1. Full Name: Hilal KAZAN
2. Date of Birth: 09.11.1985
3. Title: Professor Doctor
4. Education:

Degree	Field	University	Year
B.Sc.	Computer Engineering	Sabanci Universitesi	2007
M.Sc.	Computer Science	University of Toronto	2009
Ph.D.	Computer Science	University of Toronto	2012

5. Academic Titles:

Assistant Professorship Date: December 2012

Associate Professorship Date: April 2018

Professorship Date: August 2023

6. Supervised Master's and Ph.D. Theses
6.1. Master's Theses

Ongoing

Completed

Co-supervision: İbrahim Berber - Antalya Bilim Üniversitesi

Co-supervision: M. Edip Akay Houdjedj - Antalya Bilim Üniversitesi

Co-supervision: Yacine Marouf - Antalya Bilim Üniversitesi

Co-supervision: Aissa Houdjedj - Antalya Bilim Üniversitesi

Co-supervision: Ahmed A. T. Bahmed - Antalya Bilim Üniversitesi

Co-supervision: Ilyes Baali - Antalya Bilim Üniversitesi

Co-supervision: Rafsan Ahmed - Antalya Bilim Üniversitesi

Co-supervision: Serhan Aksoy - Antalya Bilim Üniversitesi

Supervision: Tunde Aderinwale - Antalya Bilim Üniversitesi

Co-supervision: Atefeh Lafzi - ODTÜ Enformatik Enstitüsü

Co-supervision: Saber HafezQorani - ODTÜ Enformatik Enstitüsü

Co-supervision: Udo Gieraths – Max Planck Institute in Tuebingen, Germany

6.2. Ph.D. Theses
Co-supervision: Aissa Houdjedj - Akdeniz University
7. Publications
• Articles published in international peer-reviewed journals (SCI, SSCI, Arts and Humanities)

- A Rasheed et al. (2024). *Hyperlipidemia-induced Hematopoiesis is Repressed by MLKL in Endothelial Cells of the Splenic Niche.*
Nature Cardiovascular Research. Accepted.
- A Kolaj, SK Zahr, BS Wang, T Krawec, H Kazan, G Yang, DR Kaplan, FD Miller (2023). *The P-body protein 4E-T represses translation to regulate the balance between cell genesis and establishment of the postnatal NSC pool. Cell Reports* 42(3):112242.

