1. **Adı Soyadı:** Hilal KAZAN

2. **Doğum Tarihi:** 09.11.1985

3. **Unvanı:** Profesör Doktor

4. **Öğrenim Durumu:**

Derece	Alan	Üniversite	Yıl
Lisans	Bilgisayar Muhendisligi	Sabanci Universitesi	2007
Y. Lisans	Bilgisayar Bilimi	University of Toronto	2009
Doktora	Bilgisayar Bilimi	University of Toronto	2012

5. **Akademik Unvanlar:**

Yardımcı Doçentlik Tarihi : Aralık 2012

Doçentlik Tarihi   : Nisan 2018

Profesörlük Tarihi   : Ağustos 2023

6. **Yönetilen Yüksek Lisans ve Doktora Tezleri**

   6.1.Yüksek Lisans Tezleri

   Devam edenler

   Tamamlananlar

   Eş-Danışmanlık : İbrahim Berber- Antalya Bilim Üniversitesi

   Eş-Danışmanlık : M. Edip Akay Houdjedj - Antalya Bilim Üniversitesi

   Eş-Danışmanlık : Yacine Marouf- Antalya Bilim Üniversitesi

   Eş-Danışmanlık : Aissa Houdjedj - Antalya Bilim Üniversitesi

   Eş-Danışmanlık : Ahmed A. T. Bahmed - Antalya Bilim Üniversitesi

   Eş-Danışmanlık : Ilyes Baali - Antalya Bilim Üniversitesi

   Eş-Danışmanlık : Rafsan Ahmed - Antalya Bilim Üniversitesi

   Eş-Danışmanlık : Serhan Aksoy - Antalya Bilim Üniversitesi

   Danışmanlık : Tunde Aderinwale - Antalya Bilim Üniversitesi

   Eş-danışmanlık : Atefeh Lafzi - ODTÜ Enformatik Enstitüsü

   Eş-danışmanlık: Saber HafezQorani - ODTÜ Enformatik Enstitüsü

Eş-danışmanlık: Udo Gieraths – Max Planck Institute in Tuebingen, Germany

6.2. Doktora Tezleri

Eş-danışmanlık: Aissa Houdjedj -Akdeniz University

7. Yayınlar

- **Uluslararası hakemli dergilerde yayınlanan makaleler (SCI & SSCI & Arts and Humanities)**

  - A Rasheed vd. (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, <u>H Kazan</u> (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, <u>H Kazan</u> (2020). DriveWays: a method for identifying possibly overlapping driver pathways in cancer. *Scientific Reports*, 10(1).

- M Yang,....<u>H Kazan</u>, ...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, <u>H Kazan</u>. MEXCOwalk: Mutual Exclusion and Coverage Based Random Walk to Identify Cancer Module (2019). *Bioinformatics*. doi.org/10.1093/bioinformatics/btz655.

- S HafezQorani, A Houdjedj, M Arıcı, A Said, <u>H Kazan</u>. RBPSponge. Genome-wide identification of lncRNAs that sponge RBPs (2019). *Bioinformatics*.10.1093/bioinformatics/btz448.

- DG Ozturk, M Kocak, A Akcay, K Kinoglu, E Kara, Y Buyuk, <u>H Kazan</u>, 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, <u>H Kazan</u> (2018) Predicting clinical outcomes in neuroblastoma with genomic data integration. *Biology Direct* 13 (1), 20.

- SK Zahr**,** G Yang, <u>H Kazan,</u> 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).

- <u>H Kazan</u> (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. A comprehensive database of high-throughput sequencing-based RNA secondary structure probing data (Structure Surfer) (2016). *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. Uluslararası diğer hakemli dergilerde yayınlanan makaleler

7.3 Uluslararası bilimsel toplantılarda sunulan ve bildiri kitabında (*Proceedings*) basılan bildiriler

- *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 pres.)

- *DriveWays: A Method for Identifying Possibly Overlapping Driver Pathways in Cancer oral presentation. I Baali, C Erten, H Kazan.* **ISMB** (29th Annual Conference on Intelligent Systems for Molecular Biology) 2021, virtual, July 25-30 2021 (oral pres.)

- *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) 2019, Barcelona, Nov 28-29 2019 Sayfa:119

- *A translational repression complex in developing mammalian neural stem cells that regulates neuronal specification,* SK Zahr**,** G Yang, <u>H Kazan,</u> MJ Borrett, SA Yuzwa**,** A Voronova, DR Kaplan**,** FD Miller. **Dagstuhl** (Dagstuhl Seminar 19342), Germany, 22 August 2019. Sayfa: 58

- *Predicting clinical outcomes in neuroblastoma with genomic data integration* I Baali, DAE Acar, T Aderinwale, S HafezQorani, <u>H Kazan</u> (2017) ISMB (25th Annual Conference on Intelligent Systems for Molecular Biology) 2017, CAMDA workshop, Prague, Czech Republic. (oral pres)

- S HafezQorani, <u>H Kazan.</u> (2017) Genome-wide identification of lncRNAs that sponge RNA-binding proteins. ISMB (25th Annual Conference on Intelligent Systems for Molecular Biology) 2017, RNA workshop, Prague, Czech Republic. (oral pres)

7.4. Yazılan uluslararası kitaplar veya kitaplarda bölümler

7.5. Ulusal hakemli dergilerde yayınlanan makaleler

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

7.6. Ulusal bilimsel toplantılarda sunulan ve bildiri kitabında basılan bildiriler

- *SCITUNA: A Network Alignment Approach for Integrating Multiple Single-Cell RNA-Seq Datasets.* O Dogan, BO Erten, C Erten, A Houdjedj, <u>H Kazan</u>, 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 pres.))

