JENS ALLMER

Curriculum Vitae

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EDUCATION

Habilitation	Bioinformatics, Turkish Inter-University Council (ÜAK), 09.2011
Ph. D.	Biology, University of Münster, Münster, Germany, 06.2006
M. Sc.	Zoology and Microbiology, University of Münster, Münster, Germany, 06.2002
B. Sc.	Biology, University of Münster, Münster, Germany, 03.1996

PROFESSIONAL EXPERIENCE

2019 - present	Professor, Medical Informatics and Bioinformatics, University of Applied Sciences, Hochschule Ruhr-West, Mülheim adR, Germany.
2018 - 2019	Researcher, Big Data and Machine Learning Specialist, Horticulture, Wageningen University & Research, Wageningen, the Netherlands.
2017 - 2018	Cluster Leader, Applied Bioinformatics, Wageningen University & Research, Wageningen, the Netherlands.
2016 - 2018	Visiting Professor, Workgroup for Bioinformatics, Bielefeld University, Bielefeld, Germany.
2013 - 2017	Founder and Chairman, Bionia Incorporated, IZTEKGEB, Urla, Izmir, Turkey.
2011 - 2017	Associate Professor, Dept. of Molecular Biology and Genetics, Izmir Institute of Technology, Izmir, Turkey.
2015 summer	Visiting Professor, Dept. of Knowledge Management in Bioinformatics, Institute of Computer Science, Humboldt-University, Berlin, Germany.
2013 summer	Visiting Professor, Dept. of Algorithmic Bioinformatics, Informatics Institute, Freie University, Berlin, Germany.
2008 - 2011	Assistant Professor, Dept. of Molecular Biology and Genetics, Izmir Institute of Technology, Izmir, Turkey.
2007 - 2008	Instructor, Dept. of Computer Sciences, Izmir University of Economics, Izmir, Turkey.
2006 - 2007	Post Doctorate, Dept. of Plant Biochemistry and Biotechnology, University of Münster, Münster, Germany.

PUBLICATIONS

Refereed Journal Articles

2024	Morando N, Rosenzvit MC, Pando MA, **Allmer J**, The Role of MicroRNAs in HIV Infection, *Genes* (IF: 2.8), 15, 574, doi: 10.3390/genes15050574.
2024	Hansel-Frose AFF, **Allmer J**, Friedrichs M, dos Santos HG, Dallagiovanna B, and Spangenberg L, Alternative polyadenylation and dynamic 3' UTR length is associated with polysome recruitment throughout the cardiomyogenic differentiation of hESCs, *Frontiers in Molecular Biosciences* (IF: 5.0), 11:1336336, doi: 10.3389/fmolb.2024.1336336.
2023	Yousef M, Ozdemir F, Jaber A, **Allmer J**, and Bakir-Gungor B, PriPath: identifying dysregulated pathways from differential gene expression via grouping, scoring, and modeling with an embedded feature selection approach, *BMC Bioinformatics* (IF: 3.169), 24:60, doi: 10.1186/s12859-023-05187-2.
2023	Kiran AD, Ay MC, **Allmer J**, Criteria for the Evaluation of Workflow Management Systems for Scientific Data Analysis, *Journal of Bioinformatics and Systems Biology*, 6(2):121-33, doi: 10.26502/jbsb.5107055.
2023	**Allmer J**, Noncoding RNA Databases, *Current Pharmaceutical Biotechnology* (IF: 2.829), 24(7):825-31, doi: 10.2174/1570180819666220520124511.
2023	Beukers M and **Allmer J**, Challenges for the Development of Automated RNA-seq Analyses Pipelines, *GMS Medical Informatics, Biometry and Epidemiology*, doi: 10.3205/mibe000245.
2023	Yousef M, and **Allmer J**, Deep Learning in Bioinformatics, *Turkish Journal of Biology* (IF: 2.2), 47(6):3, doi: 10.55730/1300-0152.2671
2021	Tüfekci KU, **Allmer J**, Carman KB, Bayram E, Topcu Y, Kurul SH, Genc S, and Yis U, Antiviral MicroRNA Expression Signatures are Altered in Subacute Sclerosing Panencephalitis, *Neurological Sciences and Neurophysiology* (IF: 0.06) 38(3):166-72, doi: 10.4103/nsn.nsn_57_21.
2021	Schofield AL, Brown JP, Brown J, Wilczynska A, Bell C, Glaab WE, Hackl M, Howell L, Lee S, Dear JW, Remes M, Reeves P, Zhang E, **Allmer J**, Norris A, Falciani F, Takeshita LY, Forootan SS, Sutton R, Park BK, and Goldring C, Systems analysis of miRNA biomarkers to inform drug safety, *Archives of Toxicology* (IF: 6.3) doi: 10.1007/s00204-021-03150-9.
2021	Yousef M, and **Allmer J**, Classification of Precursor MicroRNAs from Different Species Based on K-mer Distance Features, *Algorithms* (IF: 2.30) doi: 10.3390/a14050132.
2021	Gültekin V and **Allmer J**, Novel Perspectives for SARS-CoV-2 Genome Browsing, *Journal of Integrative Bioinformatics* (IF: 1.9), doi: 10.1515/jib-2021-0001.
2020	Takan T and **Allmer J**, DNMSO; an ontology for representing de novo sequencing results from TandemMS data, *PeerJ* (IF: 3.09), 8:e10216, doi: 10.7717/peerj.10216.

2019	**Allmer J**, Towards and Internet of Science, *Journal of Integrative Bioinformatics* (1.9), doi: 10.1515/jib-2019-0024.
2019	Yousef M, Abddallah L, and **Allmer J**, maTE: Discovering Expressed MicroRNA - Target Interactions, *Bioinformatics* (IF: 5.48) doi: 10.1093/bioinformatics/btz204.
2018	Öztürk SC, Göktay M, **Allmer J**, Doğanlar S, and Frary A, Development of Simple Sequence Repeat Markers in Hazelnut (Corylus avellana L.) by Next-Generation Sequencing and Discrimination of Turkish Hazelnut Cultivars, *Plant Molecular Biology Reporter* (IF: 1.84), doi: 10.1007/s11105-018-1120-0.
2018	Öztürk SE, Göktay M, Has C, Babaoğlu M, **Allmer J**, Doğanlar S, Frary A, Transcriptomic analysis of boron hyperaccumulation mechanisms in *Puccinellia distans*, *Chemosphere* (IF: 4.21), doi: 10.1016/j.chemosphere.2018.02.070.
2018	Acar IE, Sacar Demirci MD, Gross U, and **Allmer J**, The Expressed MicroRNA - mRNA Interactions of *Toxoplasma gondii*, *Frontiers in Microbiology* (IF: 4.08), doi: 10.3389/fmicb.2017.02630.
2017	Saçar Demirci MD, Baumbach J, and **Allmer J** On the performance of pre-microRNA detection algorithms, *Nature Communications* (IF: 12.12), 8(1):330, doi: 10.1038/s41467-017-00403-z.
2017	Yousef M, Nigatu D, Levy D, **Allmer J**, and Henkel W, Categorization of species based on their microRNAs employing sequence motifs, information-theoretic sequence feature extraction, and k-mers, *Journal on Advances in Signal Processing* (IF: 1.96), 2017:70, doi: 10.1186/s13634-017-0506-8.
2017	Saçar Demirci MD and **Allmer J**, Improving the Quality of Positive Datasets for the Establishment of Machine Learning Models for pre-microRNA Detection, *Journal of Integrative Bioinformatics*, 14(2), doi: 10.1515/jib-2017-0032.
2017	Saçar Demirci MD and **Allmer J**, Delineating the impact of machine learning elements in pre-microRNA detection, *PeerJ* (IF: 2.18), 5:e3131, doi: 10.7717/peerj.3131.
2017	Hamzeiy H, Suluyayla R, Brinkrolf C, Janowski SJ, Hofestaedt R, and **Allmer J**, Visualization and Analysis of MicroRNAs within KEGG Pathways using VANESA, *Journal of Integrative Bioinformatics*, doi: 10.1515/jib-2016-0004.
2017	Göl Ş, Göktay M, **Allmer J**, Doğanlar S, and Frary A, Newly Developed SSR Markers Reveal Genetic Diversity and Geographical Clustering in Spinach (*Spinacia oleracea*), *Molecular Genetics and Genomics* (IF: 2.98), doi: 10.1007/s00438-017-1314-4.
2017	Yousef M, Khalifa W, Acar İE, and **Allmer J**, MicroRNA Categorization using Sequence Motifs and k-mers, *BMC Bioinformatics* (IF: 2.45), 18(1):170 doi: 10.1186/s12859-017-1584-1.
2016	Kochetov AV, **Allmer J**, Klimenko AI, Zuraev BS, Matushkin YG, and Lashin SA, AltORFev facilitates the prediction of alternative open reading frames in eukaryotic mRNAs, *Bioinformatics* (IF: 7.31), 33(6):923-925, doi: 10.1093/bioinformatics/btw736.
2016	Saçar Demirci MD, Toprak M, and **Allmer J**, A Machine Learning Approach for MicroRNA Precursor Prediction in Retro-Transcribing Virus Genomes, Special

