

Stanford



Aziz Khan

Research Scientist, Stanford Cancer Institute

Bio

BIO

Aziz is a computational biologist in Curtis lab at the Stanford Cancer Institute, where he develops reproducible pipelines and machine learning methods for integrative analysis of multi-omics data at bulk and single-cell resolution to understand tumor evolution and chromatin regulatory dynamics of tumor growth.

Aziz completed his PhD in Bioinformatics at Tsinghua University, China in 2016 followed by a three year postdoctoral training at the University of Oslo, Norway. During PhD and Postdoc his primary research emphasis was on regulatory genomics and epigenomics. He developed computational methods, tools, and resources to understand the (epi)genomic control of gene regulation in development and disease.

Apart from research, he is advocating for open science, open source, preprints, and reproducibility in research. He is a contributor for Bioconda and also developed several open source tools and resources such as JASPAR. He is ASAPbio and eLife Community Ambassador and co-founded ECRcentral (ecrcentral.org), a community initiative for early-career researchers.

HONORS AND AWARDS

- CSC fully-funded PhD Scholarship, Chinese Scholarship Council (2012 – 2016)
- Erasmus+ mobility grant, European Commission (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)
- TWAS BIOVISION.Next Fellowship, BioVision conference, Lyon, France (2014)
- TWAS BIOVISION.Next Fellowship, BioVision conference, Lyon, France (2013)
- Research Travel Grant, Higher Education Commission (HEC), Pakistan (2012)

EDUCATION AND CERTIFICATIONS

- PhD, Tsinghua University, China , Bioinformatics (2016)
- Postdoctoral Fellow, NCMM, University of Oslo, Norway , Computational Biology (2019)

LINKS

- Personal Site: <https://asntech.github.io/>
- ECRcentral: <https://ecrcentral.org>

- JASPAR database: <http://jaspar.genereg.net>

Publications

PUBLICATIONS

- **The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution.** *Cell*
Rozenblatt-Rosen, O., Regev, A., Oberdoerffer, P., Nawy, T., Hupalowska, A., Rood, J. E., Ashenberg, O., Cerami, E., Coffey, R. J., Demir, E., Ding, L., Esplin, E. D., Ford, et al
2020; 181 (2): 236–49
- **JASPAR 2020: update of the open-access database of transcription factor binding profiles.** *Nucleic acids research*
Fornes, O., Castro-Mondragon, J. A., Khan, A., van der Lee, R., Zhang, X., Richmond, P. A., Modi, B. P., Correard, S., Gheorghe, M., Baranasic, D., Santana-Garcia, W., Tan, G., Cheneby, et al
2019
- **Modeling RNA-Binding Protein Specificity In Vivo by Precisely Registering Protein-RNA Crosslink Sites** *MOLECULAR CELL*
Feng, H., Bao, S., Rahman, M., Weyn-Vanhentenryck, S. M., Khan, A., Wong, J., Shah, A., Flynn, E. D., Krainer, A. R., Zhang, C.
2019; 74 (6): 1189–+
- **A map of direct TF-DNA interactions in the human genome** *NUCLEIC ACIDS RESEARCH*
Gheorghe, M., Sandve, G., Khan, A., Cheneby, J., Ballester, B., Mathelier, A.
2019; 47 (4): e21
- **Integrative modeling reveals key chromatin and sequence signatures predicting super-enhancers** *SCIENTIFIC REPORTS*
Khan, A., Zhang, X.
2019; 9: 2877
- **High OGT activity is essential for MYC-driven proliferation of prostate cancer cells** *THERANOSTICS*
Ikonen, H. M., Urbanucci, A., Martin, S. S., Khan, A., Mathelier, A., Thiede, B., Walker, S., Mills, I. G.
2019; 9 (8): 2183–97
- **Making genome browsers portable and personal** *GENOME BIOLOGY*
Khan, A., Zhang, X.
2018; 19: 93
- **JASPAR RESTful API: accessing JASPAR data from any programming language** *BIOINFORMATICS*
Khan, A., Mathelier, A.
2018; 34 (9): 1612–14
- **Put science first and formatting later** *EMBO REPORTS*
Khan, A., Montenegro-Montero, A., Mathelier, A.
2018; 19 (5)
- **JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework** *NUCLEIC ACIDS RESEARCH*
Khan, A., Fornes, O., Stigliani, A., Gheorghe, M., Castro-Mondragon, J. A., van der Lee, R., Bessy, A., Cheneby, J., Kulkarni, S. R., Tan, G., Baranasic, D., Arenillas, D. J., Sandelin, et al
2018; 46 (D1): D260–D266
- **Super-enhancers are transcriptionally more active and cell type-specific than stretch enhancers** *EPIGENETICS*
Khan, A., Mathelier, A., Zhang, X.
2018; 13 (9): 910–22
- **Bioconda: sustainable and comprehensive software distribution for the life sciences.** *Nature methods*
Grüning, B., Dale, R., Sjödin, A., Chapman, B. A., Rowe, J., Tomkins-Tinch, C. H., Valieris, R., Köster, J.
2018; 15 (7): 475–76
- **Intervene: a tool for intersection and visualization of multiple gene or genomic region sets** *BMC BIOINFORMATICS*
Khan, A., Mathelier, A.
2017; 18: 287

- **dbSUPER: a database of super-enhancers in mouse and human genome.** *Nucleic acids research*
Khan, A., Zhang, X.
2016; 44 (D1): D164–71