2014)

Başak Uysal, Istanbul University (2014)

Mehmet Göktay, Ege University (2012)

Elif Teke, Izmir Institute of Technology (2012)

UNDERGRADUATE STUDENTS IN MY LAB

Seçil Kapanoğlu, Molecular Biology and Genetics, Izmir Institute of Technology (2015 - present)

Semih Başlar, Molecular Biology and Genetics, Izmir Institute of Technology (2015 - present)

Çilga İscan, Molecular Biology and Genetics, Izmir Institute of Technology (2015 - present)

Taner Vatansever, Molecular Biology and Genetics, Izmir Institute of Technology (2014 - present)

Aybuğ Altay, Molecular Biology and Genetics, Izmir Institute of Technology (2013 – 2015)

Nurselin Ateş, Molecular Biology and Genetics, Izmir Institute of Technology (2013 – 2014)

Cemal Ulaş Kundakçı, Molecular Biology and Genetics, Izmir Institute of Technology (2012 – 2014)

Fatih Yergöz, Molecular Biology and Genetics, Izmir Institute of Technology (2013-2014)

Hamid Hamzeiy, Molecular Biology and Genetics, Izmir Institute of Technology (2011-2014)

Caner Bağcı, Molecular Biology and Genetics, Izmir Institute of Technology (2011-2013)

Mustafa Toprak, Computer Engineering, Izmir Institute of Technology (2010-2012)

Seçkin Boz, Molecular Biology and Genetics, Izmir Institute of Technology (2011-2012)
Erdi Okatar, Computer Engineering, Izmir Institute of Technology (2011-2012)
Nilay Peker, Molecular Biology and Genetics, Izmir Institute of Technology (2010-2011)
Emre Can Geçer, Computer Engineering, Izmir Institute of Technology (2010-2011)
Necati Batur, Computer Engineering, Izmir Institute of Technology (2009-2011)
Ferah İlhan, Molecular Biology and Genetics, Izmir Institute of Technology (2009)
Müşerref Duygu Saçar, Molecular Biology and Genetics, Izmir Institute of Technology (2008-2010)

COLLABORATIONS WITH LOCAL HIGH SCHOOLS

Çakabey College

Uncovering Hidden Evidence for Alternative Start Sites in Human Genome from Proteogenomic Data, Umutcan Savaşçı and Mert Kabasakal (2012-2013)

Selected as representative of Turkey for the International Young Scientist Competition
2nd place in the International Young Scientist Conference 2013, April, Bali Indonesia

Analyzing the Role of Regulatory miRNAs in Breast Cancer, Buğra Felekoğlu and Setenay Sinefin Yalınbaş (2010-2011)

Biology Exhibition Award from the Scientific and Technical Research Council of Turkey, High School Project Competition, Ranked 3rd in Acibadem University "Fikrine Sağlık Projesi" High School Competition, Ranked 3rd in MEF Schools Istanbul Projects Biology Section

Ödemiş High School

Hospital Decision Support System for Proper Selection of Antibiotic Agents
Çağla Gezgen (2014-2015)

PROFESSIONAL SOCIAL NETWORKS AND WEBSITES

ResearchGate: https://www.researchgate.net/profile/Jens_Allmer
LinkedIn: <http://tr.linkedin.com/in/jallmer/>
Group web page: <http://bioinformatics.iyte.edu.tr/>
Bionia: <http://www.bionia.biz>