

Zhijian Li

Institute for Computational Genomics
RWTH Aachen University
MTZ, Pauwelstr 19, 52074 Aachen
Email: zhijian.li@rwth-aachen.de
Website: <https://lzj1769.github.io/>

Education

2016 - 2022 Ph.D., Computer Science, RWTH Aachen University, Germany
2014 - 2016 M.Sc., Computer Science, Central China Normal University, China
2008 - 2012 B.S., Computer Science, Jilin University, China

Awards

2022 Outstanding Self-financed Students Abroad, China Scholarship Council (CSC)
2021 Poster Award of e:Med Meeting on Systems Medicine 2021, Germany
2016 Outstanding Master Thesis of Central China Normal University
2015 National Scholarship of China

Presentations

2021 Flash Talk & Poster Presentation, e:Med Meeting on Systems Medicine 2021, Germany
2020 Regular Talk, ECCB 2020
2020 Poster Presentation, ISMB 2020
2019 Poster Presentation, ISMB/ECCB 2019
2018 Regular Talk, ISMB 2018
2018 Poster Presentation, RECOMB 2018

Publications

Co-first authors; * Co-corresponding authors

First/co-first author papers

7. **Z Li**[#], C C Kuo[#], F Ticconi, M Shaigan, E G Gusmao, M Allhoff, M Manolov, I G Costa.
RGT: a toolbox for the integrative analysis of high throughput regulatory genomics data.
(2022) (Submitted)

6. C Kuppe[#], **Z Li**[#], R T Levinson[#], P B Mompel[#], T Lu, R Flores, M Halder, M Cheng, X Zhang, R K Schneider, R Thadhani, S Hayat, K Lim, I G Costa*, J S Rodriguez*, R Kramann*. Integrative single-cell multi-omics analysis reveals traits associated with early heart failure. (2022) (Submitted)
5. **Z Li**, J Nagai, C Kuppe, R Kramann, I G Costa. scMEGA: Single-cell Multiomic Enhancer-based Gene Regulatory Network Inference. **Biorxiv** (2022)
4. C Kuppe[#], R O R Flores[#], **Z Li**[#], S Hayat, R T Levinson, X Liao, M T Hannani, J Tanevski, F Wünnemann, J S Nagai, M Halder, D Schumacher, S Menzel, G Schäfer, K Hoeft, M Cheng, S Ziegler, X Zhang, F Peisker, N Kaesler, T Saritas, Y Xu, A Kassner, J Gummert, M Morshuis, J Amrute, R J A Veltrop, P Boor, K Klingel, L W Van Laake, A Vink, R M Hoogenboezem, E M J Bindels, L Schurgers, S Sattler, D Schapiro, R K Schneider, K Lavine, H Milting*, I G Costa*, J Saez-Rodriguez* and R Kramann*. Spatial multi-omic map of human myocardial infarction. **Nature** (2022)
3. **Z Li**[#], C Kuppe[#], S Ziegler, M Cheng, N Kabgani, S Menzel, M Zenke, R Kramann*, I G Costa*. Chromatin-accessibility estimation of single-cell ATAC-seq data with scOpen. **Nature Communications** (2021).
2. **Z Li**, M H Schulz, T Look, M Begemann, M Zenke, I G Costa. Identification of transcription factor binding sites using ATAC-seq. **Genome Biology** (2019).
1. **Z Li**, J Guo, S Yang. Improving the JADE Algorithm by Clustering Successful Parameters. **International Journal of Wireless and Mobile Computing** (2016).

Contributed papers

11. E.F Brandt, T.H Wirtz, **Z Li**, M.M Ibrahim, P Fischer, A Beckers, A Flabhove, I.G Costa, R Kramann, E.P.C van der Vorst, C Liedtke, H Sahin, C Trautwein, M.L Berres. CXCR3-expressing macrophages regulate angiogenesis, tumor cell proliferation and immune evasion in hepatocellular carcinoma. (2022) (Submitted).
10. K Ohi, J Hriczko, S Schulz, T Look, T Goodarzi, S.H Subramanyam, T Clarner, M Scheld, M Kipp, E Verjans, S Böll, I.G Costa, **Z Li**, L Gan, B Denecke, A Schippers, S Floess, J Huehn, E Schmitt, T Bopp, R Beyaert, B Lambrecht, M Zenke, N Wagner, K Tenbrock. Foxp3-specific deletion of CREB generates Th2 biased ST-2 positive regulatory T-cells with enhanced IL-10 production and suppressive capacity. (2022) (Submitted).
9. D Schumacher[#], M Cheng[#], C Kuppe, E M Bindels, R K Schneider, **Z Li**, I G Costa*, R Kramann*. Single Nucleus ATAC Sequencing Reveals Epigenomic Regulation After Myocardial Infarction. (2022) (Submitted).
8. Y Xu, C Kuppe, JP Patón, S Hayat, J Kranz, A T Abdallah, J Nagai, **Z Li**, F Peisker, T Saritas, M Halder, S Menzel, K Hoeft, A Kenter, H Kim, C van Roeyen, M Lehrke, J Moellmann, T Speer, E M Buhl, R Hoogenboezem, P Boor, J Jansen, C Knopp, I Kurth, B Smeets, E Bindels, M Reinders, C Baan, J Gribnau, E Hoorn, J Steffens, T Huber, I G Costa, J Floege, R K. Schneider, J Saez-Rodriguez, B S. Freedman and R Kramann. Adult human kidney

organoids originate from CD24+ cells and represent an advanced model for adult polycystic kidney disease. **Nature Genetics** (2022).

7. H Xu, **Z Li**, C C Kuo, K Götz, T Look, MAS de Toledo, K Seré, I G Costa and M Zenke. A lncRNA identifies IRF8 enhancer in feedback control of DC development. **Biorxiv** (2022).
6. M Cheng, **Z Li**, I G Costa. MOJITOO: a fast and universal method for integration of multi-modal single cell data. **Bioinformatics** (2022).
5. S Heller, **Z Li**, Q Lin, R Geusz, M Breunig, M Hohwieler, X Zhang, G Nair, T Seufferlein, M Hebrok, M Sander, C Julier, A Kleger*, I G Costa*. Transcriptional changes and the role of ONECUT1 in hPSC pancreatic differentiation. **Communications Biology** (2021).
4. A Philippi[#], S Heller[#], I G Costa[#], V Senée[#], M Breunig, **Z Li**, G Kwon, R Russell, A Illing, Q Lin, M Hohwieler, A Degavre, P Zalloua, S Liebau, M Schuster, J Krumm, X Zhang, R Geusz, J.R Benthuyssen, A Wang, J Chiou, K Gaulton, H Neubauer, E Simon, T Klein, M Wagner, G Nair, C Besse, C Dandine-Roulland, R Olaso, J Deleuze, B Kuster, M Hebrok, T Seufferlein, M Sander, B.O Boehm, F Oswald, M Nicolino*, C Julier*, A Kleger*. Mutations and variants of ONECUT1 in diabetes. **Nature Medicine** (2021).
3. J Guo, **Z Li**, S Yang. Accelerating differential evolution based on a subset-to-subset survivor selection operator. **Soft Computing** (2019).
2. J Guo, W Xie, **Z Li**. Enhancing JADE utilizing distance of best solutions. **Computer Engineering and Design** (2018).
1. J Guo, **Z Li**, W Xie, H Wang. Dissipative differential evolution with self-adaptive control parameters. **IEEE Congress on Evolutionary Computation** (2015).