	Issue on Computational miRNomics in *Journal of Integrative Bioinformatics*, 13(5):303, doi: 10.1515/jib-2016-303.
2016	Abuzayed M, Göktay M, **Allmer J**, Doğanlar S, and Frary A, Development of genomic simple sequence repeat markers in faba bean by next generation sequencing, *Plant Molecular Biology Reporter* (IF: 1.93), pp. 1-11, doi: 10.1007/s11105-016-1003-1.
2016	Has C, and **Allmer J**, PGMiner: Complete Proteogenomics Workflow; from Data Acquisition to Result Visualization, *Information Sciences* (IF: 4.83), 384: 126-134, doi: 10.1016/j.ins.2016.08.005.
2016	Khalifa W, Yousef M, Saçar Demirci MD, and **Allmer J**, The Impact of Feature Selection on One- and Two-class Classification Performance for Plant MicroRNAs, *PeerJ* (IF: 2.18), 4:e2135, doi: 10.7717/peerj.2135.
2016	Yousef M, Saçar Demirci MD, Khalifa W, and **Allmer J**, Feature Selection has a Large Impact on One-Class Classification Accuracy for MicroRNAs in Plants, *Advances in Bioinformatics*, 2016(5670851):1-6, doi: 10.1155/2016/5670851.
2016	Bağcı C, and **Allmer J**, One Step Forward, Two Steps Back; Xeno-MicroRNAs Reported in Breast Milk are Artifacts, *PLOS One* (IF: 3.06), doi: 10.1371/journal.pone.0145065.
2016	Yousef M, **Allmer J**, and Khalifa W, 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.
2015	Yousef M, **Allmer J**, and Khalifa W, 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.
2015	Alural B, Özderem A, **Allmer J**, Genç K, and Genç Ş, Lithium protects against paraquat neurotoxicity by NRF2 activation and miR-34a inhibition in SH-SY5Y cells, *Frontiers Neuroscience* (IF: 4.56), 9, 209, doi: 10.3389/fncel.2015.00209.
2015	Uncu A, Gültekin, V, **Allmer J**, Frary A, and Doğanlar S, Genomic Simple Sequence Repeat Markers Reveal Patterns of Genetic Relatedness and Diversity in Sesame, *The Plant Genome* (IF: 2.74), 8(2):1-12, doi: 10.3835/plantgenome2014.11.0087.
2014	Saçar MD, Bağcı C, and **Allmer J**, 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.
2014	Alural B, Duran GA, Tüfekçi KU, **Allmer J**, Önkal Z, Tunali D, Genç K, and Genç Ş, 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* (IF: 6.43), 5:475-482, doi: 10.3389/fimmu.2014.00475.
2014	Yousef M, Trinh HV, and **Allmer J**, Intersection of MicroRNA and Gene Regulatory Networks and their Implication in Cancer, *Current Pharmaceutical Biotechnology* (IF: 2.33)*, 15(5)*:445-454, doi: 10.2174/1389201015666140519120855.

2014	Hamzeiy H, Yousef M, and **Allmer J**, Computational Methods for miRNA Target Prediction, *Methods in Molecular Biology*, 1107:207-221, doi: 10.1007/978-1-62703-748-8_12.
2014	Saçar MD and **Allmer J**, Machine Learning methods for miRNA Gene prediction, *Methods in Molecular Biology*, 1107:177-187, doi: 10.1007/978-1-62703-748-8_10.
2014	**Allmer J**, Computational and Bioinformatics Methods for miRNA Gene Prediction, *Methods in Molecular Biology*, 1107:157-175, doi: 10.1007/978-1-62703-748-8_9.
2014	Çelik I, Gültekin V, **Allmer J**, Doğanlar S, and Frary A, Development of Genomic Simple Sequence Repeat Markers in Opium Poppy by Next-Generation Sequencing, *Molecular Breeding* (IF: 2.465), 34(2):323-334, doi: 10.1111/pbr.12059.
2013	Saçar MD and **Allmer J**, Current Limitations for Computational Analysis of miRNAs in Cancer, *Pakistan Journal of Clinical and Biomedical Research*, 1(2):3-5.
2013	**Allmer J**, Determining 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.
2013	Şelale H, Çelik I, Gültekin V, **Allmer J**, Doğanlar S, and Frary A, Development of EST-SSR Markers for Diversity and Breeding Studies in Opium Poppy, *Plant Breeding* (IF: 1.34), 132(3):344–351, doi: 10.1111/pbr.12059.
2012	**Allmer J**, A Call for Benchmark Data in Mass Spectrometry-Based Proteomics, *Journal of Integrative OMICS*, 2(2):1-5,doi: 10.5584/jiomics.v2012i2012.113.
2012	**Allmer J** and Yousef M, Computational Methods for *ab initio* Detection of MicroRNAs, *Frontiers in Genetics* (IF: 3.800), 3, 209, doi: 10.3389/fgene.2012.00209.
2011	**Allmer J**, Algorithms for the *De Novo* Sequencing of Peptides from Tandem Mass Spectra, *Expert Reviews of Proteomics* (IF: 3.849), 8(5):645-657, doi: 10.1586/epr.11.54.
2010	**Allmer J**, Existing bioinformatics tools for the quantitation of post translational modifications, *Amino Acids* (IF: 3.17), 42(1):129-138, doi: 10.1007/s00726-010-0614-3.
2009	**Allmer J**, Label-free quantitation, an extension to 2DB, *Amino Acids* (IF: 3.173), 38(4):1075-1087, doi: 10.1007/s00726-009-0317-9.
2009	Allmer A, **Allmer J**, Walls of the Cold War: Berlin Wall Souvenirs, *On Site review* 22(WAR):38-39.
2008	**Allmer J**, Kuhlgert S, and Hippler M, 2DB: a Proteomics database for storage, analysis, presentation, and retrieval of information from mass spectrometric experiments. *BMC Bioinformatics* (IF: 2.45), 9, 302-313, doi: 10.1186/1471-2105-9-302.
2007	Merchant S, Prochnik S, Vallon O, Harris EH, Karpowicz SJ, et al., The evolution of key animal and plant functions is revealed by analysis of the Chlamydomonas genome, *Science* (IF: 37.21), 318 (5848):245-251, doi: 10.1126/science.1143609.
2007	Naumann B, Busch A, **Allmer J**, Ostendorf E, Zeller M, Kirchhoff H and Hippler M, Comparative quantitative proteomics to investigate the remodelling of bioenergetic pathways under iron-deficiency in Chlamydomonas reinhardtii. *Proteomics* (IF: 4.04), 7 (21):3964-3979, doi: 10.1002/pmic.200700407.

2006 **Allmer J**, Naumann B, Markert C, Zhang M, and Hippler M, Mass spectrometric genomic data mining: Novel insights into bioenergetic pathways in Chlamydomonas reinhardtii, *Proteomics* (IF: 4.04), 6 (23):6207-6220, doi: 10.1002/pmic.200600208.

2004 **Allmer J**, Markert C, Stauber EJ, and Hippler M, A new approach that allows identification of intron-split peptides from mass spectrometric data in genomic databases. *FEBS letters* (IF: 3.62), 562, 202-206, doi: 10.1016/S0014-5793(04)00212-1.

Edited Volumes

2024 Abhishek Kumar and **Allmer J**, eds. Proteogenomics: Methods and Protocols, Series: Methods in Molecular Biology, *Humana Press*, ISBN: 978-1-0716-4151-4, doi: 10.1007/978-1-0716-4152-1.

2022 Allmer J and Yousef M, eds. miRNomics: MicroRNA Biology and Computational Analysis, Series: Methods in Molecular Biology, *Humana Press*, ISBN: 978-1-0716-1169-2, doi: 10.1007/978-1-0716-1170-8.

2021 **Allmer J**, Elloumi M, Comin M, and Hofestädt R, ed. Special Issue of the 1st International Applied Bioinformatics Conference (iABC'21), *Journal of Integrative Bioinformatics*, 18(4), doi: /10.1515/jib-2021-0042.2021

2021 Yousef M and **Allmer J**, miRNomics, MicroRNA Biology and Computational Analysis, Vol. 2, Series: Methods in Molecular Biology: 2257, *Humana Press*, ISBN: 978-1-0716-1170-8, doi: 10.1007/978-1-0716-1170-8.

2021 **Allmer J**, ed. Special Issue on COVID-19 Data Integration Opportunities and Vaccine Development Strategies in *Journal of Integrated Bioinformatics*, 18(1).

2021 **Allmer J** and Malik Y, miRNomics MicroRNA Biology and Computational Analysis, Series: Methods in Molecular Biology, *Humana Press*, doi: 10.1007/978-1-0716-1170-8.

2017 **Allmer J**, Brinkrolf C, Hofestaedt R and Saçar Demirci MD, eds. Computational Systems Biology - German/Russian/Turkish Network of Bioinformatics, *Shaker Verlag*, ISBN: 978-3-8440-5145-2.

2016 **Allmer J** and Yousef M, Special Issue, Computational miRNomics in *Journal of Integrated Bioinformatics*,13(5), http://journal.imbio.de/archive.php?pindex=13&iid=34.

2015 **Allmer J**, Brinkrolf C, Hofestaedt R and Saçar Demirci MD, eds. Computational Systems Biology - German/Russian/Turkish Network of Bioinformatics, *Shaker Verlag*, ISBN: 978-3-8440-4114-9.

2014 Yousef M and **Allmer J**, eds. miRNomics: MicroRNA Biology and Computational Analysis, Series: Methods in Molecular Biology, *Humana Press*, ISBN: 978-1-62703-747-1, doi: 10.1007/978-1-62703-748-8.

2014 **Allmer J**, ed. Proceedings of the 3rd International Workshop on Translational Bioinformatics and Health Informatics, Izmir, Turkey.

2012 **Allmer J**, ed. Sequence Alignment in Bioinformatics, *Nobel Publishing*, Ankara, Turkey, ISBN: 978-605-133-297-0.

2011	**Allmer J**, ed. Proceedings of the 6th International Symposium on Health Informatics and Bioinformatics, Izmir, Turkey, ISBN: 978-1-4507-7534-2.

