

Aziz Khan

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EDUCATION

Tsinghua University, Beijing, China

Ph.D. in Bioinformatics (Computational Biology) 2012 – 2016
Dissertation: Prediction, analysis and annotation of super-enhancers in the human and mouse genomes
Adviser: Prof. Xuegong Zhang

National University of Computer & Emerging Sciences, Islamabad, Pakistan

MS in Computer Science 2008 – 2010

Quaid-I-Azam University, Islamabad, Pakistan

MSc in Information Technology 2006 – 2008

Forman Christian College, Lahore, Pakistan

BSc in Mathematics and Physics 2003 – 2005

RESEARCH EXPERIENCE

Research Scientist, Curtis Lab, Stanford Cancer Institute, Stanford University 2019 – present

Postdoctoral Research Fellow, Mathelier Lab, NCMM, University of Oslo 2016 – 2019

PhD Student, Xuegong Lab, Bioinformatic Division, Tsinghua University 2012 – 2016

Rotation Student, Jingren Lab, School of Medicine, Tsinghua University 2012

Rotation Student, Tao Jiang, Tsinghua University & University of California - Riverside 2013

RESEARCH INTERESTS

Computational biology, machine learning, transcriptional gene regulation, regulatory genomics and epigenomics, integrative analysis of bulk/single-cell omics data, and resource development

PUBLICATIONS & PREPRINTS

1. Fornes O*, Castro-Mondragon JA*, **Khan A*** et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles, *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
2. **Khan A⁺**, Zhang X⁺. Integrative modeling reveals key chromatin and sequence signatures predicting super-enhancers, *Scientific Reports* 2019; 9:2877
3. Feng H, Bao S, Rahman MA, Weyn-Vanhentenryck SM, **Khan A** et al. Modeling RNA-binding protein specificity in vivo by precisely registering protein-RNA crosslink sites, *Molecular Cell* 2019; 74(6):1189-1204
4. Itkonen HM, Urbanucci A, Martin SES, **Khan A** et al. High OGT activity is essential for MYC-driven proliferation of prostate cancer cells, *Theranostics* 2019; 9(8):2183-2197
5. **Khan A⁺**, Mathelier A, Zhang X. Super-enhancers are transcriptionally more active and cell-type-specific than stretch enhancers, *Epigenetics* 2018; 13(9):910-922
6. **Khan A**, Zhang X. Making genome browsers portable and personal, *Genome Biology* 2018; 19:93
7. **Khan A⁺**, Montenegro-Montero A, Mathelier A⁺. Put science first and formatting later, *EMBO reports* 2018; 19(5):e45731
8. **Khan A***, Fornes O*, Stigliani A* et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework, *Nucleic Acids Res.* 2018; 46(D1):D260-D26
9. Gheorghe M, Sandve GK, **Khan A**, et al. A map of direct TF-DNA interactions in the human genome, *Nucleic Acids Res.* 2018; 47(4):e21
10. The Bioconda Team et al. Bioconda: sustainable and comprehensive software distribution for the life sciences, *Nature Methods* 2018; 15:475-476
11. **Khan A⁺**, Mathelier A⁺. JASPAR RESTful API: accessing JASPAR data from any programming language, *Bioinformatics* 2018; 34(9):1612-1614
12. **Khan A⁺**, Mathelier A⁺. Intervene: a tool for intersection and visualization of multiple gene or genomic region sets, *BMC Bioinformatics* 2017;18:287
13. **Khan A**, Zhang X. dbSUPER: a database of super-enhancers in mouse and human genome, *Nucleic Acids Res.* 2016, 44(D1):D164-D171

