

# JÃ¼ri Reimand

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

13,575  
citations

81900

39  
h-index

114465

63  
g-index

78  
all docs

78  
docs citations

78  
times ranked

25950  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Mutations in Noncoding <i>Cis</i> -Regulatory Elements Reveal Cancer Driver Cistromes in Luminal Breast Cancer. <i>Molecular Cancer Research</i> , 2022, 20, 102-113.  | 3.4  | 3         |
| 2  | Human phospho€ signaling networks of SARSâ€CoVâ€2 infection are rewired by population genetic variants. <i>Molecular Systems Biology</i> , 2022, 18, e10823.   | 7.2  | 8         |
| 3  | ActiveDriverDB: Interpreting Genetic Variation in Human and Cancer Genomes Using Post-translational Modification Sites and Signaling Networks (2021 Update). <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 626821.                                       | 3.7  | 12        |
| 4  | The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.   | 12.8 | 47        |
| 5  | Functional and genetic determinants of mutation rate variability in regulatory elements of cancer genomes. <i>Genome Biology</i> , 2021, 22, 133.  | 8.8  | 12        |
| 6  | Single allele loss-of-function mutations select and sculpt conditional cooperative networks in breast cancer. <i>Nature Communications</i> , 2021, 12, 5238.   | 12.8 | 8         |
| 7  | Pan-cancer analysis of non-coding transcripts reveals the prognostic onco-lncRNA HOXA10-AS in gliomas. <i>Cell Reports</i> , 2021, 37, 109873.   | 6.4  | 13        |
| 8  | Phosphoproteome and drug-response effects mediated by the three protein phosphatase 2A inhibitor proteins CIP2A, SET, and PME-1. <i>Journal of Biological Chemistry</i> , 2020, 295, 4194-4211.  | 3.4  | 48        |
| 9  | Candidate Cancer Driver Mutations in Distal Regulatory Elements and Long-Range Chromatin Interaction Networks. <i>Molecular Cell</i> , 2020, 77, 1307-1321.e10.  | 9.7  | 58        |
| 10 | Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020, 11, 735.  | 12.8 | 125       |
| 11 | Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.   | 12.8 | 73        |
| 12 | Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.  | 27.8 | 424       |
| 13 | ID1 Is Critical for Tumorigenesis and Regulates Chemoresistance in Glioblastoma. <i>Cancer Research</i> , 2019, 79, 4057-4071.   | 0.9  | 39        |
| 14 | MEDU-44. MUSASHI-1 IS A MASTER REGULATOR OF ABERRANT TRANSLATION IN GROUP 3 MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2019, 21, ii112-ii113.  | 1.2  | 0         |
| 15 | Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. <i>Nature Protocols</i> , 2019, 14, 482-517.  | 12.0 | 1,172     |
| 16 | A transcriptome-based signature of pathological angiogenesis predicts breast cancer patient survival. <i>PLoS Genetics</i> , 2019, 15, e1008482.   | 3.5  | 12        |
| 17 | Phosphoproteomics Analysis Identifies Novel Candidate Substrates of the Nonreceptor Tyrosine Kinase, Src-related Kinase Lacking C-terminal Regulatory Tyrosine and N-terminal Myristoylation Sites (SRMS). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 925-947. | 3.8  | 16        |
| 18 | Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.  | 28.9 | 620       |

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|----|--|------|-----------|
| 19 | Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. <i>Nature</i> , 2018, 553, 101-105.   | 27.8 | 170       |
| 20 | Notch1 regulates the initiation of metastasis and self-renewal of Group 3 medulloblastoma. <i>Nature Communications</i> , 2018, 9, 4121.   | 12.8 | 36        |
| 21 | Global phosphoproteomic analysis identifies SRMS-regulated secondary signaling intermediates. <i>Proteome Science</i> , 2018, 16, 16.  | 1.7  | 10        |
| 22 | ActiveDriverDB: human disease mutations and genome variation in post-translational modification sites of proteins. <i>Nucleic Acids Research</i> , 2018, 46, D901-D910.  | 14.5 | 82        |
| 23 | SubID, a non-median dichotomization tool for heterogeneous populations, reveals the pan-cancer significance of INPP4B and its regulation by EVI1 in AML. <i>PLoS ONE</i> , 2018, 13, e0191510.                     | 2.5  | 9         |
| 24 | Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017, 49, 780-788.  | 21.4 | 112       |
| 25 | Intertumoral Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2017, 31, 737-754.e6.  | 16.8 | 836       |
| 26 | Impact of outdated gene annotations on pathway enrichment analysis. <i>Nature Methods</i> , 2016, 13, 705-706.   | 19.0 | 113       |
| 27 | Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , 2016, 8, 55.  | 8.2  | 51        |
| 28 | Topoisomerase II beta interacts with cohesin and CTCF at topological domain borders. <i>Genome Biology</i> , 2016, 17, 182.  | 8.8  | 190       |
| 29 | g:Profiler—a web server for functional interpretation of gene lists (2016 update). <i>Nucleic Acids Research</i> , 2016, 44, W83-W89.  | 14.5 | 1,179     |
| 30 | Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.  | 27.8 | 266       |
| 31 | Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. <i>Cell</i> , 2016, 164, 293-309.  | 28.9 | 399       |
| 32 | New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. <i>Cell</i> , 2016, 164, 1060-1072.  | 28.9 | 702       |
| 33 | Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. <i>Cancer Cell</i> , 2015, 27, 728-743.  | 16.8 | 933       |
| 34 | Single cell-derived clonal analysis of human glioblastoma links functional and genomic heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 851-856. | 7.1  | 321       |
| 35 | Evolutionary Constraint and Disease Associations of Post-Translational Modification Sites in Human Genomes. <i>PLoS Genetics</i> , 2015, 11, e1004919.   | 3.5  | 69        |
| 36 | Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.   | 19.0 | 297       |