Refereed Book Chapters

2024	Hansel Fröse AFF, Friedrichs M and **Allmer J**, MicroRNA Databases. In: Vaschetto LM (ed.) miRNAs, Human Health and Diseases. Epigenetics and Human Health, vol 13. Springer, Cham., Sept. 2024, doi: 10.1007/978-3-031-64788-8_2.
2022	Hennig A and **Allmer J**, Künstliche Intelligenz in der Lehre für Gesundheits- und Medizintechnologien. In: Mah D-K and Torner C (eds) Künstliche Intelligenz mit offenen Lernangeboten an Hochschulen lehren, Sammelband März 2022, KI-Campus, doi: 10.5281/zenodo.6325161.
2022	Takan S, Gültekin V, and **Allmer J**, IoS: A Needed Platform for Scientific Workflow Management. In: Chen, M., Hofestädt, R. (eds) Integrative Bioinformatics. Springer, pp. 313-320, doi: 10.1007/978-981-16-6795-4_15.
2021	Odenthal L, **Allmer J**, and Yousef M, Ensemble Classifiers for Multiclass MicroRNA Classification. In: Yousef M and **Allmer J** (eds) miRNomics, MicroRNA Biology and Computational Analysis, Vol. 2, pp. 235-254, doi: 10.1007/978-1-0716-1170-8_19.
2021	Akgül B, et al., and **Allmer J**, 44 Current Challenges in miRNomics. In: Yousef M and **Allmer J** (eds) miRNomics, MicroRNA Biology and Computational Analysis, Vol. 2, pp. 235-254, doi: 10.1007/978-1-0716-1170-8_12.
2019	Saçar Demirci MD, Yousef M, and **Allmer J**, Computational Prediction of Functional MicroRNA–mRNA Interactions. In: Lai X., Gupta S., Vera J. (eds) Computational Biology of Non-Coding RNA. Methods in Molecular Biology, NY, ISBN: 978-1-4939-8981-2, pp: 175-196, *Humana Press*, New York, doi: 10.1007/978-1-4939-8982-9_7.
2016	Saçar Demirci MD, Bağcı C, and **Allmer J**, Differential Expression of *T. gondii* MicroRNAs in Murine and Human Hosts, in Non-coding RNAs and Inter-Kingdom Communication (eds. Leitao AL and Lombardo Enguita FJ), ISBN: 978-3-319-39496-1, pp: 143-159, *Springer International*, doi: 10.1007/978-3-319-39496-1_9.
2012	**Allmer J**, Pattern Matching, in Sequence Alignment in Bioinformatics (ed. **Allmer J**), pp. 11-34, *Nobel Publishing*, Ankara, Turkey, ISBN: 978-605-133-297-0.
2010	**Allmer J**, Computational approaches in microRNA analysis and storage, in MicroRNAs and the Nerve System (eds. Genç Ş and Genç K), 92-125, *Turkish Academy of Sciences (TÜBA) Publishing*, ISBN: 978-9944-252-54-6.

Proceeding Articles

2024	Erbay AK and **Allmer J**, Automatic EEG Signal Detection and Analysis of Signal Propagation Over Adjacent Electrodes, Sensorica, *IEEE Xplorer*, doi: ?.
2022	Takan S and **Allmer J** Community-wide Collaboration is a Must to Reinstall Trust in Bioinformatics Solutions and Biomedical Interpretation, *Proceedings of the International*

	Symposium on Integrative Bioinformatics 2022, *Journal of Integrative Bioinformatics*, doi: 10.1515/jib-2022-0028.
2020	Odenthal L, **Allmer J**, and Yousef M, A Machine Learning-based Approach for the Categorization of MicroRNAs to Their Species of Origin, *Proceedings of the 13th International Joint Conference on Biomedical Engineering Systems and Technologies - Volume 3 BIOINFORMATICS: BIOINFORMATICS,* ISBN 978-989-758-398-8, pp. 150-157. doi: 10.5220/0008975001500157.
2019	Yousef M and **Allmer J**, Classification of Pre-cursor microRNAs from Different Species Using a New Set of Features, pp. 15-20, in: Anderst-Kotsis G., Tjoa A., Khalil I. (eds) Database and Expert Systems Applications. DEXA 2019. *Communications in Computer and Information Science*, vol 1062. Springer, Cham, doi: 10.1007/978-3-030-27684-3_3.
2018	Hamzeiy H, Suluyayla R, Brinkrolf C, Janowski SJ, Hofestaedt R, and **Allmer J**, Visualization and Analysis of miRNAs implicated in Amyotrophic Lateral Sclerosis within Gene Regulatory Pathways, 63. Jahrestagung der Deutschen Gesellschaft für Medizinische Informatik, Biometrie und Epidemiologie e.V. (gmds), *Studies in Health Technology and Informatics*, 253:183-187, doi: 10.3233/978-1-61499-896-9-183.
2018	Yousef M, Levy D, and **Allmer J**, Species categorization based on 3'UTR microRNA target sites using sequence features, 9th *International Conference on Bioinformatics Models*, Methods and Algorithms, BIOINFORMATICS 2018.
2017	Yousef M, Khalifa W, Acar İE, and **Allmer J**, Distinguishing between MicroRNA Targets from Diverse Species using Sequence Motifs and *k*-mers, In Proceedings of the 10th International Joint Conference on Biomedical Engineering Systems and Technologies - Volume 3: BIOINFORMATICS, 133-139, Porto, Portugal, doi: 10.5220/0006137901330139.
2016	Has C, Lashin SA, Kochetov AV, and **Allmer J**, PGMiner reloaded, fully automated proteogenomic annotation tool linking genomes to proteomes, *Journal of Integrative Bioinformatics*, 13(4):293, doi: 10.2390/biecoll-jib-2016-293.
2016	Yousef M, **Allmer J**, and Khalifa W, Feature Selection for MicroRNA Target Prediction - Comparison of One-Class Feature Selection Methodologies, *Proceedings of the 9th International Joint Conference on Biomedical Engineering Systems and Technologies,* BIOINFORMATICS (3):216-225.
2013	Saçar MD and **Allmer J**, 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.
2013	Has C, Kundakci CU, Altay A, and **Allmer J**, 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.
2013	Saçar MD, Hamzeiy H and **Allmer J**, Can MiRBase Provide Positive Data for Machine Learning for the Detection of MiRNA Hairpins? *Journal of Integrative Bioinformatics*, 10(2):215-226, doi: 10.1515/jib-2013-215.

2013	Saçar MD and **Allmer J**, 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.
2012	Takan S and **Allmer J**, *De Novo* Markup Language, a Standard to Represent *De Novo* Sequencing Results from MS/MS Data, *IEEE Xplorer*, doi: 10.1109/HIBIT.2012.6209038.
2012	Bağcı C and **Allmer J**, Removing Contaminations from Genomic Sequences Based on Vector Reference Libraries, *IEEE Xplorer*, doi: 10.1109/HIBIT.2012.6209053.
2010	**Allmer J**, Label Free Quantitation in Mass Spectrometry based Proteomics, ProteomeIstanbul, *International Proteomics Workshop*, Theoretical Proceeding, pp. 112-134, Istanbul, Turkey.
2010	**Allmer J**, Guide to Practical Quantitation of Mass Spectrometric Results, ProteomeIstanbul, *International Proteomics Workshop*, Practical Proceeding, pp. 53-61, Istanbul, Turkey.
2010	**Allmer J**, Relative protein quantitation with post translational modifications in Mass spectrometry based proteomics, *IEEE Xplorer*, doi: 10.1109/HIBIT.2010.5478886.
2010	Çakır MV and **Allmer J**, Systematic Computational Analysis of Potential RNAi Regulation in *Toxoplasma gondii*, *IEEE Xplorer*, doi: 10.1109/HIBIT.2010.5478909.
2009	**Allmer J**, Kuhlgert S and Hippler M, 2DB News: Security and Functional Enhancements, *4th International Symposium on Health Informatics and Bioinformatics*, Ankara, Turkey.

Editorials

2023	Hofestädt R and **Allmer J**, Medical Omics, *GMS Medical Informatics, Biometry and Epidemiology*.
2021	**Allmer J**, Elloumi M, Comin M, and Hofestädt R, Special Issue of the 1st International Applied Bioinformatics Conference (iABC'21), *Journal of Integrative Bioinformatics*, 18(4), doi: /10.1515/jib-2021-0042.
2021	**Allmer J**, Special Issue on COVID-19 Data Integration Opportunities and Vaccine Development Strategies, *Journal of Integrative Bioinformatics*, 18(1), doi: 10.1515/jib-2021.0006.
2017	Hofestaedt R, Schreiber F, Sommer B, and **Allmer J**, Computationl miRNomics – Integrative Approaches, *Journal of Integrative Bioinformatics*, 14(1):1, doi: 10.1515/jib-2017-0012.
2016	**Allmer J** and Yousef M, Computational miRNomics, *Journal of Integrative Bioinformatics*, 13(5):1-2, doi: 10.1515/jib-2016-302.

Pre Prints

2024	Yousef M, Inal Y, Bakir Gungor B, and **Allmer J**, G-S-M: A Comprehensive Framework for Integrative Feature Selection in Omics Data Analysis and Beyond, *bioRxiv*, doi: 10.1101/2024.03.30.585514.
2022	Yousef M, Ozdemir F, Jaaber A, **Allmer J**, and Bakir-Gungor B, PriPath: Identifying Dysregulated Pathways from Differential Gene Expression via Grouping, Scoring and Modeling with an Embedded Machine Learning Approach, *ResearchSqare*, doi: 10.21203/rs.3.rs-1449467/v1.
2019	Cordero Cruz JA, Menkovski V, and **Allmer J**, Detection of pre-microRNA with Convolutional Neural Networks, *bioRxiv*, doi: 10.1101/840579.
2019	Has C, Singer J, Reinert K, and **Allmer J**, Lelantos: Fast Proteogenomic Peptide Mapping, *ResearchGate*, doi: 10.13140/RG.2.2.17540.88968.
2019	**Allmer J**, IoS: a Novel Platform for Scientific Workflow Management, *ResearchGate*, doi: 10.13140/RG.2.2.23504.66569.
2017	Öztürk SE, Göktay M, Has C, **Allmer J**, Doğanlar S, and Frary A, Boron Hyper-accumulation Mechanisms in *Puccinellia distans* as Revealed by Transcriptomic Analysis, *bioRxiv*, doi: 10.1101/110403
2016	**Allmer J**, Exact pattern matching: Adapting the Boyer-Moore algorithm for DNA searches, *PeerJ Preprints*, doi: 10.7287/peerj.preprints.1758v1.
2016	Saçar Demirci MD and **Allmer J**, izMiR: computational *ab initio* microRNA detection, *Nature Protocol Exchange*, doi: 10.1038/protex.2016.047.