*co-first authors, ⁺co-corresponding authors

AWARDS AND FELLOWSHIPS	CSC fully-funded PhD Scholarship , Tsinghua University, China	2012 – 2016
	Erasmus+ mobility grant , University of Oslo, Norway	Aug 2019
	OBF Travel Fellowship , ISMB/ECCB 2019, Basel, Switzerland	May 2019
	Biocuration Travel Fellowship , Biocuration Conference 2019, Cambridge, UK	Apr 2019
	Biocuration Travel Fellowship , Biocuration Conference 2018, Shanghai, China	Apr 2018
	Research Travel Grant , Higher Education Commission (HEC), Pakistan	2016 and 2012
	TWAS BIOVISION.Next Fellowship , BioVision conference, Lyon, France	2014 and 2013
PROFESSIONAL EXPERIENCE	Intern , Merck, Beijing, China	2014 – 2015
	Consultant , Microfinance Opportunities, Washington, D.C. USA (Freelance)	2011 – 2016
	Founder and CEO , ASN tECH, Islamabad, Pakistan	2012 – 2013
	Web Developer , Pearl Communications, Islamabad, Pakistan	2011 – 2012
	Software Engineer , Value Technologies, Islamabad, Pakistan	2010 – 2011
	Intern , a joint project by Harvard Univ & FMFB, AKDN, Islamabad, Pakistan	2009 – 2010
ADMINISTRATIVE EXPERIENCE	Co-Chair , Web Committee, ISCB Student Council	2016 – 2019
	Organizer , Young Investigator Meeting (YIM), University of Oslo, Norway	Sep 2018
	Chair Web Committee , ISCB African Student Symposium 2017, Entebbe, Uganda	Oct 2017
	Organizer , Young Investigator Meeting (YIM), University of Helsinki, Finland	Sep 2017
	Co-Chair , Tuesday Seminars, NCMM, University of Oslo	2017 – 2018
	Organizer , Tsinghua ENCODE Journal Club	2013 – 2014
PROFESSIONAL DEVELOPMENT ACTIVITIES	Co-Supervisor , Master student thesis (Kübra Altunel)	
	Reviewer , NAR, Genome Biology, Bioinformatics, BMC Bioinfo., Database, & PLOS ONE	
	Reviewer , ISCB Student Council Symposiums, 2015, 2016, 2017, 2018	
PROFESSIONAL AFFILIATIONS	Ambassador , eLife and ASAPbio	2018 – Present
	Member , International Society for Computational Biology (ISCB)	2015 – Present
	Member , NORBIS and Centre for Digital Life Norway, Norway	2017 – Present
	Member , International Society for Biocuration (ISB)	2015 – Present
PROGRAMMING & OTHER SKILLS	Languages : Python, R/Bioconductor, Shell scripting, PHP, SQL, C++	
	Tools/Resources : Bowtie, BWA, STAR, MACS, Tophat, Cufflinks, BEDTools, samtools, DEGseq, Salmon, Galaxy, MEME, HOMER, deepTools, Snakemake, Genome Browsers etc.	
	Web development : MVC, Django, Laravel, WordPress, R Shiny, jQuery/Ajax, HTML5, REST	
	Databases : MySQL, SQLite, MongoDB	
	Operating systems : Unix/Linux/Ubuntu, Mac OS, Windows	
	Other tools : Git, TravisCI, scikit-learn, Weka, Docker, L ^A T _E X, MATLAB, D3.js, Adobe Suite.	
SOFTWARE & RESOURCES DEVELOPED	JASPAR , an open and widely used database of transcription factor binding profiles - jaspar.genereg.net	
	Intervene , a Python tool for intersection & visualization of multiple sets - intervene.rtfid.io	
	dbSUPER , a database of super-enhancers - bioinfo.au.tsinghua.edu.cn/dbsuper	
	JASPAR REST API , programmatic access to TF binding profile data - jaspar.genereg.net/api	
	Intervene Shiny App , an app for intersection & visualization of sets - asntech.shinyapps.io/intervene	
	UniBind , a uniformly processed database of transcription factor binding sites - unibind.uio.no	
	mCrossBase , a database of RBP binding motifs and crosslink sites	
	ECRcentral , a central platform for early career researchers and postdocs - ecrcentral.org	
	imPROSE , Integrated methods to predict super-enhancers - asntech.github.io/improse/	