- İ Berber, C Erten, H Kazan (2023). *Predator: Predicting the impact of cancer somatic mutations on protein-protein interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics.* 10.1109/TCBB.2023.3262119.
- C Erten, A Houdjedj, H Kazan, Ahmed AT Bahmed (2022). *PersonaDrive: a method for the identification and prioritization of personalized cancer drivers. Bioinformatics,* 38(13):3407-3414.
- MA Nguyen, HD Hoang, A Rasheed, AC Duchez, H Wyatt, ML Cottee, TE Graber, L Susser, S Robichaud, İ Berber, M. Geoggrion, M Ouimet, H Kazan, L Maegdefessel, EE Mulvihill, T Alain, KJ Rayner (2022). *miR-223 Exerts Translational Control of Proatherogenic Genes in Macrophages. Circulation Research,* 131:42-58.
- R Ahmed, C Erten, A Houdjedj, H Kazan, C Yalcin. *A network-centric framework for the evaluation of mutual exclusivity tests on cancer drivers. Frontiers in Genetics.* Volume 12, 2021. https://doi.org/10.3389/fgene.2021.746495
- C Erten, A Houdjedj, H Kazan (2021). *Ranking cancer driver genes using betweenness scored random walks. BMC Bioinformatics,* 22(62), 1-16.
- A Omranovic, H Kazan, P Oblak, T Curk (2021). *Sparse data embedding and prediction by tropical matrix factorization. BMC Bioinformatics,* 22, 10.1186/s12859-021-04023-9.
- R Ahmed, I Baali, C Erten, E Hoxha, H Kazan (2020). *MEXCOwalk: mutual exclusion and coverage based random walk to identify cancer modules. Bioinformatics,* 36(3), 872-879. 10.1093/bioinformatics/btz655.
- I Baali, C Erten, H Kazan (2020). *DriveWays: a method for identifying possibly overlapping driver pathways in cancer. Scientific Reports,* 10(1).
- M Yang, ...H Kazan, ...NCI-CPTAC-DREAM-Consortium. (2020). *Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Systems,* 11(2), 186-1959.
- MJ Mason, ...H Kazan within Multiple Myeloma DREAM Consortium (2020). *Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. Leukemia.* 10.1038/s41375-020-0742-z.
- R Ahmed, I Baali, C Erten, E Hoxha, H Kazan (2019). *MEXCOwalk: Mutual Exclusion and Coverage Based Random Walk to Identify Cancer Module. Bioinformatics.* doi.org/10.1093/bioinformatics/btz655.
- S HafezQorani, A Houdjedj, M Arıcı, A Said, H Kazan (2019). *RBPSponge. Genome-wide identification of lncRNAs that sponge RBPs. Bioinformatics.* 10.1093/bioinformatics/btz448.
- DG Ozturk, M Kocak, A Akcay, K Kinoglu, E Kara, Y Buyuk, H Kazan, D Gozuacik (2018). *MITF-MIR211 axis is a novel autophagy amplifier system during cellular stress. Autophagy.* Oct 5:1-16. doi: 10.1080/15548627.2018.1531197.
- I Baali, DAE Acar, TW Aderinwale, S HafezQorani, H Kazan (2018). *Predicting clinical outcomes in neuroblastoma with genomic data integration. Biology Direct* 13(1), 20.
- SK Zahr, G Yang, H Kazan, MJ Borrett, SA Yuzwa, A Voronova, DR Kaplan, FD Miller (2018). *A translational repressor complex in developing mammalian neuronal stem cells that regulates neuronal specification. Neuron,* 97 (1-18).
- H Kazan (2016). *Modeling Gene Regulation in Liver Hepatocellular Carcinoma with Random Forests. Biomed Research International.* doi:10.1155/2016/1035945.

- A Lafzi and H Kazan (2016). *Inferring RBP-Mediated Regulation in Lung Squamous Cell Carcinoma. PloS One* 11(5): e0155354.
- N Berkowitz, I Silverman, D Childress, H Kazan, L Wang, B Gregory (2016). *A comprehensive database of high-throughput sequencing-based RNA secondary structure probing data (Structure Surfer). BMC Bioinformatics.* 10.1186/s12859-016-1071-0.
- S Chandrasekaran, M Cokol-Cakmak, N Sahin, K Yilancioglu, H Kazan, JJ Collins, M Cokol (2016). *Chemogenomics and orthology-based design of antibiotic combination therapies. Molecular Systems Biology* 12(5):872.
- S HafezQorani, A Lafzi, RG de Bruin, AJ van Zonneveld, EP van der Veer, YA Son, H Kazan (2016). *Modeling the combined effect of RNA-binding proteins and microRNAs in post-transcriptional regulation. Nucleic Acids Research.* 10.1093/nar/gkw048.
- RG de Bruin ... H Kazan, EAL Biessen, M Ares Jr, AJ van Zonneveld, EP van der Veer (2016). *Quaking promotes monocyte differentiation into pro-atherogenic macrophages by controlling pre-mRNA splicing and gene expression. Nature Communications* 7:10486.
- R Colak, T Kim, H Kazan, Y Oh, M Cruz, A Valladares-Salgado, J Peralta, J Escobedo, EJ Parra, PM Kim, A Goldenberg (2015). *JBASE: Joint Bayesian Analysis of Subphenotypes and Epistasis. Bioinformatics.* 10.1093/bioinformatics/btv504.
- K Yilancioglu, ZB Weinstein, C Meydan, A Akhmetov, I Toprak, A Durmaz, I Iossifov, H Kazan, FP Roth, M Cokol (2014). *Target-independent prediction of drug synergies using only drug lipophilicity. J Chemical Information and Modelling* 54(8):2286-2293.
- X Li, H Kazan, HD Lipshitz, QD Morris (2013). *Finding the target sites of RNA-binding proteins. WIREs RNA.* doi:10.1002/wrna.1201
- D Ray*, H Kazan*, KB Cook*, MT Weirauch*, HS Najafabadi* et al. (2013). *A compendium of RNA-binding motifs for decoding gene regulation. Nature* 499(7457): 172-177. *co-first authors*
- H Kazan, Q Morris (2013). *RBPmotif: a web server for the discovery of sequence and structure preferences of RNA-binding proteins. Nucleic Acids Research.* doi:10.1093/nar/gkt463
- ML Wilbert, SC Huelga, K Kapeli, TJ Stark, TY Liang, SX Chen, BY Yan, JL Nathanson, KR Hutt, MT Lovci, H Kazan, AQ Vu, KB Massirer, Q Morris, S Hoon, GW Yeo (2012). *LIN28 binds messenger RNAs at GGAGA motifs and regulates splicing factor abundance. Molecular Cell,* 48:1-12
- KB Cook, H Kazan, K Zuberi, Q Morris and TR Hughes (2010). *RBPDB: a database of RNA-binding specificities. Nucleic Acids Research,* 39:D301-D308
- H Kazan, D Ray, E Chan, TR Hughes and Q Morris (2010). *RNAcontext: a new method for learning the sequence and structure binding preferences of RNA-binding proteins. PLoS Computational Biology* 6(7):e1000832.
- D Ray*, H Kazan*, E Chan, LP Castillo, S Talukder, BJ Blencowe, Q Morris, TR Hughes (2009). *Rapid and systematic characterization of the RNA recognition specificities of RNA-binding proteins. Nature Biotechnology,* 27:667-670. *co-first authors*

