

Trevor Clancy

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2344770/publications.pdf>

Version: 2024-02-01

30
papers

1,082
citations

394421

19
h-index

454955

30
g-index

33
all docs

33
docs citations

33
times ranked

2329
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulators of cyclin-dependent kinases are crucial for maintaining genome integrity in S phase. <i>Journal of Cell Biology</i> , 2010, 188, 629-638.	5.2	146
2	Complete Remission with Reduction of High-Risk Clones following Haploidentical NK-Cell Therapy against MDS and AML. <i>Clinical Cancer Research</i> , 2018, 24, 1834-1844.	7.0	136
3	Remodeling of secretory lysosomes during education tunes functional potential in NK cells. <i>Nature Communications</i> , 2019, 10, 514.	12.8	103
4	The Genomic HyperBrowser: inferential genomics at the sequence level. <i>Genome Biology</i> , 2010, 11, R121.	9.6	78
5	Artificial intelligence predicts the immunogenic landscape of SARS-CoV-2 leading to universal blueprints for vaccine designs. <i>Scientific Reports</i> , 2020, 10, 22375.	3.3	56
6	Metastasis-associated protein S100A4 induces a network of inflammatory cytokines that activate stromal cells to acquire pro-tumorigenic properties. <i>Cancer Letters</i> , 2014, 344, 28-39.	7.2	46
7	CLC and IFNAR1 are differentially expressed and a global immunity score is distinct between early- and late-onset colorectal cancer. <i>Genes and Immunity</i> , 2011, 12, 653-662.	4.1	40
8	Melanoma brain colonization involves the emergence of a brain-adaptive phenotype. <i>Oncoscience</i> , 2014, 1, 82-94.	2.2	39
9	Identification of eight candidate target genes of the recurrent 3p12â€“p14 loss in cervical cancer by integrative genomic profiling. <i>Journal of Pathology</i> , 2013, 230, 59-69.	4.5	37
10	From proteomes to complexomes in the era of systems biology. <i>Proteomics</i> , 2014, 14, 24-41.	2.2	35
11	Naive Donor NK Cell Repertoires Associated with Less Leukemia Relapse after Allogeneic Hematopoietic Stem Cell Transplantation. <i>Journal of Immunology</i> , 2016, 196, 1400-1411.	0.8	35
12	NeoMutate: an ensemble machine learning framework for the prediction of somatic mutations in cancer. <i>BMC Medical Genomics</i> , 2019, 12, 63.	1.5	35
13	Intra-lineage Plasticity and Functional Reprogramming Maintain Natural Killer Cell Repertoire Diversity. <i>Cell Reports</i> , 2019, 29, 2284-2294.e4.	6.4	33
14	The Genomic HyperBrowser: an analysis web server for genome-scale data. <i>Nucleic Acids Research</i> , 2013, 41, W133-W141.	14.5	32
15	Improved HLA typing of Class I and Class II alleles from nextâ€“generation sequencing data. <i>Hla</i> , 2019, 94, 504-513.	0.6	31
16	Hypoxia-independent gene expression signature associated with radiosensitisation of prostate cancer cell lines by histone deacetylase inhibition. <i>British Journal of Cancer</i> , 2016, 115, 929-939.	6.4	28
17	Profiling networks of distinct immune-cells in tumors. <i>BMC Bioinformatics</i> , 2016, 17, 263.	2.6	26
18	Combining Network Modeling and Gene Expression Microarray Analysis to Explore the Dynamics of Th1 and Th2 Cell Regulation. <i>PLoS Computational Biology</i> , 2010, 6, e1001032.	3.2	21

#	ARTICLE	IF	CITATIONS
19	Predicting Physical Interactions between Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1723-1734.	3.8	21
20	Immunological network signatures of cancer progression and survival. <i>BMC Medical Genomics</i> , 2011, 4, 28.	1.5	17
21	Membranous Expression of Ectodomain Isoforms of the Epidermal Growth Factor Receptor Predicts Outcome after Chemoradiotherapy of Lymph Node–Negative Cervical Cancer. <i>Clinical Cancer Research</i> , 2011, 17, 5501-5512.	7.0	15
22	Molecular profiling of tumor-specific T _H 1 cells activated in vivo. <i>Oncolmmunology</i> , 2013, 2, e24383.	4.6	13
23	Characterization of the Small Intestinal Lesion in Celiac Disease by Label-Free Quantitative Mass Spectrometry. <i>American Journal of Pathology</i> , 2018, 188, 1563-1579.	3.8	12
24	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. <i>Current Pharmaceutical Design</i> , 2017, 23, 4716-4725.	1.9	11
25	The differential disease regulome. <i>BMC Genomics</i> , 2011, 12, 353.	2.8	9
26	Personalized HLA typing leads to the discovery of novel HLA alleles and tumor-specific HLA variants. <i>Hla</i> , 2022, 99, 313-327.	0.6	7
27	Differential Protein Network Analysis of the Immune Cell Lineage. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	5
28	Connectivity can be used to identify key genes in DNA microarray data: a study based on gene expression in nasal polyps before and after treatment with glucocorticoids. <i>Acta Oto-Laryngologica</i> , 2007, 127, 1074-1079.	0.9	4
29	The T Cell Epitope Landscape of SARS-CoV-2 Variants of Concern. <i>Vaccines</i> , 2022, 10, 1123.	4.4	4
30	Identifying pathogenic processes by integrating microarray data with prior knowledge. <i>BMC Bioinformatics</i> , 2014, 15, 115.	2.6	2