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Current Position:

University of Texas, MD Anderson Cancer Center — Houston, TX
Instructor — 2018-Present

Education:

Ph.D. in Biomedical Sciences	UT GSBS/MD Anderson Cancer Center	2008 – 2013
B.S. in Genetic and Bioengineering	Yeditepe University (Istanbul/Turkey)	2003 – 2007
B.S. in Computer Engineering	Yeditepe University (Istanbul/Turkey)	2004 – 2008

Honors and Awards:

NCI – MD Anderson Brain SPORE CEP Award ($50K, role: PI)	2019-2020
Emerson Collective Cancer Research Fund ($200K, role: PI)	2018-2020
NSF, Junior Scientist Travel Award for CSHL Nuclear Organization Meeting	2016
Amazon Cloud AWG credit ($10K, role: co-PI)	2013
Best Poster - Graduate Student Award in Basic Science	2012
Graduate School Travel Award	2011
Center for Cancer Epigenetic Fellowship (full tuition & stipend support)	2010-2011
Yeditepe University Deans Scholar (full tuition & life expense support)	2003-2008

Research Experience and Training:

UT MD Anderson Cancer Center — Houston, TX
Post-doctoral Fellow. Advisor: Dr. Andrew Futreal — 2013-2018

- Chromatin dysregulation in cancer cells

UT MD Anderson Cancer Center — Houston, TX
Graduate Research Assistant. Advisors: Dr. Michelle Barton and Dr. Wei Li — 2008-2013

- Genome-wide profiling of p53 in human embryonic stem cells

Harvard Medical School — Cambridge, MA
Intern with Dr. Manoj Bhasin — Summer 2007

- A web-portal to query Microarray Output

Yeditepe University — Istanbul, Turkey
Undergraduate Research Assistant. Advisor: Dr. Hasan Out — 2007-2008

- A Genetic Algorithm to Cluster Microarray Data

Publications

Akdemir KC[#], Le V, Kim J, Killcoyne S, King DE, Inoue A, Amin S, Robinson FS, Nimmakayalu M, Herrera RE, Lynn EJ, Chan K, Seth S, Klimczak LJ, Gerstung M, Gordenin DA, O'Brien J, Li L, Deribe YL, Fitzgerald R, Campbell P, Verhaak RG, Gordenin D, Morrison A, Dixon J[#], Futreal PA[#]. Process-specific somatic mutation distributions vary with three-dimensional genome structure. *Nature Genetics (in press)*.
Co-corresponding authors

Akdemir KC, Le V, Chandran S, Li Y, Verhaak RG, Beroukhim R, Campbell P, Chin L, Dixon J, Futreal PA. Chromatin folding domain disruptions by somatic genome rearrangements in human cancers. *Nature Genetics (2020)*.

Genovese G, Carugo A, Tepper J, Robinson FS, Li L, Svelto M, Nezi L, Corti D, Minelli R, Pettazzoni P, Gutschner T, **Akdemir KC**, et al. 2017. Synthetic vulnerabilities of mesenchymal subpopulations in pancreatic cancer. *Nature* 542:362-6

Barthel FP, Wei W, Tang M, Martinez-Ledesma E, Hu X, Amin SB, **Akdemir KC**, Seth S, Song X, Wang Q, Lichtenberg T, Hu J, et al. 2017. Systematic analysis of telomere length and somatic alterations in 31 cancer types. *Nature Genetics* 49:349-57

Fiziev P*, **Akdemir KC*,** Miller JP, Keung EZ, Samant NS, Sharma S, Natale CA, Terranova CJ, Maitituoheti M, Amin SB, Martinez-Ledesma E, Dhamdhere M, et al. 2017. Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. *Cell Reports* 19:875-89.
* These authors contributed equally

Smyk M*, **Akdemir KC*,** Stankiewicz P. 2017. SOX9 chromatin folding domains correlate with its real and putative distant cis-regulatory elements. *Nucleus* 8:182-7. * These authors contributed equally

