## Zeynep Kalender Atak

## List of Publications by Year

 in descending orderSource: https:/|exaly.com/author-pdf/9460958/publications.pdf
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| 1 | A Multi-Omics Analysis of Metastatic Melanoma Identifies a Germinal Center-Like Tumor Microenvironment in HLA-DR-Positive Tumor Areas. Frontiers in Oncology, 2021, 11, 636057. | 1.3 | 8 |
| :---: | :---: | :---: | :---: |
| 2 | $14 q 32$ rearrangements deregulating <i>BCL11B </i>mark a distinct subgroup of T and myeloid immature acute leukemia. Blood, 2021, 138, 773-784. | 0.6 | 19 |
| 3 | Interpretation of allele-specific chromatin accessibility using cell stateâ€"aware deep learning. Genome Research, 2021, 31, 1082-1096. | 2.4 | 34 |
| 4 | Robust gene expression programs underlie recurrent cell states and phenotype switching in melanoma. Nature Cell Biology, 2020, 22, 986-998. | 4.6 | 148 |
| 5 | Yin Yang 1 sustains biosynthetic demands during brain development in a stage-specific manner. Nature Communications, 2019, 10, 2192. | 5.8 | 28 |
| 6 | Yin Yang 1 Orchestrates a Metabolic Program Required for Both Neural Crest Development and Melanoma Formation. Cell Stem Cell, 2019, 24, 637-653.e9. | 5.2 | 44 |
| 7 | Mapping gene regulatory networks from single-cell omics data. Briefings in Functional Genomics, 2018, 17, 246-254. | 1.3 | 194 |
| 8 | A comprehensive inventory of TLX1 controlled long non-coding RNAs in T-cell acute lymphoblastic leukemia through polyA+ and total RNA sequencing. Haematologica, 2018, 103, e585-e589. | 1.7 | 20 |
| 9 | Decoding transcriptional states in cancer. Current Opinion in Genetics and Development, 2017, 43, 82-92. | 1.5 | 7 |

10 SCENIC: single-cell regulatory network inference and clustering. Nature Methods, 2017, 14, 1083-1086. 9.0 3,086
Identification of cis-regulatory mutations generating de novo edges in personalized cancer gene 11 regulatory networks. Genome Medicine, 2017, 9, 80.
3.6 ..... 17
Multiplex enhancer-reporter assays uncover unsophisticated TP53 enhancer logic. Genome Research, ..... 2.4 ..... 70
2016, 26, 882-895.
1.5 ..... 21Identification of High-Impact cis-Regulatory Mutations Using Transcription Factor Specific RandomForest Models. PLoS Computational Biology, 2015, 11, e1004590.Decoding the regulatory landscape of melanoma reveals TEADS as regulators of the invasive cellstate. Nature Communications, 2015, 6, 6683.

20 Comprehensive Analysis of Transcriptome Variation Uncovers Known and Novel Driver Events in