AWARDS

2018	Montpellier Université D'Excellence (MUSE), mobility support, host: Stephan Köhler, CNRS, Montpellier, France.
2017	Deutscher Akademischer Austausch Dienst (DAAD), Research Stays for University Academics and Scientists, host Prof. Dr. Al Dahouk, Federal Institute for Risk Assessment, Berlin, Germany (3 months).
2013	European Molecular Biology Organization (EMBO), Short Term Fellowship, host Prof. Dr. Knut Reintert, Freie University Berlin, Germany (3 months).
2013	Deutscher Akademischer Austausch Dienst (DAAD), Research Stays for University Academics and Scientists (declined).
2011	Habilitation (Tenure), Bioinformatics, Turkish Inter-University Council.
2010	Turkish Academy of Sciences (TÜBA), Outstanding Young Researcher Award (GEBIP). Award for most promising bioinformatician.

GRANTS

Allmer J (2022 -2023) CleanIt, HPC University of Paderborn (500,000 CPU hours).

Allmer J (2022 -2023) Expressed Zika Virus pre-miRNAs in Human samples, HPC University of Paderborn (~1,000,000 CPU hours).

Allmer J (2021 - 2022) Determining expressed regulatory motifs for boron hyperaccumulation in *Puccinellia distans*, HPC University of Paderborn (~60,000 CPU hours).

Allmer J (03-08 2021) Zika Virus MicroRNAs Regulate Human Gene Expression, RWTH Compute Cluster (~15,000 CPU hours).

Allmer J (01-02 2021), Test account high performance compute cluster University of Paderborn (~1,000 CPU hours).

Allmer J, Ralf Dieckmann, and Sasha Al Dahouk (2018 - 2020) Analysis of the biocide-induced bacterial cell response using genomics, transcriptomics, and proteomics, Federal Institute for Risk Assessment, Berlin, Germany (~60,000€).

Allmer J (2016 - 2017) Facilitating pre-microRNA Detection in Higher Eukaryotes using AWS, Amazon Web Services (7000€).

Allmer J, Nalbant A, and Akgül B (2016 - 2019) Investigation of the effects on apoptotic pathways of circular RNAs: the new regulators of gene expression, The Scientific and Technological Research Council of Turkey (TÜBITAK), 215Z081 (120.000€).

Allmer J (2016) Travel grant to attend H2020 partnering meeting, Brussels, Belgium, The Scientific and Technological Research Council of Turkey (*TÜBITAK)*, 330238 (1500€).

Allmer J (2015) IBM Global Entrepreneur Program for Cloud Startups ($12.000 + Education).

ERASMUS Teaching Staff Mobility Grant awarded to **Allmer J** (2015): Freie University, Berlin, Germany 17-21.08.2015, European Commission (Travel).

Allmer J (2014 - 2018) Novel Human Proteins, Detection and Validation of Alternative Open Reading Frames, The Scientific and Technological Research Council of Turkey (*TÜBITAK)*, 114Z177 (110.000€).

Allmer J (2014 - 2017) A Datawarehouse For The Analysis Of Micro-RNA Metabolic Network Control, The Scientific and Technological Research Council of Turkey (*TÜBITAK)*, 113E326 (120.000€ + Travel).

Frary A, **Allmer J**, Yalçın T, and Doğanlar S (2014 - 2017) Investigating tolerance to abiotic stress and boron accumulation in Puccinellia via comparative proteomics, The Scientific and Technological Research Council of Turkey *(TÜBITAK)*, 113Z930 (135.000€ + Travel).

Allmer J (2014) Support for the 3rd International Workshop on Translational Bioinformatics and Health Informatics, The Scientific and Technological Research Council of Turkey (*TÜBITAK)*, 1929B021400101 (15.000€).

Allmer J (2014) Creating a Ground-Truth Benchmark Dataset for Fine-Tuning Peptide MS/MS Spectrum Scoring Functions, *PRIME-XS* 230 (Travel + MS measurements).

Has C, Gültekin V, and **Allmer J** (2013 - 2014) ProteoGaia: A Novel Approach to *de novo* Sequencing, Technology and Innovation Funding Directorate (*TEYDEB)*, 2130354 (38.000€).

Allmer J (2013 - 2015) Employing human blood plasma mass spectrometric data for accurate gene annotation, Faculty Research Development Grant Project, *IzTech*, 2013IYTE04 (8000€).

ERASMUS Teaching Staff Mobility Grant awarded to **Allmer J** (2012): Bielefeld University, Germany 30-31.08.2012, European Commission (Travel).

Allmer J (2011 - 2012) RAy: A Profile-based Approach for Homology Matching of Tandem-MS Spectra to Sequence Databases, Short Term R&D Funding Program, *TÜBITAK*, 111E139 (9.000€).

Allmer J (2009 - 2010) Accuracy Assessment of Label-Free Protein Quantitation using MS/MS, Faculty Research Development Grant Project, *IzTech*, 2009IYTE30 (3.000€).

Allmer J (2008), PTMPredictor, Research Project, *CPU Turkey* (Software + Machinery +Travel).

PATENTS

2005	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.
2004	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.

INVITED TALKS

2017	On the state of the art in pre-miRNA detection algorithms, B-Wise Bioinformatics Series, Wageningen, the Netherlands (Sept. 5).
2017	BioInfOMICS, Flash Presentation, Bioinformatics year closing, Wageningen, the Netherlands (Jul. 5).
2017	The Intracellular Pathogen *Toxoplasma gondii* Hijacks Host MicroRNAs to Regulate its Environment; a Computational Study, Bioscience, Wageningen University and Research, Wageningen, the Netherlands (Jul. 4).
2017	The Intracellular Pathogen *Toxoplasma gondii* Hijacks Host MicroRNAs to Regulate its Environment; a Computational Study, Georg-August University, Göttingen, Germany (Mar. 30).
2016	Machine Learning for MicroRNA Detection and its Application to Cross-Kingdom-Communication, Eastern Mediterranean University, Famagusta, North Cyprus.
2013	BioInfOmics; or from Genomics via Transcriptomics and Proteomics to ProteoGenomics, Boağziçi University, Istanbul, Turkey.

2011	Hamzeiy H, Saçar MD and **Allmer J**, MicroRNA Hairpin Prediction Accuracy, Concordia University, Montreal, Canada.
2011	Bioinformatics in Turkey, Informatics Institute 15th Anniversary Celebration, Middle East Technical University, Ankara, Turkey.
2007	Enhanced Gene Annotation by Mass Spectrometry and Proteomics, Dokuz Eylül University, Izmir, Turkey.
2006	High throughput mass spectrometric analysis of the thylakoid proteome of Chlamydomonas reinhardtii coupled to computational data mining, invited talk, Münster University, Münster, Germany.
2006	From Problem to Solution: Software Development to Enhance and Facilitate Analysis of Mass Spectrometric Data, Izmir University of Economics, Izmir, Turkey.
2006	GenomicPeptideFinder: enhanced protein identification and gene annotation from MS/MS data, Ernst Moritz Arndt University, Greifswald, Germany.
2006	Development of algorithms for peptide identification from mass spectrometric data in genomic databases, Middle East Technical University, Ankara, Turkey.

CONFERENCE ACTIVITY

Conference Organization

2021	Co-organizer Workshop Medical OMICS, part of the 66. GMDS-Jahrestagung 2021, Online Conference.
2021	Oganizer Workshop Medical OMICS, part of the 1st International Applied Bioinformatics Conference (Online).
2021	Conference co-chair, 1st International Applied Bioinformatics Conference (Online).
2020	Co-organizer Workshop Medical OMICS, part of the 65. GMDS-Jahrestagung 2020, Online Conference.
2019	Co-organizer Workshop Medical Omics, part of the 64. GMDS-Jahrestagung 2019 "Wandel gestalten - Kreative Lösungen für innovative Medizin", Dortmund.
2019	Conference chair Mini Conference on Advances in Applied Bioinformatics, Mülheim an der Ruhr, Germany.
2019	Co-organizer GMDS Workshop "Medical Omics", Bielefeld, Germany.
2017	Co-Organizer for the Scientific-Software Development Workshop, Wageningen, the Netherlands.
2017	Organizer for the Seminar on Integrative Bioinformatics, Wageningen, the Netherlands.
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.
2012	Organizer and chair of the 2nd Translational Bioinformatics and Health Informatics workshop, 7th International Symposium on Health Informatics and Bioinformatics, Cappadocia, Turkey.
2011	Conference chair, 6th International Symposium on Health Informatics and Bioinformatics, Izmir, Turkey.

Member of Organization or Program Committee

2023	Programm Chair, 10th International Conference on Bioinformatics Research and Applications (ICBRA 2023), Barcelona, Spain.
2023	Member of the program committee, BIOKDD, DEXA Conferences ans Workshops, Penang, Malaysia.
2022	Programm Chair, 9th International Conference on Bioinformatics Research and Applications (ICBRA 2022), Berlin, Germany.
2021	Programm Chair, 8th International Conference on Bioinformatics Research and Applications (ICBRA 2021), virtual, Germany.
2020	Programm Co-Chair, 7th International Conference on Bioinformatics Research and Applications (ICBRA 2020), virtual.
2020	Member of technical program committee, The Twelfth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies, Venice, Italy.
2019	Member of program committee, The Fourth International Conference on Informatics and Assistive Technologies for Health-Care, Medical Support and Wellbeing HEALTHINFO 2019, Valencia, Spain.
2019	Member of scientific committee, 12th International Symposium on Health Informatics and Bioinformatics (HIBIT), Izmir, Turkey.
2019	Member of technical committee, 11th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2019), Stockholm, Sweden.
2019	Member of program committee, BIOINFORMATICS, 12th International Joint Conference on Biomedical Engineering Systems and Technologies, Prague, Czech Republic.
2018	Member of program committee, 11th International Symposium on Health Informatics and Bioinformatics, Antalya, Turkey.
2018	Member of program committee, BIOINFORMATICS, 11th International Joint Conference on Biomedical Engineering Systems and Technologies, Madeira, Portugal.
2017	Member of program committee, 10th International Symposium on Health Informatics and Bioinformatics, Güzelyurt, Northern Cyprus.
2017	Member of scientific committee, The International DNA Day and Genome Congress, Kirsehir, Turkey.