7.2. Articles published in other international peer-reviewed journals

7.3. Papers presented at international scientific meetings and published in proceedings

- *Ranking Cancer Drivers via Betweenness-based Outlier Detection and Random Walks.* C Erten, A Houdjedj, H Kazan. ISMB (29th Annual Conference on Intelligent Systems for Molecular Biology), 2021, virtual, July 25-30, 2021 (oral presentation).

- *DriveWays: A Method for Identifying Possibly Overlapping Driver Pathways in Cancer.* I Baali, C Erten, H Kazan. ISMB (29th Annual Conference on Intelligent Systems for Molecular Biology), 2021, virtual, July 25-30, 2021 (oral presentation).
- *MEXCOWalk: Mutual Exclusion and Coverage Based Random Walk to Identify Cancer Modules.* R Ahmed, I Baali, C Erten, E Hoxha, H Kazan. ISMB (27th Annual Conference on Intelligent Systems for Molecular Biology), 2019, Basel, July 21-25, 2019 (poster).
- *MEXCOWalk: Mutual Exclusion and Coverage Based Random Walk to Identify Cancer Modules.* R Ahmed, I Baali, C Erten, E Hoxha, H Kazan. AdvCompBio 2019 (Advances in Computational Biology), Barcelona, Nov 28-29, 2019, p.119.
- *A translational repression complex in developing mammalian neural stem cells that regulates neuronal specification.* SK Zahr, G Yang, H Kazan, MJ Borrett, SA Yuzwa, A Voronova, DR Kaplan, FD Miller. Dagstuhl Seminar 19342, Germany, 22 August 2019, p.58.
- *Predicting clinical outcomes in neuroblastoma with genomic data integration.* I Baali, DAE Acar, T Aderinwale, S HafezQorani, H Kazan (2017). ISMB (25th Annual Conference on Intelligent Systems for Molecular Biology), CAMDA workshop, Prague, Czech Republic (oral presentation).
- S HafezQorani, H Kazan (2017). *Genome-wide identification of lncRNAs that sponge RNA-binding proteins.* ISMB (25th Annual Conference on Intelligent Systems for Molecular Biology), RNA workshop, Prague, Czech Republic (oral presentation).