- *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, <u>H Kazan</u>. HIBIT **(**The International Symposium on Health Informatics and Bioinformatics) 2022, Oct 20-21 2022, METU campus in Erdemli, Mersin. (oral pres. 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, 10-11 Sept, Bilkent University, conducted online. (poster pres)

- *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, 10-11 Sept, Bilkent University, conducted online. (oral pres)

- *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 pres.)

- *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 pres)

- *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 Sayfa: 58. (oral pres)

- *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. Sayfa: 231 (poster pres)

- *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 pres)

- *MEXCOwalk: Kanser ile İlişkili Gen Modüllerinin Çıkarımı Üzerine bir Yöntem.* R Ahmed, I Baali, C Erten, E Hoxha, H Kazan. 4. Yaşam Bilimleri Kongresi, Kayseri, 22 Şubat 2019. (oral pres.)

- *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 pres.)

- *Integrating multiple data types for cancer subtype discovery.* T Aderinwale, H Kazan. HIBIkakaT 2017, 10th International Symposium on Health Informatics and Bioinformatics, Girne, Cyprus, June 28-30, 2017. (oral pres.)

- PUM1(2) proteinlerinin gen ifadesine olan etkilerinin susturma deneyi ile incelenmesi. S HafezQorani, H Kazan (2016). 5th National Molecular Biology and Biotechnology Congress, Ko67898787987nya, 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. Diğer yayınlar

7.8. Uluslararası Atıflar

Google Scholar'a gore toplam 4688 atıf bulunmaktadır.

8. Projeler

- **Araştırmacı: Tübitak 1001 projesi (2025-devam)**
  - İlaç Dirençli Üçlü Negatif Meme Kanserinin Tespitinde snoRNA-miRNA Tabanlı Biyobelirteç Paneli Oluşturulması
- **Araştırmacı: TÜSEB 202 B-01 (2023-2025)**
  - Tümörle ilişkili makrofajların plastisilerinde alternatif transcript izoformlarının biyobelirteç özelliklerinin tek hücre RNA sekanslama yaklaşımı ile araştırılması (16428)
- **Yürütücü: Tübitak 1001 Projesi (2022-2024)**

- ◦ Tek hücre veri setlerinin entegrasyonu için ağ hizalama tabanlı yenilikçi yaklaşımlar (121E491)
- **Yürütücü: TÜSEB 2019-TA-01 ARGE projesi (2020-2023)**
  - ◦ Omik verileriyle kişiye özgü kanser sürücü gen keşfine yönelik özgün hesapsal yaklaşımlar (4069)
- **Yürütücü: Hollanda ve Kanada ile ortak ERA-NET CVD Projesi (2019-2022)**
  - ◦ Nöroimmun rehberlik işaretleri, MikroRNAlar & İltihabi Tepki: Kardiyovsasküler hastalıklarda cinsiyet farklılıkları (118S930)
- **Yürütücü: TÜBİTAK 1001 Projesi (2018-2021)**
  - ◦ Kanserde gen ifadesinin çok boyutlu genomik verilerle incelenmesi ve kanser alt gruplarının belirlenmesi (117E789)
- **Yürütücü: FP7 Marie Curie Kariyer Projesi (2014-2018)**
  - ◦ Systematic study of post-transcriptional regulation mediated by RNA-binding proteins and miRNAs
- **Yürütücü: TÜBİTAK 3501 Kariyer Projesi (2013-2015)**
  - ◦ Mesajcı RNA'ların transkripsiyon sonrası regulasyonunda rol oynayan etmenlerin saptanması (113E159)

9. **İdari Görevler**
- Bilgisayar Mühendisliği Bölüm Başkan Yardımcılığı (2017 Mart-devam)
- Fen Bilimleri Enstitüsü Müdürlüğü (2015 Eylül-2017 Eylül)
- Bilgisayar Mühendisliği Bölüm Başkanlığı (2016 Eylül-2017 Şubat)

10. **Bilimsel ve Mesleki Kuruluşlara Üyelikler**

International Society of Computational Biology (ISCB)

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

12. **Son iki yılda verdiğiniz lisans ve lisansüstü düzeydeki dersler için aşağıdaki tabloyu doldurunuz.**

Akademik Yıl	Dönem	Dersin Adı	Haftalık Saati		Öğrenci Sayısı
			Teorik	Uygulama	
2023	Güz				
	İlkbahar	CS 445 – Makine Öğrenmesi (Lisans)	3		168
		DS 701- Veri Bilimine Giriş (Y. Lisans)	3		15
		DS 702 – Veri Bilimi İçin Uygulamalı İstatistik (Y. Lisans)	3		11
		ECE 700 – Seminer (Y. Lisans)	2		4
2022	Güz	CS 303 Programlama Dillerinin Temelleri (Lisans)	3		65
		DS 703 Makine Öğrenmesi (Y. Lisans)	3		13
		ECE 700 – Seminer (Y. Lisans)	2		1
	İlkbahar	CS 445 Makine Öğrenmesi (Lisans)	3		8
		DS 502 Veri Bilimi İçin Uygulamalı İstatistik (Y. Lisans)	3		4
		ECE 584 Graduate Seminar (Y. Lisans)	2		1

Not: Açılmışsa, yaz döneminde verilen dersler de tabloya ilave edilecektir.