2017	Member of program committee, 13th International Symposium on Integrative Bioinformatics, Odense, Denmark.
2017	Session organizer, 21st Conference of the International Federation of Operational Research Societies, Quebec City, Canada.
2017	Member of program committee, BIOINFORMATICS, Porto, Portugal.
2017	**Allmer J** and Yousef M, Organizers of the Computational miRNomics Satellite Workshop at the BIOINFORMATICS Conference, Porto, Portugal.
2016	Session chair for MicroRNA and Integrative Analysis, 12th International Symposium on Integrative Bioinformatics, Bielefeld, Germany.
2016	Member of the organizing committee, 12th International Symposium on Integrative Bioinformatics, Bielefeld, Germany.
2016	Session chair, X Annual Congress of the European Proteomics Association, Istanbul, Turkey.
2016	Member of program committee, BioTechno 2016, Lisbon, Portugal.
2016	Member of program committee, BIOINFORMATICS, Rome, Italy.
2016	Member of organizing committee, Integrative Bioinformatics, Bielefeld, Germany.
2016	Member of organizing committee, EURO CBBM, Istanbul, Turkey.
2015	Member of program committee, BIOINFORMATICS, Lisbon, Portugal.
2015	Member of 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	Member of scientific committee, NETTAB and Integrative Bioinformatics, Bari, Italy.
2014	Member of program committee, CELLmicrocosmos neXt workshop, Bielefeld, Germany.
2014	Member of scientific committee, 3rd International Congress of the Molecular Biology Association of Turkey, Izmir, Turkey.
2014	Member of organizing committee, International Workshop on Proteomics, Bioinformatics and Health Informatics, Izmir, Turkey.
2014	Member of program committee, BIOINFORMATICS, Barcelona, Spain.
2013	Member of program committee, 8th International Symposium on Health Informatics and Bioinformatics, Ankara, Turkey.

2012	Scientific advisor, and member of program committee, 7th International Symposium on Health Informatics and Bioinformatics, Cappadocia, Turkey.
2010	Member of program committee, 5th International Symposium on Health Informatics and Bioinformatics, Antalya, Turkey.
2009	Member of organizing committee, 4th International Symposium on Health Informatics and Bioinformatics, Ankara, Turkey.

Invited Conference Presentations

2024	MicroRNAs; Regulation and Prediction, Raesfeld (Mar. 24).
2020	Keynote, Pre-microRNA Prediction from Machine Learning to Deep Learning, 1st International Conference on Data Science in Biology (ICDSB), virtual (Sept. 05).
2018	Bioinformatics approaches to microRNA analysis (data mining, use in model generation, read-across, translation), Workshop on the use of microRNAs in drug safety assessment, Centre for Drug Safety Science (MRC), Liverpool, UK (Oct. 04).
2017	Database Integration Facilitating the Merging of MicroRNA and Gene Regulatory Pathways in ALS, Seminar on Integrative Bioinformatics (Sept. 12).
2017	Keynote, Database Integration Facilitating the Merging of MicorRNA and Gene Regulatory Pathways in ALS, 13th International Conference Beyond Databases Architectures and Structures, Ustron, Poland (May 30 – Jun. 02).
2017	On the State-of-the-Art in Computational Protein Identification and Sequencing from Mass Spectrometric Measurements, 2nd Life Science Congress, Kayseri, Turkey (Feb. 22-25).
2016	Has C, Mungan MD, Toprak M, and **Allmer J**, On the Accuracy of Peptide Identification from MS/MS Spectra Using Database Search, X Annual Congress of the European Proteomics Association, Istanbul, Turkey (Jun. 22-25).
2015	Göktay M, Ayvaz M, un-Hua Liu C, Smith W, Zhang HB, and **Allmer J**, 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 (Jun. 25-27).
2015	Bağcı C and **Allmer J**, 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 (Jun. 25-27).
2015	Suluyayla R, Saçar MD, and **Allmer J**, Analysis of Features Describing pre-microRNAs, International German/Turkish/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany (Jun. 25-27).
2015	Bağcı C and **Allmer J**, Next Generation Sequencing's Sensitivity is both Boon and Bane, 2nd International Congress on Biosensors, Gediz University, Izmir, Turkey (Jun. 10-12).

2015	Bağcı C and **Allmer J**, How to Avoid Pitfalls in Next Generation Sequencing Data Analysis, 2nd International Congress on Biosensors, Gediz University, Izmir, Turkey (Jun. 10-12).
2014	Saçar MD, Bağcı C, and **Allmer J**, *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 (Nov. 4-5).
2014	Suluyayla R, Has C, and **Allmer J**, 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 (Jun. 2-3).
2012	Sacar MD, Hamzeiy H, and **Allmer J**, Have Features for miRNA Hairpin Detection been Saturated?, 3rd International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany (Jun. 18-19).
2012	A Bioinformatics View on Sequence Similarity and Homology, 3rd International German/Russian Summer School on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany (Jun. 18-19).
2011	Hamzeiy H, Saçar MD and **Allmer J**, A Handful of miRNA Fingerprints, 2nd International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany (Jun. 4-5).
2011	Bioinformatics in Turkey, Informatics Institute 15th Anniversary Celebration, Middle East Technical University, Ankara, Turkey (Jun. 9-10).
2011	Computationally Establishing miRNA Regulatory Networks from Seed Genes, VIII. International Molecular Biology and Genetics Student Winter School, Istanbul University, Istanbul, Turkey (Feb 24-26).
2010	Mass Spectrometry Based Proteomics, 4th Moleküler Biyoloji ve Genetik Araştırma we Uygulama Platformu, Izmir, Turkey (Mar. 9-10).
2010	Label Free Quantitation in Mass Spectrometry based Proteomics, ProteomeIstanbul, International Proteomics Workshop, Istanbul, Turkey (Jul. 12-17).
2010	Guide to Practical Quantitation of Mass Spectrometric Results, ProteomeIstanbul, International Proteomics Workshop, Istanbul, Turkey (Jul. 12-17).

Solicited Conference Presentations

2024	Erbay AK and **Allmer J**, Automatic EEG Signal Detection and Analysis of Signal Propagation Over Adjacent Electrodes, Sensorica, Mülheim adR., (Jun 24).
2022	Cantet F, **Allmer J**, Al Dahouk S, Bonazzi M, and Köhler S, RNA-immunoprecipitation/miRNA-Seq reveals miRNA-like, small noncoding RNAs of *Brucella suis*, translocated into the cytoplasm of infected murine macrophages, Brucellosis, Teramo, Italy (Sept. 16-19).
2019	**Allmer J**, The Internet of Science, Advances in Applied Bioinformatics, Mülheim an der Ruhr, Germany (July 19).

2019	**Allmer J** and Yousef M, Towards an Internet of Science, 13th ILAIS Conference, Tel Aviv, Israel (June 24).
2018	Saçar Demirci MD and **Allmer J**, izMiR 2.0: an Enhanced Version of Consensus miRNA Prediction Method, 11th International Symposium on Health Informatics and Bioinformatics, Antalya, Turkey (Oct. 25-27).
2016	Has C, Lashin SA, Kochetov VK, and **Allmer J**, PGMiner reloaded, fully automated proteogenomic annotation tool linking genomes to proteomes, 12th International Symposium on Integrative Bioinformatics, Bielefeld, Germany (Sept. 21-23).
2016	Hamzeiy H, Suluyayla R, Brinkrolf C, Janowski SJ, Hofestaedt R, and **Allmer J**, VANESA Provides a Platform for the Visualization and Analysis of MicroRNAs within KEGG Pathways, 12th International Symposium on Integrative Bioinformatics, Bielefeld, Germany (Sept. 21-23).
2016	Yousef M, **Allmer J**, and Khalifa W, Feature Selection for MicroRNA Target Prediction - Comparison of One-Class Feature Selection Methodologies, 7th International Conference on Bioinformatics Models, Methods and Algorithms, Rome, Italy (Feb. 21-23).
2016	Saçar Demirci MD, Toprak M, and **Allmer J**, A Machine Learning Approach for MicroRNA Precursor Prediction in Retro-Transcribing Virus Genomes, 12th International Symposium on Integrative Bioinformatics, Bielefeld, Germany (Sept. 21-23).
2015	Has C, Mungan MD, Çiftçi C, and **Allmer J**, 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 (Aug. 3-7).
2015	Kochetov AV, Lashin SA, Zuraev BS, Matushkin YG, and **Allmer J**, Dissecting eukaryotic mRNAs: an algorithm for prediction of efficiently translated hidden alternative ORFs, 6th International German/Turkish/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany (Jun. 25-27).
2015	Hamzeiy H, Janowski SJ, Hofestaedt R, and **Allmer J**, Visualisation and Analysis of MicroRNAs within KEGG Pathways, 6th International German/Turkish/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany (Jun. 25-27).
2015	Göktay M, Ayvaz M, un-Hua Liu C, Smith W, Zhang HB, and **Allmer J**, 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 (Jun. 25-27).
2015	Bağcı C and **Allmer J**, 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 (Jun. 25-27).