Szafranski P, Gambin T, Dharmadhikari AV, **Akdemir KC**, Jhangiani SN, Schuette J, Godiwala N, Yatsenko SA, Sebastian J, Madan-Khetarpal S, Surti U, Abellar RG, et al. 2016. Pathogenetics of alveolar capillary dysplasia with misalignment of pulmonary veins. *Human Genetics* 135:569-86

Lissanu Deribe Y, Shi Y, Rai K, Nezi L, Amin SB, Wu CC, **Akdemir KC**, Mahdavi M, Peng Q, Chang QE, Hornigold K, Arold ST, et al. 2016. Truncating PREX2 mutations activate its GEF activity and alter gene expression regulation in NRAS-mutant melanoma. *Proc Natl Acad Sci* U S A 113:E1296-305

Jain AK, Xi Y, McCarthy R, Allton K, **Akdemir KC**, Patel LR, Aronow B, Lin C, Li W, Yang L, Barton MC. 2016. LncPRESS1 Is a p53-Regulated LncRNA that Safeguards Pluripotency by Disrupting SIRT6-Mediated De-acetylation of Histone H3K56. *Molecular Cell* 64:967-81

Carugo A, Genovese G, Seth S, Nezi L, Rose JL, Bossi D, Cicalese A, Shah PK, Viale A, Pettazzoni PF, **Akdemir KC**, Bristow CA, et al. 2016. In Vivo Functional Platform Targeting Patient-Derived Xenografts Identifies WDR5-Myc Association as a Critical Determinant of Pancreatic Cancer. *Cell Reports* 16:133-47

Rai K, **Akdemir KC**, Kwong LN, Fiziev P, Wu CJ, Keung EZ, Sharma S, Samant NS, Williams M, Axelrad JB, Shah A, Yang D, et al. 2015. Dual Roles of RNF2 in Melanoma Progression. *Cancer Discovery* 5:1314-27

Keung EZ, **Akdemir KC**, Al Sannaa GA, Garnett J, Lev D, Torres KE, Lazar AJ, Rai K, Chin L. 2015. Increased H3K9me3 drives dedifferentiated phenotype via KLF6 repression in liposarcoma. *J Clin Invest* 125:2965-78

Akdemir KC, Chin L. 2015. HiCPlotter integrates genomic data with interaction matrices. *Genome Biology* 16:198

Akdemir KC*, Jain AK*, Allton K, Aronow B, Xu X, Cooney AJ, Li W, Barton MC. 2014. Genome-wide profiling reveals stimulus-specific functions of p53 during differentiation and DNA damage of human embryonic stem cells. *Nucleic Acids Res* 42:205-23. * These authors contributed equally

Henry SP, Liang S**, Akdemir KC**, de Crombrugghe B. 2012. The postnatal role of Sox9 in cartilage. *J Bone Miner Res* 27:2511-25

Wilson MA, Koutelou E, Hirsch C, **Akdemir K**, Schibler A, Barton MC, Dent SY. 2011. Ubp8 and SAGA regulate Snf1 AMP kinase activity. *Molecular Cell Biology* 31:3126-35

Tsai WW, Wang Z, Yiu TT, **Akdemir KC**, Xia W, Winter S, Tsai CY, Shi X, Schwarzer D, Plunkett W, Aronow B, Gozani O, et al. 2010. TRIM24 links a non-canonical histone signature to breast cancer. *Nature* 468:927-32

Kurinna S, Stratton SA, Tsai WW, **Akdemir KC**, Gu W, Singh P, Goode T, Darlington GJ, Barton MC. 2010. Direct activation of forkhead box O3 by tumor suppressors p53 and p73 is disrupted during liver regeneration in mice. *Hepatology* 52:1023-32

Consortia

Akdemir KC as part of PCAWG6 Structural Variations Subgroup:

The ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Network. Pan-cancer analysis of whole genomes. Nature (in press)

Li Y, Roberts ND, Weischenfeldt J, Wala JA, Shapira O, Schumacher SE, et al. Patterns of somatic structural variation in human cancer genomes. Nature (in press)

