Jean-Pierre A Kocher

List of Publications by Year
in descending order

70	4,955	159585 30	102487 66
papers	citations	h-index	g-index

76	76	76	11489
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Telogator: a method for reporting chromosome-specific telomere lengths from long reads. Bioinformatics, 2022, 38, 1788-1793.	4.1	2
2	CpGtools: a python package for DNA methylation analysis. Bioinformatics, 2021, 37, 1598-1599.	4.1	19
3	Re-Evaluate Fusion Genes in Prostate Cancer. Cancer Informatics, 2021, 20, 117693512110275.	1.9	5
4	Elevated expression of plasminogen activator inhibitor (PAI-1/SERPINE1) is independent from rs1799889 genotypes in arthrofibrosis. Meta Gene, 2021, 28, 100877.	0.6	1
5	P2T2: Protein Panoramic annoTation Tool for the interpretation of protein coding genetic variants. JAMIA Open, 2021, 4, ooab065.	2.0	1
6	PB-Motifâ€"A Method for Identifying Gene/Pseudogene Rearrangements With Long Reads: An Application to CYP21A2 Genotyping. Frontiers in Genetics, 2021, 12, 716586.	2.3	5
7	Surface Roughness of Titanium Orthopedic Implants Alters the Biological Phenotype of Human Mesenchymal Stromal Cells. Tissue Engineering - Part A, 2021, 27, 1503-1516.	3.1	14
8	Exogene: A performant workflow for detecting viral integrations from paired-end next-generation sequencing data. PLoS ONE, 2021, 16, e0250915.	2.5	3
9	Combining copy number, methylation markers, and mutations as a panel for endometrial cancer detection via intravaginal tampon collection. Gynecologic Oncology, 2020, 156, 387-392.	1.4	22
10	ExÂVivo Cell Therapy by Ectopic Hepatocyte Transplantation Treats the Porcine Tyrosinemia Model of Acute Liver Failure. Molecular Therapy - Methods and Clinical Development, 2020, 18, 738-750.	4.1	8
11	A Potential Theragnostic Regulatory Axis for Arthrofibrosis Involving Adiponectin (ADIPOQ) Receptor 1 and 2 (ADIPOR1 and ADIPOR2), TGFÎ²1, and Smooth Muscle Î±-Actin (ACTA2). Journal of Clinical Medicine, 2020, 9, 3690.	2.4	8
12	Aberrant immunohistochemical expression of <scp>CD4</scp> as a rare finding in metastatic melanoma. Journal of Cutaneous Pathology, 2020, 47, 1223-1226.	1.3	1
13	Prognostic subclass of intrahepatic cholangiocarcinoma by integrative molecularâ€"clinical analysis and potential targeted approach. Hepatology International, 2019, 13, 490-500.	4.2	36
14	Ccne1 Overexpression Causes Chromosome Instability in Liver Cells and Liver Tumor Development in Mice. Gastroenterology, 2019, 157, 210-226.e12.	1.3	50
15	Recurrent MSCE116K mutations in ALK-negative anaplastic large cell lymphoma. Blood, 2019, 133, 2776-2789.	1.4	55
16	Predict drug sensitivity of cancer cells with pathway activity inference. BMC Medical Genomics, 2019, 12, 15.	1.5	36
17	Prevalent Homozygous Deletions of Type I Interferon and Defensin Genes in Human Cancers Associate with Immunotherapy Resistance. Clinical Cancer Research, 2018, 24, 3299-3308.	7.0	37
18	Early genetic aberrations in patients with sporadic colorectal cancer. Molecular Carcinogenesis, 2018, 57, 114-124.	2.7	23

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19	A data science approach for the classification of low-grade and high-grade ovarian serous carcinomas. BMC Genomics, 2018, 19, 841.	2.8	1
20	Detection and visualization of complex structural variants from long reads. BMC Bioinformatics, 2018, 19, 508.	2.6	25
21	Indel sensitive and comprehensive variant/mutation detection from RNA sequencing data for precision medicine. BMC Medical Genomics, 2018, 11, 67.	1.5	5
22	Novel Neural Network Approach to Predict Drug-Target Interactions Based on Drug Side Effects and Genome-Wide Association Studies. Human Heredity, 2018, 83, 79-91.	0.8	2
23	Improving Single-Nucleotide Polymorphism-Based Fetal Fraction Estimation of Maternal Plasma Circulating Cell-Free DNA Using Bayesian Hierarchical Models. Journal of Computational Biology, 2018, 25, 1040-1049.	1.6	3
24	HGT-ID: an efficient and sensitive workflow to detect human-viral insertion sites using next-generation sequencing data. BMC Bioinformatics, 2018, 19, 271.	2.6	14
25	The impact of pharmacokinetic gene profiles across human cancers. BMC Cancer, 2018, 18, 577.	2.6	3
26	mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers. Nucleic Acids Research, 2017, 45, W215-W221.	14.5	12
27	Exploring genetic associations with ceRNA regulation in the human genome. Nucleic Acids Research, 2017, 45, 5653-5665.	14.5	39
28	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
29	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. Genome Biology, 2017, 18, 52.	8.8	33
30	UClncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. Scientific Reports, 2017, 7, 14196.	3.3	29
31	Adipose tissue DNA methylome changes in development of new-onset diabetes after kidney transplantation. Epigenomics, 2017, 9, 1423-1435.	2.1	8
32	Linnorm: improved statistical analysis for single cell RNA-seq expression data. Nucleic Acids Research, 2017, 45, e179-e179.	14.5	100
33	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	61
34	CircularLogo: A lightweight web application to visualize intra-motif dependencies. BMC Bioinformatics, 2017, 18, 269.	2.6	5
35	Experience with precision genomics and tumor board, indicates frequent target identification, but barriers to delivery. Oncotarget, 2017, 8, 27145-27154.	1.8	55
36	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. Rare Tumors, 2017, 9, 50-53.	0.6	8