7.4. International books authored or book chapters

7.5. Articles published in national peer-reviewed journals

- H Kazan (2016). *Computational Prediction of RNA-protein Interactions. APJES* 4:3. doi:10.21541/apjes.92217

7.6. Papers presented at national scientific meetings and published in proceedings

- *SCITUNA: A Network Alignment Approach for Integrating Multiple Single-Cell RNA-Seq Datasets.* O Dogan, BO Erten, C Erten, A Houdjedj, H Kazan, M Krichen and Y Marouf. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2022, Oct 20-21, 2022, METU campus in Erdemli, Mersin (poster presentation).
- *Sex-biased expression of neuroimmune guidance cues in cardiovascular diseases.* Y Marouf, SO Doğan, ED Benavente, G Pasterkamp, HM den Ruijter, Jv Gils, K Rayner, H Kazan. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2022, Oct 20-21, 2022, METU campus in Erdemli, Mersin (oral presentation in Student Symposium).
- *Predicting the impact of cancer somatic mutations on protein-protein interactions.* I Berber, C Erten and H Kazan. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2021, Sept 10-11, Bilkent University, conducted online (poster presentation).
- *PersonaDrive: A Computational Approach for Prioritization of Patient-specific Cancer Drivers.* C Erten, A Houdjedj, H Kazan and AAT Bahmed. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2021, Sept 10-11, Bilkent University, conducted online (oral presentation).

- *DriveWays: a method for identifying possibly overlapping driver pathways in cancer.* I Baali, C Erten, H Kazan. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2020, Sabancı Universitesi, conducted online (oral presentation).
- *A novel network-centric framework for evaluating epistasis in cancer.* R Ahmed, C Erten, H Kazan, C Yalcin. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2020, Sabancı Universitesi, conducted online (poster presentation).
- *MEXCOWalk: Mutual Exclusion and Coverage Based Random Walk to Identify Cancer Modules.* R Ahmed, I Baali, C Erten, E Hoxha, H Kazan. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2019, İzmir, October 17-18, 2019, p.58 (oral presentation).
- *An integrative network-based approach for prioritizing driver genes for breast cancer.* AAT Bahmed, C Erten, A Houdjedj, H Kazan. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2019, İzmir, October 17-18, 2019, p.231 (poster presentation).
- *MexCoGrowth: a seed-and-extend based algorithm to identify overlapping cancer driver modules.* I Baali, C Erten, H Kazan. HIBIT (The International Symposium on Health Informatics and Bioinformatics), 2019, İzmir, October 17-18, 2019 (poster presentation).
- *MEXCOwalk: Kanser ile İlişkili Gen Modüllerinin Çıkarımı Üzerine bir Yöntem.* R Ahmed, I Baali, C Erten, E Hoxha, H Kazan. 4th Life Sciences Congress, Kayseri, 22 February 2019 (oral presentation).
- *Genome-wide analysis for identification of lncRNAs that sponge RNA-binding proteins.* S HafezQorani, H Kazan. HIBIT 2017, 10th International Symposium on Health Informatics and Bioinformatics, Girne, Cyprus, June 28-30, 2017. Poster No: 66.
- *Identification of dysregulated pathways across multiple cancer types.* C Erten, E Hoxha, H Kazan, E Tepe. HIBIT 2017, 10th International Symposium on Health Informatics and Bioinformatics, Girne, Cyprus, June 28-30, 2017 (oral presentation).
- *Integrating multiple data types for cancer subtype discovery.* T Aderinwale, H Kazan. HIBIT 2017, 10th International Symposium on Health Informatics and Bioinformatics, Girne, Cyprus, June 28-30, 2017 (oral presentation).
- *PUM1(2) proteinlerinin gen ifadesine olan etkilerinin susturma deneyi ile incelenmesi.* S HafezQorani, H Kazan (2016). 5th National Molecular Biology and Biotechnology Congress, Konya, Turkey, July 18-21, 2016.
- *Investigating the role of alternative polyadenylation in lung squamous cell carcinoma.* H Kazan (2016). 6th Multidisciplinary Cancer Research Congress, Konya, Turkey, October 27-30, 2016.
- *Identifying the interactions between RNA-binding proteins and miRNAs.* A Lafzi, S HafezQorani, YA Son, H Kazan. Conference on Medical Informatics in Europe, 2014, İstanbul.
- *A compendium of RNA-binding motifs for decoding gene regulation.* D Ray, H Kazan, E Chan, LP Castillo, S Talukder, BJ Blencowe, Q Morris, TR Hughes. HIBIT 2013, 8th International Symposium on Health Informatics and Bioinformatics, Ankara.
- *Learning binding preferences of RNA-binding proteins inferred from large scale binding assays.* H Kazan, X Liu, KB Cook, W Jiao, HD Lipshitz, TR Hughes, Q Morris (2010). RECOMB Satellite on Regulatory Genomics, New York City, USA.