2015	Erkan EP, Dinc M, Eren E, **Allmer J**, Yalcin T, Genc, Ş, A cell division cycle 7-related protein kinase inhibitor suppresses glioblastoma cell growth in vitro, 12th European Meeting on Glial Cell Function in Health and Disease, 63:E461-E462, T17-04A Bilbao, Spain.
2015	Suluyayla R, Saçar MD, and **Allmer J**, Analysis of Features Describing pre-microRNAs, 6th International German/Turkish/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld University, Bielefeld, Germany (Jun. 25-27).
2014	Bağcı C and **Allmer J**, 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 (Jun. 2-3).
2014	Suluyayla R, Has C, and **Allmer J**, OMSSA was discontinued by NCBI; did its performance cause this decision? International Workshop on MS-Based Proteomics, Bioinformatics, and Health Informatics, Izmir, Turkey (May 19-21).
2014	Saçar MD and **Allmer J**, An Integrative Data Mining Approach for MicroRNA Detection in Human. 3rd International Workshop on Translational Bioinformatics and Medical Informatics, Izmir, Turkey (May 21-23).
2013	Has C, Toprak M, and **Allmer J**, AthenaDB, Data Integration for Protein Secondary Structure Analyses, 4th International German/Russian Workshop on Integrative Biological Pathway Analysis and Simulation, Bielefeld, Germany (Jun. 24-25).
2013	Saçar MD and **Allmer J**, Comparison of Four *Ab Initio* MicroRNA Prediction Tools, 4th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2013, p. 66, Barcelona, Spain (Feb. 11-14).
2012	Hamzeiy H, Saçar MD, and **Allmer J**, 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 (Feb 24-26).
2012	Has C, Göktay M, Teke E, Tosun C, and **Allmer J**, 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 (Nov. 29-30).
2012	Hamzeiy H, Saçar MD, and **Allmer J**, A Closer Look at Features Used in In Silico miRNA Hairpin Fingerprinting and Predicting, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey (Apr. 19-23).
2011	Hamzeiy H, Saçar MD, and **Allmer J**, 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 (Jul. 4-8).
2010	**Allmer J**, Mass Spectrometry Based Proteomics, 4. Moleküler Biyoloji ve Genetik Araştırma ve Uygulama Platformu, p. 19, Izmir, Turkey (Aug. 27-30).
2010	Has C and **Allmer J**, An integrative view on protein secondary structure prediction, 5th Int. Symposium on Health Informatics and Bioinformatics, p. 233, Antalya, Turkey (Apr. 19-23).

2010	*De Novo* Amino Acid Sequencing in Mass Spectrometry based Proteomics, 9th GEBIP Annual Meeting, Istanbul, Turkey (Sept. 17-19).
2009	Enabling the quantitation of post translational modifications, 11th International Congress on Amino Acids, Peptides and Proteins, *Amino Acids* 37, S32 (Aug. 2-8).

Posters

2021	Yousef M, Ozdemir F, Jabeer A, **Allmer J**, and Bakir-Gungor B, GeNetKEGG: Gene Expression Based KEGG PathWay Grouping and Scoring, 5th International Symposium on Bioinformatics (Dec. 15-17).
2020	Odenthal L, **Allmer J**, and Yousef M, A Machine Learning-based Approach for the Categorization of MicroRNAs to Their Species of Origin, 13th International Joint Conference on Biomedical Engineering Systems and Technologies. BIOINFORMATICS 2020 (Feb. 24-26).
2019	Yousef M, Abddallah L, and **Allmer J**, maTE: Discovering Expressed MicroRNA - Target Interactions, 27th Conference on Intelligent Systems for Molecular Biology, Basel, Switzerland (May 21-25), doi: 10.7490/f1000research.1117194.1.
2019	**Allmer J** and Gedikli F, Testgesteuertes Lernen von Programmierfähigkeiten und Online Prüfungen, E-Learning Day, Bottrop, Germany (May 22).
2019	Yousef M, Abddallah L, and **Allmer J**, maTE: Discovering Expressed MicroRNA - Target Interactions, 3rd Annual MAQC Society Conference - in Collaboration with CHARME, Riva Del Garda - Trentino – Italy (Apr. 8-10).
2018	Saçar Demirci MD and **Allmer J**, izMiR 2.0: an Enhanced Version of Consensus miRNA Prediction Method, 11th International Symposium on Health Informatics and Bioinformatics, Antalya, Turkey (Oct. 25-27).
2018	Brinkrolf C, Hofestaedt R, and **Allmer J**, VANESA, Facilitating the Integrated Analysis of Gene and MicroRNA-based Regulation, 63. Jahrestagung der Deutschen Gesellschaft für Medizinische Informatik, Biometrie und Epidemiologie (Sept. 2-6).
2018	Yousef M, Levy D, and **Allmer J**, Species categorization based on 3'UTR microRNA target sites using sequence features, 9th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2018 (Jan. 19-21). Received the best poster award.
2016	Acar İE, Ekren R, and **Allmer J**, Detection of Alternative Explanations for Cancer Causes in Publicly Available Next Generation Sequencing Data, German Conference on Bioinformatics, Berlin, Germany (Sept. 12-15).
2016	Sweef O, Ahmadov U, Yarimcam MC, **Allmer J**, Nalbant A, and Akgül B, Long Non-coding RNAs Are Differentially Expressed During Apoptosis in the Jurkat Human Acute T-Cell Leukaemia Cell Line, III. Experimental Hematology Congress, DOI: 10.13140/RG.2.1.4186.2808 (May 12).
2016	Ahmadov U, Bağcı C, Yildiz R, Yarimcam MC, Sweef O, **Allmer J**, Nalbant A, and Akgül B, Long Noncoding RNAs: Potential Regulatory Players of Apoptosis, 1st

	International Cell Death Research Congress, DOI: 10.13140/RG.2.1.1466.5366 (May 4-7).
2016	Bağcı C, Saçar Demirci MD, Has C, and **Allmer J**, Integrative Multi-Omics Analysis of *Toxoplasma gondii* MicroRNAs and their Effects; Powered by KNIME, 9th KNIME User Group Meeting and Summit, Berlin, Germany (Mar. 15-17).
2016	Ahmadov U, Bağcı C, Yildiz R, Yarimcam MC, Sweef O, **Allmer J**, Nalbant A, and Akgül B, Long non-coding RNAs are differentially expressed in a pathway-specific manner during apoptosis in human. Systems biology of non-coding RNAs, Rehovot, Israel (Feb. 8-11).
2015	Ahmadov U, Bağcı C, Yildiz R, Yarimcam MC, Sweef O, **Allmer J**, Nalbant A, and Akgül B, Long non-coding RNAs are differentially expressed in a pathway-specific manner during apoptosis in human. International Congress of the Molecular Biology, Ankara, Turkey (Nov. 27-29).
2015	Erkan EP, Dinç M, Eren E, **Allmer J**, Yalçın T, Genç Ş, A Cell Division Cycle 7-related Protein Kinase Inhibitor Suppresses Giloblastoma 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 (Jul. 15-18).
2015	Has C, Mungan MD, Çiftçi C, and **Allmer J**, Preparing Sequence Databases for Application in Proteogenomics, 14th International Conference on Amino Acids, Peptides and Proteins (ICAAPP14), Vienna, Austria (Aug. 3-7).
2015	Has C, Mungan MD, Çiftçi C, and **Allmer J**, 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 (Mar. 22-25).
2014	Hamzeiy H and **Allmer J**, MicroRNA Data Analysis: A Special Focus on Console Applications, WiBioSE Conference, Arandjelovac and Belgrade, Serbia (Feb. 2-8).
2012	Has C, Boz S, **Allmer J**, Using Human Blood Plasma Proteomics Data for the Validation of Gene Models, ECCB'12, 11th European Conference on Computational Biology, Basel, Switzerland (Sept. 9-12).
2012	Has C, Toprak M, **Allmer J**, PROMETHEUS: Secondary Structural Elements' Profiles of Proteins, ECCB'12, 11th European Conference on Computational Biology, Basel, Switzerland (Sept. 9-12).
2012	Has C, Yılmaz Ş, Aytun B, **Allmer J**, 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 (Sept. 9-12).
2012	Akçimen F, Sayın S, Bakırbaş A, Firatligil B, Has C, and **Allmer J**, Genome Annotation of Sesamum Indicum, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey (Apr. 19-23).

2012	Boz S, Has C, and **Allmer J**, Using Proteomics Data for the Validation of Gene Models, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey (Apr. 19-23).
2012	Toprak M, Has C, and **Allmer J**, Prometheus Secondary Structural Elements' Profiles of Proteins, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey (Apr. 19-23).
2012	Hamzeiy H, Saçar MD, and **Allmer J**, The Predictive Power of Specific Features Used for miRNA Discovery, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey (Apr. 19-23).
2012	Yilmaz S and **Allmer J**, RAy: Increasing the Scope of Mass Spectrometry-Homology Based Database Search, 7th International Symposium on Health Informatics and Bioinformatics, Capadocia, Turkey (Apr. 19-23).
2012	Doğanlar S, Gültekin V, **Allmer J**, and Frary A, Development of Genomic Tools for Eggplant, International Symposium on Biotechnology and other Omics in Vegetable Science, Antalya, Turkey (Apr. 29-May 2).
2011	Şelale H, Çelik I, **Allmer J**, Frary A, and Doğanlar S, Development of EST-SSR markers for opium poppy (Papaver somniferum), Plant Genomics European Meeting, Istanbul, Turkey (May 4-7).
2011	Çelik I, Gültekin V, **Allmer J**, Doğanlar S, and Frary A, Development of SSR Markers Derived from Genomic Sequence of Papaver somniferum L., The International Congress on Bioinformatics and Biomics, Kusadasi, Turkey (May 18-22).
2010	Aytun B and **Allmer J**, Tandem MS Fragment Ion Naming for Enhancement of *de novo* Sequencing, 5th Int. Symposium on Health Informatics and Bioinformatics, p. 232, Antalya, Turkey (Apr. 19-23).
2010	Geçer EC, Batur N, and **Allmer J**, Sequential Process Management System 'KERB', 5th Int. Symposium on Health Informatics and Bioinformatics, p. 224, Antalya, Turkey (Apr. 19-23).
2009	**Allmer J**, Label-free quantitation with 2DB, 11th International Congress on Amino Acids, Peptides and Proteins, *Amino Acids* 37, S123 (Aug. 2-8).
2009	Batur N and **Allmer J**, Database Management System Independence by Amending 2DB with a Database Access Layer, 4th International Symposium on Health Informatics and Bioinformatics, Ankara, Turkey (Apr. 19-23).
2008	Kırmacı E, İnce T, and **Allmer J**, PTM Predictor, Güncel, Gömsis, CPU Turkey, Istanbul, Turkey (Nov. 3-5).
2008	**Allmer J**, Efficient String Matching, 3rd International Symposium on Health Informatics and Bioinformatics, Istanbul, Turkey (May 18-20).
2007	Kuhlgert, S. and **Allmer J**, 2DB: a publication grade proteomics database poster presentation, 2nd International Symposium on Health Informatics and Bioinformatics, Belek, Turkey (Apr. 30-May 2).

