JÃ¼ri Reimand

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3496262/publications.pdf

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	g:Profilerâ€”a web-based toolset for functional profiling of gene lists from large-scale experiments. Nucleic Acids Research, 2007, 35, W193-W200.	14.5	1,203
2	g:Profilerâ€”a web server for functional interpretation of gene lists (2016 update). Nucleic Acids Research, 2016, 44, W83-W89.	14.5	1,179
3	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. Nature Protocols, 2019, 14, 482-517.	12.0	1,172
4	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. Cancer Cell, 2015, 27, 728-743.	16.8	933
5	Intertumoral Heterogeneity within Medulloblastoma Subgroups. Cancer Cell, 2017, 31, 737-754.e6.	16.8	836
6	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
7	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. Cell, 2016, 164, 1060-1072.	28.9	702
8	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
9	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
10	g:Profilerâ€”a web server for functional interpretation of gene lists (2011 update). Nucleic Acids Research, 2011, 39, W307-W315.	14.5	454
11	Comprehensive identification of mutational cancer driver genes across 12 tumor types. Scientific Reports, 2013, 3, 2650.	3.3	437
12	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
13	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. Cell, 2016, 164, 293-309.	28.9	399
14	Single cell-derived clonal analysis of human glioblastoma links functional and genomic heterogeneity. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 851-856.	7.1	321
15	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	19.0	297
16	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. Molecular Systems Biology, 2013, 9, 637.	7.2	267
17	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
18	Topoisomerase II beta interacts with cohesin and CTCF at topological domain borders. Genome Biology, 2016, 17, 182.	8.8	190

#	Article	IF	Citations
19	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. Nature, 2018, 553, 101-105.	27.8	170
20	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	19.0	161
21	The mutational landscape of phosphorylation signaling in cancer. Scientific Reports, 2013, 3, 2651.	3.3	149
22	Mining for coexpression across hundreds of datasets using novel rank aggregation and visualization methods. Genome Biology, 2009, 10, R139.	9.6	133
23	Integrative pathway enrichment analysis of multivariate omics data. Nature Communications, 2020, 11, 735.	12.8	125
24	Impact of outdated gene annotations on pathway enrichment analysis. Nature Methods, 2016, 13, 705-706.	19.0	113
25	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	21.4	112
26	Research Resource: Interactome of Human Embryo Implantation: Identification of Gene Expression Pathways, Regulation, and Integrated Regulatory Networks. Molecular Endocrinology, 2012, 26, 203-217.	3.7	107
27	Comprehensive reanalysis of transcription factor knockout expression data in Saccharomyces cerevisiae reveals many new targets. Nucleic Acids Research, 2010, 38, 4768-4777.	14.5	102
28	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. Nature Communications, 2015, 6, 8554.	12.8	102
29	ActiveDriverDB: human disease mutations and genome variation in post-translational modification sites of proteins. Nucleic Acids Research, 2018, 46, D901-D910.	14.5	82
30	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. Nucleic Acids Research, 2008, 36, W452-W459.	14.5	81
31	MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. Nature Methods, 2015, 12, 531-533.	19.0	75
32	EAG2 potassium channel with evolutionarily conserved function as a brain tumor target. Nature Neuroscience, 2015, 18, 1236-1246.	14.8	74
33	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	12.8	73
34	Evolutionary Constraint and Disease Associations of Post-Translational Modification Sites in Human Genomes. PLoS Genetics, 2015, 11, e1004919.	3.5	69
35	Mid-Gestational Gene Expression Profile in Placenta and Link to Pregnancy Complications. PLoS ONE, 2012, 7, e49248.	2.5	69
36	Candidate Cancer Driver Mutations in Distal Regulatory Elements and Long-Range Chromatin Interaction Networks. Molecular Cell, 2020, 77, 1307-1321.e10.	9.7	58