VOLUNTEER & SOCIAL WORK	Volunteer , ISMB/ECCB 2017, Prague	Jul 2017
	Volunteer , ISMB/ECCB 2015, Dublin	Jul 2015
	Volunteer , ICML (International Conference on Machine Learning), Beijing	Jun 2014
	Web administrator , Migrant Children’s Foundation (MCF), China	2013 – 2018
	Volunteer , RECOMB 2013, Beijing	Apr 2013
TALKS AND POSTER PRESENTATIONS	1. ECRcentral: Bringing early-career researchers and funding opportunities together, <i>ISMB/ECCB 2019</i> , Basel, Switzerland. Jul 2017. - [Talk and Poster]	
	2. Facilitating community-based curation of transcription factor binding profiles in JASPAR, <i>12th International Biocuration Conference</i> , Cambridge, UK Apr 2019. - [Poster]	
	3. A dynamic landscape of enhancer clusters during mouse development, <i>CSHL meeting on Epigenetics and Chromatin</i> , New York, USA. Sep 2018. - [Poster]	
	4. Towards a format-free submission policy: Let’s put science first, <i>2nd annual conference of Digital Life Norway Research School</i> , Stiklestad, Norway. Jun 2018. - [Talk]	
	5. JASPAR: a comprehensive database of transcription factor binding profiles, <i>11th International Biocuration Conference</i> , Shanghai Apr 2018. - [Poster and Talk]	
	6. A novel web framework and RESTful API for the JASPAR database of transcription factor binding profiles, <i>3rd annual conference of NORBIS</i> , Tromsø, Norway. Nov 2017. - [Poster]	
	7. JASPAR RESTful API: accessing JASPAR data from any programming languages, <i>GREEKC Training on Knowledge Commons and Tools interoperability</i> , Lisbon, Portugal Oct 2017. - [Talk]	
	8. Intervene: a tool for intersection and visualization of multiple gene or genomic region sets, <i>ISCB Student Council Symposium, ISMB/ECCB</i> , Prague, Czech Republic. Jul 2017. - [Talk and Poster]	
	9. Comprehensive analysis, prediction, and annotation of super-enhancers, <i>Sven Furberg Seminar in Bioinformatics and Statistical Genomics</i> , Oslo, Norway, Apr 2017. - [Talk]	
	10. Integrative analysis reveals significant differences between super and stretch enhancers, <i>Gene Expression Data Analysis</i> , Mainz, Germany, Nov 2016. - [Poster and Talk]	
	11. Computational prediction, characterization & annotation of super-enhancers & analysis of their key features, <i>CSHA - Chromatin, Epig. & Trans.</i> , Suzhou, China, May 2016. - [Poster]	
	12. dbSUPER - an extensive and interactive database of super-enhancers, <i>CSHA/AACR Meeting - Big Data, Comp. & Sys. Bio. in Cancer</i> , Suzhou, China, Dec 2015. - [Poster]	
	13. Super-enhancer prediction from epigenetic signatures and sequence motif data, <i>ISMB/ECCB 2015</i> , Dublin, Ireland, Jul 2015. - [Poster]	
	14. An extensive and interactive database of super-enhancers – dbSUPER, <i>ISCB Student Council Symposium 2015</i> , Dublin, Ireland, Jul 2015. - [Poster]	
	15. An extensive and interactive database of super-enhancers – dbSUPER, <i>8th International Biocuration Conference (IBC)</i> , Beijing Apr 2015. - [Poster]	
	16. Integration of ChIP-seq and machine learning reveals super-enhancers and features of biological significance, <i>Synthetic Biology Workshops</i> , Tsinghua University, May 2014. - [Talk]	
LANGUAGES	English: Fluent (speaking, reading, writing) Urdu: Native language Shinah: Mother tongue Chinese: Basic Norwegian: Basic	
INTERESTS	Volunteering, sports (football and badminton), gardening, photography, and cooking.	
REFERENCES	References are available upon request.	