7.7. Other publications

7.8. International Citations

According to Google Scholar, there are a total of 4,688 citations.

8. Projects

- Researcher: TÜBİTAK 1001 Project (2025-present)
    - Establishment of a snoRNA-miRNA-based biomarker panel for the detection of drug-resistant triple-negative breast cancer
- Researcher: TÜSEB 202 B-01 (2023-2025)
    - Investigation of the biomarker properties of alternative transcript isoforms in the plasticity of tumor-associated macrophages using a single-cell RNA sequencing approach (16428)
- Principal Investigator: TÜBİTAK 1001 Project (2022-2024)
    - Innovative network alignment-based approaches for the integration of single-cell datasets (121E491)
- Principal Investigator: TÜSEB 2019-TA-01 R&D Project (2020-2023)
    - Novel computational approaches for personalized cancer driver gene discovery using omics data (4069)
- Principal Investigator: ERA-NET CVD Project in collaboration with the Netherlands and Canada (2019-2022)
    - Neuroimmune guidance cues, microRNAs, and inflammatory response: sex differences in cardiovascular diseases (118S930)
- Principal Investigator: TÜBİTAK 1001 Project (2018-2021)
    - Investigation of gene expression in cancer using multidimensional genomic data and identification of cancer subtypes (117E789)
- Principal Investigator: FP7 Marie Curie Career Project (2014-2018)
    - Systematic study of post-transcriptional regulation mediated by RNA-binding proteins and miRNAs
- Principal Investigator: TÜBİTAK 3501 Career Project (2013-2015)
    - Identification of factors involved in the post-transcriptional regulation of messenger RNAs (113E159)

9. Administrative Duties

- Vice Chair, Department of Computer Engineering (March 2017-present)
- Director, Graduate School of Natural and Applied Sciences (September 2015-September 2017)
- Chair, Department of Computer Engineering (September 2016-February 2017)

10. Membership in Scientific and Professional Organizations

International Society of Computational Biology (ISCB)

11. Awards

- Grace Hopper Celebration of Women in Computing Scholarship Award, 2008
- Sabanci University Certificate of High Honor for five semesters
- Sabanci University Faculty of Engineering and Natural Sciences High Honor Scholarship, 2003-2007

12. Courses Taught at Undergraduate and Graduate Levels in the Last Two Years

Academic Year	Semester	Course Title	Weekly Hours (Theoretical)	Weekly Hours (Practical)	Number of Students
2023	Fall				
2023	Spring	CS 445 – Machine Learning (Undergraduate)	3		168
2023	Spring	DS 701 – Introduction to Data Science (M.Sc.)	3		15
2023	Spring	DS 702 – Applied Statistics for Data Science (M.Sc.)	3		11
2023	Spring	ECE 700 – Seminar (M.Sc.)	2		4
2022	Fall	CS 303 – Fundamentals of Programming Languages (Undergraduate)	3		65
2022	Fall	DS 703 – Machine Learning (M.Sc.)	3		13
2022	Fall	ECE 700 – Seminar (M.Sc.)	2		1
2022	Spring	CS 445 – Machine Learning (Undergraduate)	3		8
2022	Spring	DS 502 – Applied Statistics for Data Science (M.Sc.)	3		4
2022	Spring	ECE 584 – Graduate Seminar (M.Sc.)	2		1

Note: If offered, courses taught during the summer term should also be added to the table.