

Andreas Scherer

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,485
citations

394421

19
h-index

214800

47
g-index

54
all docs

54
docs citations

54
times ranked

4349
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. <i>Genome Biology</i> , 2022, 23, 2.	8.8	18
2	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.	4.1	11
3	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. <i>Briefings in Bioinformatics</i> , 2021, 22, 1656-1678.	6.5	66
4	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.	5.8	3
5	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
6	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	8.8	20
7	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.	8.8	29
8	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	17.5	66
9	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.	17.5	39
10	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. <i>Scientific Data</i> , 2021, 8, 296.	5.3	15
11	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
12	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.	4.1	7
13	The SEQC2 epigenomics quality control (EpiQC) study. <i>Genome Biology</i> , 2021, 22, 332.	8.8	20
14	Site-directed attachment of photoexcitable spin labels for light-induced pulsed dipolar spectroscopy. <i>Chemical Communications</i> , 2020, 56, 14669-14672.	4.1	12
15	Optimising broadband pulses for DEER depends on concentration and distance range of interest. <i>Magnetic Resonance</i> , 2020, 1, 59-74.	1.9	5
16	AXL targeting reduces fibrosis development in experimental unilateral ureteral obstruction. <i>Physiological Reports</i> , 2019, 7, e14091.	1.7	13
17	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.	2.7	15
18	Detection of CNVs in NGS Data Using VS-CNV. <i>Methods in Molecular Biology</i> , 2018, 1833, 115-127.	0.9	9

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19	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.	4.1	3
20	Reproducibility in biomarker research and clinical development: a global challenge. <i>Biomarkers in Medicine</i> , 2017, 11, 309-312.	1.4	11
21	Matched preclinical designs for improved translatability. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	2
22	Bridging the translational innovation gap through good biomarker practice. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 587-588.	46.4	48
23	Time-, spectral- and spatially resolved EPR spectroscopy enables simultaneous monitoring of diffusion of different guest molecules in nano-pores. <i>Journal of Magnetic Resonance</i> , 2017, 283, 45-51.	2.1	9
24	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.	2.4	8
25	Clear Cell Renal Cell Carcinoma is linked to Epithelial-to-Mesenchymal Transition and to Fibrosis. <i>Physiological Reports</i> , 2017, 5, e13305.	1.7	36
26	Renal Fibrosis mRNA Classifier: Validation in Experimental Lithium-Induced Interstitial Fibrosis in the Rat Kidney. <i>PLoS ONE</i> , 2016, 11, e0168240.	2.5	7
27	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.	1.0	18
28	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.	1.8	7
29	Concepts and Relevance of Genome-Wide Association Studies. <i>Science Progress</i> , 2016, 99, 59-67.	1.9	30
30	Distinct protein signature of hypertension-induced damage in the renal proteome of the two-kidney, one-clip rat model. <i>Journal of Hypertension</i> , 2015, 33, 126-135.	0.5	14
31	Gene expression profiling of immunomagnetically separated cells directly from stabilized whole blood for multicenter clinical trials. <i>Clinical and Translational Medicine</i> , 2014, 3, 36.	4.0	9
32	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	17.5	420
33	Alteration of human blood cell transcriptome in uremia. <i>BMC Medical Genomics</i> , 2013, 6, 23.	1.5	31
34	Robust and tissue-independent gender-specific transcript biomarkers. <i>Biomarkers</i> , 2013, 18, 436-445.	1.9	32
35	Clinical and ethical considerations of massively parallel sequencing in transplantation science?. <i>World Journal of Transplantation</i> , 2013, 3, 62.	1.6	1
36	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.	2.9	39

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37	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.	2.8	18
38	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.	17.5	795
39	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.	0.7	39
40	Functional Genomic Analysis of Peripheral Blood During Early Acute Renal Allograft Rejection. <i>Transplantation</i> , 2009, 88, 942-951.	1.0	33
41	MDQC: a new quality assessment method for microarrays based on quality control reports. <i>Bioinformatics</i> , 2007, 23, 3162-3169.	4.1	34
42	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.	3.5	3
43	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.	1.0	96
44	Calmodulin Differentially Modulates Smad1 and Smad2 Signaling. <i>Journal of Biological Chemistry</i> , 2000, 275, 41430-41438.	3.4	50
45	Reuse of CAD designs by a neural-network approach. <i>Engineering Applications of Artificial Intelligence</i> , 1996, 9, 413-421.	8.1	9
46	The database group at University of Hagen. <i>SIGMOD Record</i> , 1995, 24, 79-84.	1.2	0
47	The ribose 5-phosphate isomerase-encoding gene is located immediately downstream from that encoding murine immunoglobulin μ . <i>Gene</i> , 1995, 156, 191-197.	2.2	29
48	Problem solving in federative environments: The FRESCO concept of cooperative agents. <i>Lecture Notes in Computer Science</i> , 1992, , 185-203.	1.3	4