

# Hedi Peterson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2371318/publications.pdf>

Version: 2024-02-01

36  
papers

7,657  
citations

331670

21  
h-index

315739

38  
g-index

43  
all docs

43  
docs citations

43  
times ranked

16473  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic quantification of immunosenescent CD8 <sup>+</sup> TEMRA cells in human blood. <i>Aging Cell</i> , 2022, 21, e13607.	6.7	18
2	Post-Aire Medullary Thymic Epithelial Cells and Hassall's Corpuscles as Inducers of Tonic Pro-Inflammatory Microenvironment. <i>Frontiers in Immunology</i> , 2021, 12, 635569.	4.8	12
3	PAWER: protein array web exploreR. <i>BMC Bioinformatics</i> , 2020, 21, 411.	2.6	4
4	A framework to assess the quality and impact of bioinformatics training across ELIXIR. <i>PLoS Computational Biology</i> , 2020, 16, e1007976.	3.2	7
5	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	30.7	23
6	gprofiler2 – an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. <i>F1000Research</i> , 2020, 9, 709.	1.6	128
7	gprofiler2 – an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. <i>F1000Research</i> , 2020, 9, 709.	1.6	331
8	Co-expression analysis reveals interpretable gene modules controlled by trans-acting genetic variants. <i>ELife</i> , 2020, 9, .	6.0	24
9	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , 2019, 20, 164.	8.8	39
10	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019, 6, 151.	5.3	34
11	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq1 1 0.784314 rgBT /Overlock 10	14.5	3,302
12	Multiplex analysis of 40 cytokines do not allow separation between endometriosis patients and controls. <i>Scientific Reports</i> , 2019, 9, 16738.	3.3	12
13	funcExplorer: a tool for fast data-driven functional characterisation of high-throughput expression data. <i>BMC Genomics</i> , 2018, 19, 817.	2.8	5
14	Fingerprinting of neurotoxic compounds using a mouse embryonic stem cell dual luminescence reporter assay. <i>Archives of Toxicology</i> , 2017, 91, 365-391.	4.2	16
15	Signs of innate immune activation and premature immunosenescence in psoriasis patients. <i>Scientific Reports</i> , 2017, 7, 7553.	3.3	34
16	Autoantibody Repertoire in APECED Patients Targets Two Distinct Subgroups of Proteins. <i>Frontiers in Immunology</i> , 2017, 8, 976.	4.8	48
17	Using bio.tools to generate and annotate workbench tool descriptions. <i>F1000Research</i> , 2017, 6, 2074.	1.6	7
18	C-reactive protein upregulates the whole blood expression of CD59 - an integrative analysis. <i>PLoS Computational Biology</i> , 2017, 13, e1005766.	3.2	44

#	ARTICLE	IF	CITATIONS
19	Endometrial transcriptome analysis indicates superiority of natural over artificial cycles in recurrent implantation failure patients undergoing frozen embryo transfer. <i>Reproductive BioMedicine Online</i> , 2016, 32, 597-613.	2.4	38
20	AIRE-Deficient Patients Harbor Unique High-Affinity Disease-Ameliorating Autoantibodies. <i>Cell</i> , 2016, 166, 582-595.	28.9	228
21	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
22	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	14.5	113
23	Human three-dimensional engineered neural tissue reveals cellular and molecular events following cytomegalovirus infection. <i>Biomaterials</i> , 2015, 53, 296-308.	11.4	18
24	The relationship between brain tumor cell invasion of engineered neural tissues and in vivo features of glioblastoma. <i>Biomaterials</i> , 2013, 34, 8279-8290.	11.4	20
25	Human embryonic stem cell-derived test systems for developmental neurotoxicity: a transcriptomics approach. <i>Archives of Toxicology</i> , 2013, 87, 123-143.	4.2	222
26	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. <i>Frontiers in Physiology</i> , 2013, 4, 303.	2.8	15
27	MicroRNA Expression Profiles of Human Blood Monocyte-derived Dendritic Cells and Macrophages Reveal miR-511 as Putative Positive Regulator of Toll-like Receptor 4. <i>Journal of Biological Chemistry</i> , 2011, 286, 26487-26495.	3.4	121
28	Genome-wide promoter analysis of histone modifications in human monocyte-derived antigen presenting cells. <i>BMC Genomics</i> , 2010, 11, 642.	2.8	29
29	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
30	A Data Integration Approach to Mapping OCT4 Gene Regulatory Networks Operative in Embryonic Stem Cells and Embryonal Carcinoma Cells. <i>PLoS ONE</i> , 2010, 5, e10709.	2.5	81
31	VisHiC—hierarchical functional enrichment analysis of microarray data. <i>Nucleic Acids Research</i> , 2009, 37, W587-W592.	14.5	7
32	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
33	Mining for coexpression across hundreds of datasets using novel rank aggregation and visualization methods. <i>Genome Biology</i> , 2009, 10, R139.	9.6	133
34	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. <i>Nucleic Acids Research</i> , 2008, 36, W452-W459.	14.5	81
35	KEGGanim: pathway animations for high-throughput data. <i>Bioinformatics</i> , 2008, 24, 588-590.	4.1	31
36	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