

# Aziz Khan

Centre for Molecular Medicine Norway (NCMM), University of Oslo, Norway  
aziz.khan@ncmm.uio.no • +47 -46379301 • asntech.github.io • github.com/asntech • publons.com/a/382123 • orcid.org/0000-0002-6459-6224

## EDUCATION

**Tsinghua University**, Beijing, China

Ph.D. in Control Science and Engineering (**Bioinformatics**) 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

**Postdoctoral Research Fellow**, Mathelier Lab, NCMM, University of Oslo 2016 - present

**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. **A. Khan**<sup>+</sup> and X. Zhang<sup>+</sup>, Integrative modeling reveals key chromatin and sequence signatures predicting super-enhancers, *Scientific Reports* 2019; doi:10.1038/s41598-019-38979-9.
2. H. Feng, S. Bao, S.M. Weyn-Vanhentenryck, **A. Khan** et al. Modeling RNA-binding protein specificity in vivo by precisely registering protein-RNA crosslink sites, *Molecular Cell* 2019; 74(6):1189-1204.e6
3. H.M. Itkonen, A. Urbanucci, S.ES Martin, **A. Khan** et al. High OGT activity is essential for MYC-driven proliferation of prostate cancer cells, *Theranostics* 2019; 9(8):2183-2197
4. **A. Khan**<sup>+</sup>, A. Mathelier and X. Zhang, Super-enhancers are transcriptionally more active and cell-type-specific than stretch enhancers, *Epigenetics* 2018. doi: 10.1080/15592294.2018.1514231.
5. **A. Khan** and X. Zhang, Making genome browsers portable and personal, *Genome Biology* 2018; 19:93, doi: 10.1186/s13059-018-1470-9.
6. **A. Khan**<sup>+</sup>, A. Montenegro-Montero and A. Mathelier<sup>+</sup>, Put science first and formatting later, *EMBO reports* 2018; 19(5):e45731, doi: 10.15252/embr.201845731.
7. **A. Khan**<sup>\*</sup>, O. Fornes<sup>\*</sup>, A. Stigliani<sup>\*</sup> 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.
8. M. Gheorghe, GK Sandve, **A. Khan**, et al. A map of direct TF-DNA interactions in the human genome, *Nucleic Acids Res.* 2018; doi: 10.1093/nar/gky1210.
9. The Bioconda Team et al., Bioconda: sustainable and comprehensive software distribution for the life sciences, *Nature Methods* 2018, 15:475–476.
10. **A. Khan**<sup>+</sup> and A. Mathelier<sup>+</sup>, JASPAR RESTful API: accessing JASPAR data from any programming language, *Bioinformatics* 2018; 34(9):1612-1614.
11. **A. Khan**<sup>+</sup> and A. Mathelier<sup>+</sup>, Intervene: a tool for intersection and visualization of multiple gene or genomic region sets, *BMC Bioinformatics* 2017;18:287.
12. **A. Khan** and X. Zhang, dbSUPER: a database of super-enhancers in mouse and human genome, *Nucleic Acids Res.* 2016, 44(D1):D164–D171.
13. M. Ishtiaq<sup>\*</sup>, **A. Khan**<sup>\*</sup>, M.A. Jaffar, H.J. Kim, A hybrid feature selection approach by combining miD and miQ, *ITFE Summer Conference* 2011, South Korea, (1), 367-373.

<sup>\*</sup>co-first authors, <sup>+</sup>co-corresponding authors

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

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