2007 Hippler M, Busch A, **Allmer J**, Ostendorf E, Zeller M, Kirchhoff H, and Naumann B, Comparative quantitative proteomics to investigate the remodelling of bioenergetic pathways under iron-deficiency in Chlamydomonas reinhardtii, *Photosynthesis research*, 91(2-3): 290-290, PS2226.

2006 Naumann B, **Allmer J**, Zhang M, and Hippler M, 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, Montepellier, France (Jul. 3-7).

2004 **Allmer J**, Markert C, Stauber EJ, and Hippler M, A new approach that allows identification of intron-split peptides from mass spectrometric data in genomics databases. 13th International Congress on Photosynthesis, p. 20, Montréal, Québec, Canada (Aug 28-Sept 1).

2004 **Allmer J**, Markert C, Meyer H, and Hippler M, 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 (Aug 28-Sept 1).

2004 **Allmer J**, Markert C, Stauber EJ, and Hippler M, 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 (May 11-15).

2002 **Allmer J**, Seidl MD, Pirow R, and Paul RJ, Physiological responses of Hb-poor and Hb-rich Daphnia pulex to sudden hypoxia. International Symposium on Animal Physiology, p1, Alexisbad, Germany (May 23-25).

Non Scientific Workshop Participation

2019 Seminar Hochschullehre für neuberufene Professorinnen und Professoren, Hagen, Germany (Sept. 26,27; Oct. 28; Nov. 25, 26).

2019 Stimmtraining: Stimme und Rhetorik für Fortgeschrittene, Bielefeld, Germany (Sept. 20)

2019 Nonverbale Kommunikation in der Lehre, Dortmund, Germany (Jul. 18).

2019 HRW Neuberufenen Teamevent, Hagen, Germany (Feb. 8,9).

2018 Management Training Workshop, Wageningen University and Research, Wageningen, the Netherlands (Jan. 17-18).

2016 Participated in HealthBE2016, Horizon 2020 Health Partnering Day, Brussels, Belgium (Jul. 7).

2014 Attended the Symposium "Excellence in Science, Enabling Young Researchers" by The Turkish Academy of Sciences on invitation (Aug. 30).

2013 Attended the workshop on innovations in health sciences and technology transfer, Dokuz Eylül Univesity, Izmir, Turkey (Mar. 15).

IN PRESS

2020	Interview Deutschlandfunk Topic: parallel computing and Coronavirus. Interviewer Thomas Reintjes. https://www.deutschlandfunknova.de/beitrag/crowd-science-gemeinsam-gegen-sars-cov-2, https://ondemand-mp3.dradio.de/file/dradio/2020/05/22/deutschlandfunknova_crowd_science_20200522_9c5aef4c.mp3.
2019	Invitation video to the medical OMICS workshop organized by Hofestädt R and **Allmer J** at the 64. Meeting of the GMDS: https://youtu.be/0YmQJr3_XQ0.
2017	Small molecules, high impact: MicroRNAs in gene regulation, de Gruyter, http://sciencediscoveries.degruyter.com/small-molecules-high-impact-micrornas-gene-regulation/, summarizing the article:" Hamzeiy H, Suluyayla R, Brinkrolf C, Janowski SJ, Hofestaedt R, and **Allmer J**, VANESA Provides a Platform for the Visualization and Analysis of MicroRNAs within KEGG Pathways, *Journal of Integrative Bioinformatics*, 14(1), doi: 10.1515/jib-2016-0004." in laymen terms.
2015	Interview by Lutz Steinbrück for the German University Journal (DUZ).
2006	**Allmer J** and Hippler M, Interview by Proteomics, for the most influential article of the month, available as podcast (*Proteomics*, 6, 23).

TEACHING EXPERIENCE

Hochschule Ruhr West, Sole Instructor

Information Systems in Healthcare, Databases and data security (2019 - present, yearly in the spring semester)

Personalized Healthcare Technologies (2019 - present, yearly in the spring semester)

Medical OMICS (2020 - present, yearly in the spring semester)

Datamining and Machine Learning (2019 – present, yearly in the fall semester)

Basics of Informatics and Programming Languages (2019 – present. yearly in the fall semester)

Syntactic and Semantic Interoperability and Standards (2019 – present, yearly in the fall semester)

Medical Informatics (fall 2022, then yearly in the spring semester)

Izmir Institute of Technology, Sole Instructor

Introduction to Programming (winter 2016)

Applied Bioinformatics (spring/fall 2009, fall 2010, spring 2011, fall 2012, fall 2013, fall 2014, fall 2015, fall 2016)

Computational Biology (fall 2008, fall 2009, spring 2010, fall 2011, fall 2012, spring 2014, spring 2015, spring 2016, spring 2017)

Algorithms in Bioinformatics (spring/fall 2010, spring 2011, spring 2012, spring 2013, fall 2014, spring 2016)

Proteomics Data Analysis (spring 2011, spring 2012, fall 2013, spring 2015)

Genomics (spring 2014, fall 2015, spring 2017)

Freie University Berlin, Sole Instructor

Proteomics Data Analysis (summer 2015)

Bielefeld University, Sole Instructor

Computational Proteomics (summer 2013)

Dokuz Eylül University, Sole Instructor

Bioinformatics in Genomics and Proteomics (fall 2007)

Izmir University of Economics, Sole Instructor

Bioinformatics (spring 2008)

Introduction to Software Engineering (spring 2008)

Introduction to Computers and Information Systems (spring/fall 2007, spring 2008)

Database Management Systems (spring/summer 2007, spring 2008)

Data Mining (fall 2007)

Advanced Programming (spring 2007)

System Analysis and Design (fall 2007)

University of Münster, Co-Instructor

Methods in Functional Proteomics (fall 2006)

Doctoral Theses

Visam Gültekin (2021 - present) The Human Transcriptome (co-Advisor with Ralf Hofestädt, University of Bielefeld).

Aruana Fagundes Fiuza Hansel Fröse (2022 – 2023) Part of her doctoral thesis was performed as a co-supervised internship with Prof. Dr. Ralf Hofestädt (Bielefeld University, Germany).

Müşerref Duygu Saçar Demirci (2013 - 2017) Computational Establishment of MicroRNA Metabolic Networks, Department of Molecular Biology and Genetics, IYTE.

Canan Has (2012 - 2017) Enhancement and validation of current human genome annotation via new proteogenomic methods, Department of Molecular Biology and Genetics, IYTE.

Master Theses

Marko Petkovic (2021 – 2022) Simulating and Generating pre-miRNA using Variational Auto-Encoders, (Co-Advisor with Vlado Menkowski, Technical University Eindhoven), Department of Mathematics and Computer Science.

Irma Brandt (2020 – 2022) Towards Concept-based Interpretability of Pre-miRNA Detection using Convolutional Neural Networks, (Co-Advisor with Vlado Menkowski, Technical University Eindhoven), Department of Mathematics and Computer Science.

Mokhlis El Houcine (2020 - 2021) „Maßnahmen gegen Over- und Underfitting für Convolutional Neuronales Netzwerk" (2nd Advisor with Zhichun Lee), Hochschule Ruhr West.

Jorge Cordero (2018 - 2019) Application of deep learning to pre-miRNA detection using Google Tensor Flow (Co-Advisor with Vlado Menkowski, Technical University Eindhoven), Department of Mathematics and Computer Science.

Luise Odenthal (2018 - 2019) Framework for the automatic categorization of hairpins to their species of origin (Co-Advisor with Malik Yousef and Ralf Hofestädt), Department of Computer Engineering, IYTE and Department of Bioinformatics and Medical Informatics, Bielefeld University.

İlhan Erkin Acar (2015 - 2017) Improving MicroRNA Target Prediction Employing Integrative Data Mining, Department of Biotechnology, IYTE.

Mehmet Direnç Mungan (2014 - 2017) Importance of Database Normalization for Reliable Protein Identification in Mass Spectrometry-Based Proteomics, Department of Biotechnology, IYTE.

Caner Bağcı, Biotechnology (2013 - 2016) Automatic, Fast and Accurate Sequence Decontamination (co-Advisor with Dr. Selma Tekir, Department of Computer Engineering, IYTE), Biotechnology, IYTE.

Rabia Suluyayla (2013 - 2016) Cost and Benefit Analysis of Features used in Machine Learning based pre-miRNA Detection, Department of Molecular Biology and Genetics, IYTE.

Mustafa Toprak (2013 - 2015) 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.

Mehmet Göktay (2013 - 2015) 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.

Müşerref Duygu Saçar (2011 - 2013) An Integrative Data Mining Approach for MicroRNA Detection in Human, Department of Molecular Biology and Genetics, IYTE.

Visam Gültekin, (2010 - 2013) Quality Assessment of *De Novo* Sequence Assembly Tools, Department of Molecular Biology and Genetics, IYTE.