Rheinbay E, Nielsen MM, Abascal F, Tiao G, Hornshøj H, Hess JM, et al. On the discovery of somatic driver events in >2,500 whole cancer genomes. Nature (in press)

Rodriguez-Martin B, Alvarez EG, Baez-Ortega A, Zamora J, Supek F, Demeulemeester J, et al. Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics (in press)

Yuan Y, Ju YS, Kim Y, Li J, Wang Y, Yoon C, et al. Comprehensive Molecular Characterization of Mitochondrial Genomes in Human Cancers. Nature Genetics (in press)

Sieverling L, Hong C, Koser SD, Ginsbach P, Kleinheinz K, Hutter B, et al. Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications (in press)

Cortes-Ciriano I, Lee J-K, Xi R, Jain D, Jung YL, Yang L, et al. Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics (in press)

Akdemir KC as part of Analysis Working Group:

Cancer Genome Atlas N. 2015. Genomic Classification of Cutaneous Melanoma. *Cell* 161:1681-96

Commentary

Sarabipour S, Wissik EM, Burgess SJ, Hensel Z, Debat H, Emmott E, Akay A, **Akdemir KC**, Schwessinger B. 2018. Preprints: good for science and public. *Nature*.
Preprint available at: https://peerj.com/preprints/27098/

Presentations

Invited Talks

2020	NCI Multi-center BRAIN SPORE Meeting
2020	Telluride Science Research Center Workshop on Physical Genomics and Transcriptional Engineering
2019	Oregon Health and Science University, Portland, OR
2019	MD Anderson Cancer Medicine Grand Rounds
2019	Genentech, San Francisco, CA
2018	Ontario Institute of Cancer Research (OICR), Toronto, ON, Canada
2018	University of Rochester, Wilmot Cancer Institute, NY

Conference Talks (selected based on an abstract)

2018	American Society of Human Genetics (ASHG), San Diego, CA
2017	Society of Molecular Biology and Evolution Annual Meeting (SMBE), Austin, TX
2017	CSHL System Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY
2017	Keystone Conference: Epigenetic and Human Diseases, Seattle, WA
2016	Genomics of Common Diseases, Baltimore, MD
2016	CSHL Nuclear Organization and Function, Cold Spring Harbor, NY
2015	Human Genome Organization Annual International Meeting (HUGO), Houston, TX
2014	3rd TCGA Scientific Symposium, NIH, Bethesda, MD

Poster Presentations

2019	American Society of Human Genetics (ASHG), Houston, TX – *Reviewer's Choice Award*
2019	American Association of Cancer Research (AACR), Atlanta, GA
2018	CSHL Nuclear Organization and Function, Cold Spring Harbor, NY
2018	American Association of Cancer Research (AACR), Chicago, IL
2016	Epigenomic 2016, San Juan, PR
2016	NY Epigenomics Symposium, New York Genome Center, New York, NY
2015	Keystone Conference: Epigenomic and DNA Methylation, Keystone, CO
2013	4th NIGMS Workshop on Human Stem Cell Research, NIH, Bethesda, MD
2011	CSHL Genome Informatics, Cold Spring Harbor, NY

Teaching and Services

2019	Mentoring CPRIT Summer Student – Justin Kim, Brown University (Extrachromosomal oncogene amplifications in osteosarcoma tumors)
2017-18	eLife Early Career Research Ambassador (Promoting preprints and reproducible science)
2018	Mentoring CPRIT Summer Student – Caleb Kroll, Dartmouth College (BLC11B translocations in mixed lineage leukemia cells)
2015-present	Ad hoc reviewer with BMC Bioinformatics, Genome Biology, NAR Cancer
2012	Graduate School Bioinformatics Workshop Series Organizer (A set of hands-on workshops on online bioinformatics tools – Galaxy or Genome Browsers)
2006	Undergraduate Peer Teaching Assistant (C-Programming, Data Structure Labs)

References

P. Andrew Futreal, Ph.D. (Post-doctoral advisor)

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Michelle C. Barton, Ph.D. (Thesis advisor)

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Updated on July 27, 2020