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|----|--|------|-----------|
| 37 | MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. <i>Nature Methods</i> , 2015, 12, 531-533.   | 19.0 | 75        |
| 38 | EAG2 potassium channel with evolutionarily conserved function as a brain tumor target. <i>Nature Neuroscience</i> , 2015, 18, 1236-1246.   | 14.8 | 74        |
| 39 | Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. <i>Nature Communications</i> , 2015, 6, 8554.   | 12.8 | 102       |
| 40 | Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. <i>Molecular Systems Biology</i> , 2014, 10, .  | 7.2  | 4         |
| 41 | HyperModules: identifying clinically and phenotypically significant network modules with disease mutations for biomarker discovery. <i>Bioinformatics</i> , 2014, 30, 2230-2232.                             | 4.1  | 28        |
| 42 | Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.  | 16.8 | 627       |
| 43 | Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.   | 19.0 | 161       |
| 44 | Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. <i>Molecular Systems Biology</i> , 2013, 9, 637.  | 7.2  | 267       |
| 45 | Comprehensive identification of mutational cancer driver genes across 12 tumor types. <i>Scientific Reports</i> , 2013, 3, 2650.   | 3.3  | 437       |
| 46 | The mutational landscape of phosphorylation signaling in cancer. <i>Scientific Reports</i> , 2013, 3, 2651.  | 3.3  | 149       |
| 47 | Research Resource: Interactome of Human Embryo Implantation: Identification of Gene Expression Pathways, Regulation, and Integrated Regulatory Networks. <i>Molecular Endocrinology</i> , 2012, 26, 203-217. | 3.7  | 107       |
| 48 | Disruption of <i>Abi1/Hssh3bp1</i> expression induces prostatic intraepithelial neoplasia in the conditional <i>Abi1/Hssh3bp1</i> KO mice. <i>Oncogenesis</i> , 2012, 1, e26-e26.                            | 4.9  | 20        |
| 49 | Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.   | 27.8 | 761       |
| 50 | m:Explorer: multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence. <i>Genome Biology</i> , 2012, 13, R55.   | 9.6  | 7         |
| 51 | Domain-mediated protein interaction prediction: From genome to network. <i>FEBS Letters</i> , 2012, 586, 2751-2763.  | 2.8  | 48        |
| 52 | Mid-Gestational Gene Expression Profile in Placenta and Link to Pregnancy Complications. <i>PLoS ONE</i> , 2012, 7, e49248.  | 2.5  | 69        |
| 53 | g:Profiler—a web server for functional interpretation of gene lists (2011 update). <i>Nucleic Acids Research</i> , 2011, 39, W307-W315.  | 14.5 | 454       |
| 54 | Comprehensive reanalysis of transcription factor knockout expression data in <i>Saccharomyces cerevisiae</i> reveals many new targets. <i>Nucleic Acids Research</i> , 2010, 38, 4768-4777.                  | 14.5 | 102       |

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|----|--|------|-----------|
| 55 | Relicensing of Transcriptionally Inactivated Replication Origins in Budding Yeast. <i>Journal of Biological Chemistry</i> , 2010, 285, 40004-40011.                    | 3.4  | 27        |
| 56 | Comprehensive transcriptome analysis of mouse embryonic stem cell adipogenesis unravels new processes of adipocyte development. <i>Genome Biology</i> , 2010, 11, R80. | 9.6  | 29        |
| 57 | VisHiC–hierarchical functional enrichment analysis of microarray data. <i>Nucleic Acids Research</i> , 2009, 37, W587-W592.  | 14.5 | 7         |
| 58 | Ranking Genes by Their Co-expression to Subsets of Pathway Members. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 1-13.                              | 3.8  | 11        |
| 59 | Mining for coexpression across hundreds of datasets using novel rank aggregation and visualization methods. <i>Genome Biology</i> , 2009, 10, R139.                    | 9.6  | 133       |
| 60 | The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. <i>PLoS ONE</i> , 2009, 4, e6804.  | 2.5  | 54        |
| 61 | GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. <i>Nucleic Acids Research</i> , 2008, 36, W452-W459.                 | 14.5 | 81        |
| 62 | KEGGanim: pathway animations for high-throughput data. <i>Bioinformatics</i> , 2008, 24, 588-590.  | 4.1  | 31        |
| 63 | g:Profiler—a web-based toolset for functional profiling of gene lists from large-scale experiments. <i>Nucleic Acids Research</i> , 2007, 35, W193-W200.               | 14.5 | 1,203     |