Andreas Scherer

List of Publications by Year
in descending order

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	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	3.8	18
2	Consensus guidelines for the validation of qRT-PCR assays in clinical research by the CardioRNA consortium. Molecular Therapy - Methods and Clinical Development, 2022, 24, 171-180.	1.8	11
3	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. Briefings in Bioinformatics, 2021, 22, 1656-1678.	3.2	66
4	Biomarker Research and Development for Coronavirus Disease 2019 (COVID-19): European Medical Research Infrastructures Call for Global Coordination. Clinical Infectious Diseases, 2021, 72, 1838-1842.	2.9	3
5	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	9.4	126
6	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
7	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	3.8	29
8	FC 019PROTEOMIC PROFILING OF GLOMERULI FROM KIDNEYS WITH HYPERTENSIVE NEPHROPATHY REVEALS SIGNATURE OF DISEASE PROGRESSION. Nephrology Dialysis Transplantation, 2021, 36, .	0.4	0
9	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	9.4	66
10	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	9.4	39
11	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. Scientific Data, 2021, 8, 296.	2.4	15
12	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
13	AGAP2-AS1 as a prognostic biomarker in low-risk clear cell renal cell carcinoma patients with progressing disease. Cancer Cell International, 2021, 21, 690.	1.8	7
14	The SEQC2 epigenomics quality control (EpiQC) study. Genome Biology, 2021, 22, 332.	3.8	20
15	AGAP2-AS1 as a potential marker for development of distant metastases in surgically treated low-risk clear cell renal cell carcinoma.. Journal of Clinical Oncology, 2020, 38, 732-732.	0.8	1
16	AXL targeting reduces fibrosis development in experimental unilateral ureteral obstruction. Physiological Reports, 2019, 7, e14091.	0.7	13
17	Transcriptome-proteome integration of archival human renal cell carcinoma biopsies enables identification of molecular mechanisms. American Journal of Physiology - Renal Physiology, 2019, 316, F1053-F1067.	1.3	15
18	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. International Journal of Molecular Sciences, 2018, 19, 803.	1.8	3

#	Article	IF	Citations
19	Reproducibility in biomarker research and clinical development: a global challenge. Biomarkers in Medicine, 2017, 11, 309-312.	0.6	11
20	Matched preclinical designs for improved translatability. Science Translational Medicine, 2017, 9, .	5.8	2
21	Bridging the translational innovation gap through good biomarker practice. Nature Reviews Drug Discovery, 2017, 16, 587-588.	21.5	48
22	Renal carcinoma/kidney progenitor cell chimera organoid as a novel tumourigenesis gene discovery model. DMM Disease Models and Mechanisms, 2017, 10, 1503-1515.	1.2	8
23	Clear Cell Renal Cell Carcinoma is linked to Epithelial-to-Mesenchymal Transition and to Fibrosis. Physiological Reports, 2017, 5, e13305.	0.7	36
24	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. PLoS ONE, 2016, 11, e0149743.	1.1	50
25	Renal Fibrosis mRNA Classifier: Validation in Experimental Lithium-Induced Interstitial Fibrosis in the Rat Kidney. PLoS ONE, 2016, 11, e0168240.	1.1	7
26	Development and confirmation of potential gene classifiers of human clear cell renal cell carcinoma using next-generation RNA sequencing. Scandinavian Journal of Urology, 2016, 50, 452-462.	0.6	18
27	Proteomic Analysis of Minimally Damaged Renal Tubular Tissue from Two-Kidney-One-Clip Hypertensive Rats Demonstrates Extensive Changes Compared to Tissue from Controls. Nephron, 2016, 132, 70-80.	0.9	7
28	The use of haplotype-specific transcripts improves sample annotation consistency. Biomarker Research, 2014, 2, 17.	2.8	1
29	Metzincins and related genes in experimental renal ageing: towards a unifying fibrosis classifier across species. Nephrology Dialysis Transplantation, 2014, 29, 1177-1185.	0.4	10
30	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	9.4	420
31	Robust and tissue-independent gender-specific transcript biomarkers. Biomarkers, 2013, 18, 436-445.	0.9	32
32	Clinical and ethical considerations of massively parallel sequencing in transplantation science?. World Journal of Transplantation, 2013, 3, 62.	0.6	1
33	Differential suppression of epidermal antimicrobial protein expression in atopic dermatitis and in EFAD mice by pimecrolimus compared to corticosteroids. Experimental Dermatology, 2011, 20, 783-788.	1.4	39
34	A subset of metzincins and related genes constitutes a marker of human solid organ fibrosis. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2011, 458, 487-496.	1.4	18
35	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	9.4	795
36	Transcriptome changes in renal allograft protocol biopsies at 3 months precede the onset of interstitial fibrosis/tubular atrophy (IF/TA) at 6 months. Nephrology Dialysis Transplantation, 2009, 24, 2567-2575.	0.4	39

#	Article	IF	Citations
37	Functional Genomic Analysis of Peripheral Blood During Early Acute Renal Allograft Rejection. Transplantation, 2009, 88, 942-951.	0.5	33
38	VeloceGenomics: An Accelerated in Vivo Drug Discovery Approach to Rapidly Predict the Biologic, Drug-Like Activity of Compounds, Proteins, or Genes. Pharmaceutical Research, 2005, 22, 1597-1613.	1.7	3
39	Early prognosis of the development of renal chronic allograft rejection by gene expression profiling of human protocol biopsies. Transplantation, 2003, 75, 1323-1330.	0.5	96
40	Calmodulin Differentially Modulates Smad1 and Smad2 Signaling. Journal of Biological Chemistry, 2000, 275, 41430-41438.	1.6	50
41	The ribose 5-phosphate isomerase-encoding gene is located immediately downstream from that encoding murine immunoglobulin Îº. Gene, 1995, 156, 191-197.	1.0	29