#	Article	IF	Citations
37	The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. PLoS ONE, 2009, 4, e6804.	2.5	54
38	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. Genome Medicine, 2016, 8, 55.	8.2	51
39	Domainâ€mediated protein interaction prediction: From genome to network. FEBS Letters, 2012, 586, 2751-2763.	2.8	48
40	Phosphoproteome and drug-response effects mediated by the three protein phosphatase 2A inhibitor proteins CIP2A, SET, and PME-1. Journal of Biological Chemistry, 2020, 295, 4194-4211.	3.4	48
41	The transcriptional landscape of Shh medulloblastoma. Nature Communications, 2021, 12, 1749.	12.8	47
42	ID1 Is Critical for Tumorigenesis and Regulates Chemoresistance in Glioblastoma. Cancer Research, 2019, 79, 4057-4071.	0.9	39
43	Notch1 regulates the initiation of metastasis and self-renewal of Group 3 medulloblastoma. Nature Communications, 2018, 9, 4121.	12.8	36
44	KEGGanim: pathway animations for high-throughput data. Bioinformatics, 2008, 24, 588-590.	4.1	31
45	Comprehensive transcriptome analysis of mouse embryonic stem cell adipogenesis unravels new processes of adipocyte development. Genome Biology, 2010, 11, R80.	9.6	29
46	HyperModules: identifying clinically and phenotypically significant network modules with disease mutations for biomarker discovery. Bioinformatics, 2014, 30, 2230-2232.	4.1	28
47	Relicensing of Transcriptionally Inactivated Replication Origins in Budding Yeast. Journal of Biological Chemistry, 2010, 285, 40004-40011.	3.4	27
48	Disruption of Abi1/Hssh3bp1 expression induces prostatic intraepithelial neoplasia in the conditional Abi1/Hssh3bp1 KO mice. Oncogenesis, 2012, 1, e26-e26.	4.9	20
49	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). Molecular and Cellular Proteomics, 2018, 17, 925-947.	3.8	16
50	Pan-cancer analysis of non-coding transcripts reveals the prognostic onco-lncRNA HOXA10-AS in gliomas. Cell Reports, 2021, 37, 109873.	6.4	13
51	A transcriptome-based signature of pathological angiogenesis predicts breast cancer patient survival. PLoS Genetics, 2019, 15, e1008482.	3.5	12
52	ActiveDriverDB: Interpreting Genetic Variation in Human and Cancer Genomes Using Post-translational Modification Sites and Signaling Networks (2021 Update). Frontiers in Cell and Developmental Biology, 2021, 9, 626821.	3.7	12
53	Functional and genetic determinants of mutation rate variability in regulatory elements of cancer genomes. Genome Biology, 2021, 22, 133.	8.8	12
54	Ranking Genes by Their Coâ€expression to Subsets of Pathway Members. Annals of the New York Academy of Sciences, 2009, 1158, 1-13.	3.8	11

#	Article	IF	Citations
55	Global phosphoproteomic analysis identifies SRMS-regulated secondary signaling intermediates. Proteome Science, 2018, 16, 16.	1.7	10
56	SubID, a non-median dichotomization tool for heterogeneous populations, reveals the pan-cancer significance of INPP4B and its regulation by EVI1 in AML. PLoS ONE, 2018, 13, e0191510.	2.5	9
57	Single allele loss-of-function mutations select and sculpt conditional cooperative networks in breast cancer. Nature Communications, 2021, 12, 5238.	12.8	8
58	Human phosphoâ€signaling networks of SARSâ€CoVâ€2 infection are rewired by population genetic variants. Molecular Systems Biology, 2022, 18, e10823.	7.2	8
59	VisHiC--hierarchical functional enrichment analysis of microarray data. Nucleic Acids Research, 2009, 37, W587-W592.	14.5	7
60	m:Explorer: multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence. Genome Biology, 2012, 13, R55.	9.6	7
61	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. Molecular Systems Biology, 2014, 10, .	7.2	4
62	Mutations in Noncoding Cis-Regulatory Elements Reveal Cancer Driver Cistromes in Luminal Breast Cancer. Molecular Cancer Research, 2022, 20, 102-113.	3.4	3
63	MEDU-44. MUSASHI-1 IS A MASTER REGULATOR OF ABERRANT TRANSLATION IN GROUP 3 MEDULLOBLASTOMA. Neuro-Oncology, 2019, 21, ii112-ii113.	1.2	0