Priit Adler

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/12085407/publications.pdf

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17 papers	6,034 citations	687363 13 h-index	888059 17 g-index
18 all docs	18 docs citations	18 times ranked	12841 citing authors

#	ARTICLE	IF	CITATIONS
1	PAWER: protein array web exploreR. BMC Bioinformatics, 2020, 21, 411.	2.6	4
2	Healthspan pathway maps in C. elegans and humans highlight transcription, proliferation/biosynthesis and lipids. Aging, 2020, 12, 12534-12581.	3.1	12
3	HENA, heterogeneous network-based data set for Alzheimerâ€™s disease. Scientific Data, 2019, 6, 151.	5.3	34
4	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	14.5	3,302
5	Prostaglandin D2 Receptor DP1 Antibodies Predict Vaccine-induced and Spontaneous Narcolepsy Type 1: Large-scale Study of Antibody Profiling. EBioMedicine, 2018, 29, 47-59.	6.1	21
6	funcExplorer: a tool for fast data-driven functional characterisation of high-throughput expression data. BMC Genomics, 2018, 19, 817.	2.8	5
7	Meta-signature of human endometrial receptivity: a meta-analysis and validation study of transcriptomic biomarkers. Scientific Reports, 2017, 7, 10077.	3.3	182
8	Autoantibody Repertoire in APECED Patients Targets Two Distinct Subgroups of Proteins. Frontiers in Immunology, 2017, 8, 976.	4.8	48
9	g:Profilerâ€”a web server for functional interpretation of gene lists (2016 update). Nucleic Acids Research, 2016, 44, W83-W89.	14.5	1,179
10	TRIB3 enhances cell viability during glucose deprivation in HEK293-derived cells by upregulating IGFBP2, a novel nutrient deficiency survival factor. Biochimica Et Biophysica Acta - Molecular Cell Research, 2015, 1853, 2492-2505.	4.1	17
11	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. Molecular Biology of the Cell, 2014, 25, 2522-2536.	2.1	44
12	Robust rank aggregation for gene list integration and meta-analysis. Bioinformatics, 2012, 28, 573-580.	4.1	875
13	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
14	Mining for coexpression across hundreds of datasets using novel rank aggregation and visualization methods. Genome Biology, 2009, 10, R139.	9.6	133
15	The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. PLoS ONE, 2009, 4, e6804.	2.5	54
16	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. Nucleic Acids Research, 2008, 36, W452-W459.	14.5	81
17	KEGGanim: pathway animations for high-throughput data. Bioinformatics, 2008, 24, 588-590.	4.1	31