Savaş Takan (2010 - 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 (2010 - 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 (2009 - 2012) Evaluations of Protein Secondary Structure Prediction Algorithms on a New Advanced Benchmark DataSet, Department of Molecular Biology and Genetics, IYTE.

Belgin Aytun (2009 - 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 (2007 - 2009) Systematic Computational Analysis of Potential RNAi Regulation in *Toxoplasma gondii,* Department of Molecular Biology and Genetics, IYTE.

Bachelor Theses

Gamze Temur (tbd), Entwicklung eines wissenschaftlichen Knowledgegraphen, Hochschule Ruhr West

Tara Fereydooni-Lotfabadi (tbd), De novo Sequnzierung von Plaques im Gehirn von Alzheimer Patienten, Hochschule Ruhr West

Firdaous Amatalla (tbd), Digitalisierung und Interoperabilität bezüglich der Netzwerkstrukturen in Gesundheitseinrichtungen mit Blick auf die Auslastung von Sonografiegeräten, Hochschule Ruhr West

Luis Enrique Rodriguez Ingenpaß (2024), Instrumentarium für den Transfer einer prä-operativen Hüftplanung in den OP, Hochschule Ruhr West

Lucica Bettina Aleman (2024), Toxoplasmosis and Ocular Toxoplasmosis: A Comprehensive Review of Clinical Features and Modern Diagnostic Approaches Incorporating Next-Generation Sequencing, Hochschule Ruhr West

Alpay-Kaan Erbay (2023) Automatische EEG-Signalerkennung und Analyse der Signalausbreitung über benachbarte Elektroden, Hochschule Ruhr West

Meenujan Sritharan (2023) Prozessoptimierung im Krankenhaus durch eine digitale Lagerstation: Konzept, HL7 Standard, Realisierung und Implementierung, Hochschule Ruhr West

Paul Philipp (2023) Extended Reality in Childhood Autism: Detection, Prognosis, and Treatment, Hochschule Ruhr West

Tim Bonetzki (2022) Klassifizierung von Patientenanliegen als Anwendungsfall von Natural Language Processing, Hochschule Ruhr West

Stefanie Martin (2022) Evaluation von Verfahren der Merkmalsselektion im Kontext der Semi-Supervised Anomaliedetektion auf eingebetteten Systemen in der Industrie 4.0, Hochschule Ruhr West

Ömer Aktas (2022) Schwachstellenanalyse und Optimierung der Restanodenreinigungsanlage im Rahmen der Aluminiumherstellung, Hochschule Ruhr West

Daniel Rempel (2021) Adaptive Erkenntnisgewinnung durch Auswertung von Produktionsdaten für einen neuen IoT-Baukasten, Hochschule Ruhr West

Internships

Mehmet Can Ay (summer 2022), ERASMUS Internship, Workflow Management System Evaluation, Hochschule Ruhr West

Dilan (summer 2022), ERASMUS Internship, Workflow Management System Evaluation, Hochschule Ruhr West

Akin Deniz Altan (Aug. 2019), maTEjs, a generalized and improved version of maTE, Hochschule Ruhr West, Medical Informatics and Bioinformatics, Mülheim an der Ruhr.

Matthieu Beukers (Feb.-Jun. 2018), Comparison of CLC Workbench, Konstanz Information Miner, and Galaxy for the Development of Reproducible Integrated RNA-seq Analysis Workflows, Applied Bioinformatics, Bioscience, Wageningen University and Research.

PROFESSIONAL SERVICE

Editorship

Member of the editorial board for Journal of Integrative Bioinformatics, 2015-present

Editor for Journal of Integrative Bioinformatics Tools, 2013-present

Associate Editor for the Journal of Integrated Omics, 2012-present

Grant Refereeing/ External Expert

European Commission, Reviewer of the Marie Skłodowska-Curie European Postdoctoral Fellowships, 2020 - present

AQAS Program Accreditation, 2020, 2022.

The Scientific and Technological Research Council of Turkey, 2012 - 2016

Israeli Ministry of Health, 2016

National Science Center, Poland, 2016

Natural Sciences and Engineering Research Council of Canada, 2014

Peer Review

PeerJ. 2014 - present

Journal of Integrative Bioinformatics, 2012 - present

BMC Genomics, 2014 - present

PLoS One, 2014 - present

IEEE Transactions on Computational Biology and Bioinformatics (TCBB), 2013 – present.

BMC Bioinformatics, 2009 - present

Oxford Journal of Bioinformatics, 2009 – 2016.

Expert Review of Proteomics, 2012.

Molecular Biosystems, 2013 – 2015.

Briefings in Bioinformatics, 2016.

Open Peer Review

Review for: Uptake of dietary milk miRNAs by adult humans: a validation study, *F1000/research*, doi: 10.5256/f1000research.9200.r13515

Review for: Alternative miRNAs? Human sequences misidentified as plant miRNAs in plant studies and in human plasma, *F1000/research*, doi: 10.5256/f1000research.15294.r31318

To Profession

Member of the Research and Transfer Committee, Hochschule Ruhr West (2022 - present).

Head of hiring committee for Digital Engineering, Hochschule Ruhr West (2022-2023).

Head of the hiring committee for Ingenieurinformatk, Hochschule Ruhr West (2021).

Member of the Studieneingangsphase (STEP) committee, Hochschule Ruhr West (2019).

Member of the PhD committee, Molecular Biology and Genetics, Izmir Institute of Technology, Izmir, Turkey (2013-present).

Website development coordinator, Department of Molecular Biology and Genetics, Izmir Institute of Technology, Izmir, Turkey (2008-2013).

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

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

Ph. D. Committee Membership

Cassandra Königs, PharMeBINet; a general-purpose approach for the integration of heterogeneous biomedical data sources and its application to drug-drug interaction prediction, Bielefeld University, Bielefeld, Germany (2024).

Florent Jouy, Effects of Chemicals on Human Immune Cells Through Quantitative Proteomics, Molecular Systems Biology, Helmholtz Centre for Environmental Research, Leipzig, Germany (2017).

Nimet İlke Akçay, Petri Net-Based Quantitative Modeling and Validation of p16-mediated Signaling Pathway, Applied Mathematics and Computer Science, Eastern Mediterranean University, Famagusta, North Cyprus (2016).

Çağdaş Taşoğlu, Fragmentation Reaction Mechanism of Peptides Containing Glutamic Acid and Glutamine in Gas Phase: Comparison of Electron Transfer Dissociation with Collision-Induced Dissociation using Mass Spectrometry, Chemistry Izmir Institute of Technology, Izmir, Turkey (2015).

Ahmet Emin Atik, Gas-Phase Fragmentation Mechanisms of Peptides by Mass Spectrometry, Chemistry, Izmir Institute of Technology, Izmir, Turkey (2013).

Tunca Doğan, Automatic Identification of Evolutionary and Sequence Relationships in Large Scale Protein Data Using Computational and Graph-Theoretical Analyses, Bioengineering, Izmir Institute of Technology, Izmir, Turkey (2012).

Collaborations with Local High Schools

Çağla Gezgen, Hospital Decision Support System for Proper Selection of Antibiotic Agents, Ödemiş High School (2014-2015).

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

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

Student Organizations

Capoeira club founder at the Izmir Institute of Technology (2010 - 2016).

Acted as trainer for the Capoeira club at the Izmir Institute of Technology (2010 - 2014).

OTHER

Management Training Workshop, Wageningen University and Research, Wageningen, the Netherlands (17-18.01.2018).

PROFESSIONAL AFFILIATIONS

GMDS – Deutsche Gesellschaft für Medizinische Informatik Biometrie und Epidemiologie e.V. (German Society of Medical Informatics, Biometry and Epidemiology), 2019-present

ISCB - International Society for Computational Biology, 2012-present

BID - Turkish Bioinformatics Society, 2012- present

TUPA – Turkish Proteomics Association, 2013-present

EURO - The Association of European Operational Research Societies, 2013-present

TURKMIA - Turkish Society of Medical Informatics, 2014-present

PROFESSIONAL SOCIAL NETWORKS AND WEBSITES

ResearchGate:	Profile: https://www.researchgate.net/profile/Jens_Allmer Top 3% of RG according to Research Interest Score
ChronicleVitae:	https://chroniclevitae.com/people/800974-jens-allmer
Academia:	https://hochschule-ruhr-west.academia.edu/JensAllmer
LinkedIn:	http://tr.linkedin.com/in/jallmer/

LANGUAGE SKILLS

	Reading	**Writing**	**Speaking**	**Listening**
German	native	native	native	native
English	idiomatic	idiomatic	idiomatic	idiomatic
Dutch	advanced	advanced	advanced	advanced
Turkish	advanced	intermediate	intermediate	advanced
French	advanced	intermediate	intermediate	advanced
Portuguese	beginner	beginner	beginner	beginner
Spanish	beginner	beginner	beginner	beginner

REFERENCES

Michael Hippler
Plant Biochemistry and Biotechnology
Münster University
Schlossplatz 8
48143 Münster, Germany
Email: mhippler@uni-muenster.de
Phone: +49 251 832-4790

Ralf Hofestaedt
Bielefeld University
Faculty of Technology
Bioinformatics Department
Universitätsstraße 25
33615 Bielefeld, Germany
Email: hofestae@techfak.uni-bielefeld.de
Phone: +49 521 106-5283

Alexey Kochetov
Plant Gene Engineering Laboratory
Institute of Cytology and Genetics
Russian Academy of Sciences
10, pr. Lavrentieva
Novosibirsk, 630090, Russia
Email: ak@bionet.nsc.ru
Phone: +7 913 744 9511

Anne Frary (can also evaluate teaching abilities)
Molecular Biology and Genetics
Izmir Institute of Technology
Plant Genetics and Breeding
Gulbahce Kampus
35430 Urla, Izmir, Turkey
Email: annefrary@iyte.edu.tr
Phone: +90 232 750 7303