

Andreas Scherer

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

2,387
citations

489802

18
h-index

312153

41
g-index

44
all docs

44
docs citations

44
times ranked

4664
citing authors

#	ARTICLE	IF	CITATIONS
1	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	9.4	795
2	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	9.4	420
3	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
4	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	9.4	126
5	Early prognosis of the development of renal chronic allograft rejection by gene expression profiling of human protocol biopsies. <i>Transplantation</i> , 2003, 75, 1323-1330.	0.5	96
6	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. <i>Briefings in Bioinformatics</i> , 2021, 22, 1656-1678.	3.2	66
7	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	9.4	66
8	Calmodulin Differentially Modulates Smad1 and Smad2 Signaling. <i>Journal of Biological Chemistry</i> , 2000, 275, 41430-41438.	1.6	50
9	Transcriptome Sequencing (RNAseq) Enables Utilization of Formalin-Fixed, Paraffin-Embedded Biopsies with Clear Cell Renal Cell Carcinoma for Exploration of Disease Biology and Biomarker Development. <i>PLoS ONE</i> , 2016, 11, e0149743.	1.1	50
10	Bridging the translational innovation gap through good biomarker practice. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 587-588.	21.5	48
11	Transcriptome changes in renal allograft protocol biopsies at 3 months precede the onset of interstitial fibrosis/tubular atrophy (IF/TA) at 6 months. <i>Nephrology Dialysis Transplantation</i> , 2009, 24, 2567-2575.	0.4	39
12	Differential suppression of epidermal antimicrobial protein expression in atopic dermatitis and in EFAD mice by pimecrolimus compared to corticosteroids. <i>Experimental Dermatology</i> , 2011, 20, 783-788.	1.4	39
13	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	9.4	39
14	Clear Cell Renal Cell Carcinoma is linked to Epithelial-to-Mesenchymal Transition and to Fibrosis. <i>Physiological Reports</i> , 2017, 5, e13305.	0.7	36
15	Functional Genomic Analysis of Peripheral Blood During Early Acute Renal Allograft Rejection. <i>Transplantation</i> , 2009, 88, 942-951.	0.5	33
16	Robust and tissue-independent gender-specific transcript biomarkers. <i>Biomarkers</i> , 2013, 18, 436-445.	0.9	32
17	The ribose 5-phosphate isomerase-encoding gene is located immediately downstream from that encoding murine immunoglobulin μ . <i>Gene</i> , 1995, 156, 191-197.	1.0	29
18	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	3.8	29

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19	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	3.8	20
20	The SEQC2 epigenomics quality control (EpiQC) study. <i>Genome Biology</i> , 2021, 22, 332.	3.8	20
21	A subset of metzincins and related genes constitutes a marker of human solid organ fibrosis. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2011, 458, 487-496.	1.4	18
22	Development and confirmation of potential gene classifiers of human clear cell renal cell carcinoma using next-generation RNA sequencing. <i>Scandinavian Journal of Urology</i> , 2016, 50, 452-462.	0.6	18
23	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. <i>Genome Biology</i> , 2022, 23, 2.	3.8	18
24	Transcriptome-proteome integration of archival human renal cell carcinoma biopsies enables identification of molecular mechanisms. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, F1053-F1067.	1.3	15
25	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. <i>Scientific Data</i> , 2021, 8, 296.	2.4	15
26	AXL targeting reduces fibrosis development in experimental unilateral ureteral obstruction. <i>Physiological Reports</i> , 2019, 7, e14091.	0.7	13
27	Reproducibility in biomarker research and clinical development: a global challenge. <i>Biomarkers in Medicine</i> , 2017, 11, 309-312.	0.6	11
28	Consensus guidelines for the validation of qRT-PCR assays in clinical research by the CardioRNA consortium. <i>Molecular Therapy - Methods and Clinical Development</i> , 2022, 24, 171-180.	1.8	11
29	Metzincins and related genes in experimental renal ageing: towards a unifying fibrosis classifier across species. <i>Nephrology Dialysis Transplantation</i> , 2014, 29, 1177-1185.	0.4	10
30	Renal carcinoma/kidney progenitor cell chimera organoid as a novel tumourigenesis gene discovery model. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 1503-1515.	1.2	8
31	Renal Fibrosis mRNA Classifier: Validation in Experimental Lithium-Induced Interstitial Fibrosis in the Rat Kidney. <i>PLoS ONE</i> , 2016, 11, e0168240.	1.1	7
32	Proteomic Analysis of Minimally Damaged Renal Tubular Tissue from Two-Kidney-One-Clip Hypertensive Rats Demonstrates Extensive Changes Compared to Tissue from Controls. <i>Nephron</i> , 2016, 132, 70-80.	0.9	7
33	AGAP2-AS1 as a prognostic biomarker in low-risk clear cell renal cell carcinoma patients with progressing disease. <i>Cancer Cell International</i> , 2021, 21, 690.	1.8	7
34	VeloceGenomics: An Accelerated in Vivo Drug Discovery Approach to Rapidly Predict the Biologic, Drug-Like Activity of Compounds, Proteins, or Genes. <i>Pharmaceutical Research</i> , 2005, 22, 1597-1613.	1.7	3
35	Expanding the Utilization of Formalin-Fixed, Paraffin-Embedded Archives: Feasibility of miR-Seq for Disease Exploration and Biomarker Development from Biopsies with Clear Cell Renal Cell Carcinoma. <i>International Journal of Molecular Sciences</i> , 2018, 19, 803.	1.8	3
36	Biomarker Research and Development for Coronavirus Disease 2019 (COVID-19): European Medical Research Infrastructures Call for Global Coordination. <i>Clinical Infectious Diseases</i> , 2021, 72, 1838-1842.	2.9	3

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37	Matched preclinical designs for improved translatability. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	2
38	The use of haplotype-specific transcripts improves sample annotation consistency. <i>Biomarker Research</i> , 2014, 2, 17.	2.8	1
39	Clinical and ethical considerations of massively parallel sequencing in transplantation science?. <i>World Journal of Transplantation</i> , 2013, 3, 62.	0.6	1
40	AGAP2-AS1 as a potential marker for development of distant metastases in surgically treated low-risk clear cell renal cell carcinoma.. <i>Journal of Clinical Oncology</i> , 2020, 38, 732-732.	0.8	1
41	FC 019PROTEOMIC PROFILING OF GLOMERULI FROM KIDNEYS WITH HYPERTENSIVE NEPHROPATHY REVEALS SIGNATURE OF DISEASE PROGRESSION. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, .	0.4	0