Hedi Peterson

List of Publications by Year
in descending order

36	7,657	331670	315739
papers	citations	21	38
		h-index	g-index

43	43	43	16473
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq1 1 0.784314 rgBT /Overlock 1	14.5	3,302
2	g:Profiler—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
3	g:Profiler—a web server for functional interpretation of gene lists (2016 update). Nucleic Acids Research, 2016, 44, W83-W89.	14.5	1,179
4	gprofiler2 -- an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. F1000Research, 2020, 9, 709.	1.6	331
5	AIRE-Deficient Patients Harbor Unique High-Affinity Disease-Ameliorating Autoantibodies. Cell, 2016, 166, 582-595.	28.9	228
6	Human embryonic stem cell-derived test systems for developmental neurotoxicity: a transcriptomics approach. Archives of Toxicology, 2013, 87, 123-143.	4.2	222
7	Mining for coexpression across hundreds of datasets using novel rank aggregation and visualization methods. Genome Biology, 2009, 10, R139.	9.6	133
8	gprofiler2 -- an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. F1000Research, 2020, 9, 709.	1.6	128
9	MicroRNA Expression Profiles of Human Blood Monocyte-derived Dendritic Cells and Macrophages Reveal miR-511 as Putative Positive Regulator of Toll-like Receptor 4. Journal of Biological Chemistry, 2011, 286, 26487-26495.	3.4	121
10	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
11	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. Nucleic Acids Research, 2008, 36, W452-W459.	14.5	81
12	A Data Integration Approach to Mapping OCT4 Gene Regulatory Networks Operative in Embryonic Stem Cells and Embryonal Carcinoma Cells. PLoS ONE, 2010, 5, e10709.	2.5	81
13	Autoantibody Repertoire in APECED Patients Targets Two Distinct Subgroups of Proteins. Frontiers in Immunology, 2017, 8, 976.	4.8	48
14	C-reactive protein upregulates the whole blood expression of CD59 - an integrative analysis. PLoS Computational Biology, 2017, 13, e1005766.	3.2	44
15	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	8.8	39
16	Endometrial transcriptome analysis indicates superiority of natural over artificial cycles in recurrent implantation failure patients undergoing frozen embryo transfer. Reproductive BioMedicine Online, 2016, 32, 597-613.	2.4	38
17	Signs of innate immune activation and premature immunosenescence in psoriasis patients. Scientific Reports, 2017, 7, 7553.	3.3	34
18	HENA, heterogeneous network-based data set for Alzheimer's disease. Scientific Data, 2019, 6, 151.	5.3	34

#	Article	IF	Citations
19	KEGGanim: pathway animations for high-throughput data. Bioinformatics, 2008, 24, 588-590.	4.1	31
20	Genome-wide promoter analysis of histone modifications in human monocyte-derived antigen presenting cells. BMC Genomics, 2010, 11, 642.	2.8	29
21	Comprehensive transcriptome analysis of mouse embryonic stem cell adipogenesis unravels new processes of adipocyte development. Genome Biology, 2010, 11, R80.	9.6	29
22	Co-expression analysis reveals interpretable gene modules controlled by trans-acting genetic variants. ELife, 2020, 9, .	6.0	24
23	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
24	The relationship between brain tumor cell invasion of engineered neural tissues and inÂvivo features of glioblastoma. Biomaterials, 2013, 34, 8279-8290.	11.4	20
25	Human three-dimensional engineered neural tissue reveals cellular and molecular events following cytomegalovirus infection. Biomaterials, 2015, 53, 296-308.	11.4	18
26	Epigenetic quantification of immunosenescent CD8^{+} TEMRA cells in human blood. Aging Cell, 2022, 21, e13607.	6.7	18
27	Fingerprinting of neurotoxic compounds using a mouse embryonic stem cell dual luminescence reporter assay. Archives of Toxicology, 2017, 91, 365-391.	4.2	16
28	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. Frontiers in Physiology, 2013, 4, 303.	2.8	15
29	Multiplex analysis of 40 cytokines do not allow separation between endometriosis patients and controls. Scientific Reports, 2019, 9, 16738.	3.3	12
30	Post-Aire Medullary Thymic Epithelial Cells and Hassallâ€™s Corpuscles as Inducers of Tonic Pro-Inflammatory Microenvironment. Frontiers in Immunology, 2021, 12, 635569.	4.8	12
31	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
32	VisHiC--hierarchical functional enrichment analysis of microarray data. Nucleic Acids Research, 2009, 37, W587-W592.	14.5	7
33	A framework to assess the quality and impact of bioinformatics training across ELIXIR. PLoS Computational Biology, 2020, 16, e1007976.	3.2	7
34	Using bio.tools to generate and annotate workbench tool descriptions. F1000Research, 2017, 6, 2074.	1.6	7
35	funcExplorer: a tool for fast data-driven functional characterisation of high-throughput expression data. BMC Genomics, 2018, 19, 817.	2.8	5
36	PAWER: protein array web exploreR. BMC Bioinformatics, 2020, 21, 411.	2.6	4