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37	A comprehensive analysis of breast cancer microbiota and host gene expression. PLoS ONE, 2017, 12, e0188873.	2.5	111
38	Circular RNAs and their associations with breast cancer subtypes. Oncotarget, 2016, 7, 80967-80979.	1.8	140
39	Predicting regulatory variants with composite statistic. Bioinformatics, 2016, 32, 2729-2736.	4.1	40
40	CpGFilter: model-based CpG probe filtering with replicates for epigenome-wide association studies. Bioinformatics, 2016, 32, 469-471.	4.1	27
41	Targeted alignment and end repair elimination increase alignment and methylation measure accuracy for reduced representation bisulfite sequencing data. BMC Genomics, 2016, 17, 149.	2.8	3
42	Measure transcript integrity using RNA-seq data. BMC Bioinformatics, 2016, 17, 58.	2.6	187
43	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2016, 44, D869-D876.	14.5	184
44	Epidaurus: aggregation and integration analysis of prostate cancer epigenome. Nucleic Acids Research, 2015, 43, e7-e7.	14.5	10
45	PVAAS: identify variants associated with aberrant splicing from RNA-seq. Bioinformatics, 2015, 31, 1668-1670.	4.1	3
46	TP53mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. Nucleic Acids Research, 2015, 43, 6945-6958.	14.5	46
47	Chromosome X genomic and epigenomic aberrations and clinical implications in breast cancer by base resolution profiling. Epigenomics, 2015, 7, 1099-1110.	2.1	12
48	Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. Epigenomics, 2015, 7, 813-828.	2.1	97
49	Text mining facilitates database curation - extraction of mutation-disease associations from Bio-medical literature. BMC Bioinformatics, 2015, 16, 185.	2.6	23
50	glmgraph: an R package for variable selection and predictive modeling of structured genomic data. Bioinformatics, 2015, 31, 3991-3993.	4.1	23
51	PANDA: pathway and annotation explorer for visualizing and interpreting gene-centric data. PeerJ, 2015, 3, e970.	2.0	3
52	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. PLoS ONE, 2014, 9, e114804.	2.5	110
53	Application of whole exome sequencing in undiagnosed inherited polyneuropathies. Journal of Neurology, Neurosurgery and Psychiatry, 2014, 85, 1265-1272.	1.9	43
54	Transcriptional atlas of cardiogenesis maps congenital heart disease interactome. Physiological Genomics, 2014, 46, 482-495.	2.3	47

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55	Integrated Genomic Characterization Reveals Novel, Therapeutically Relevant Drug Targets in FGFR and EGFR Pathways in Sporadic Intrahepatic Cholangiocarcinoma. PLoS Genetics, 2014, 10, e1004135.	3.5	292
56	Murine Leukemia Virus Uses NXF1 for Nuclear Export of Spliced and Unspliced Viral Transcripts. Journal of Virology, 2014, 88, 4069-4082.	3.4	36
57	Comprehensive Assessment of Genetic Variants WithinTCF4in Fuchs' Endothelial Corneal Dystrophy. , 2014, 55, 6101.		31
58	Aberrant signature methylome by DNMT1 hot spot mutation in hereditary sensory and autonomic neuropathy 1E. Epigenetics, 2014, 9, 1184-1193.	2.7	55
59	The Biological Reference Repository (BioR): a rapid and flexible system for genomics annotation. Bioinformatics, 2014, 30, 1920-1922.	4.1	67
60	RVboost: RNA-seq variants prioritization using a boosting method. Bioinformatics, 2014, 30, 3414-3416.	4.1	34
61	MACE: model based analysis of ChIP-exo. Nucleic Acids Research, 2014, 42, e156-e156.	14.5	84
62	The eSNV-detect: a computational system to identify expressed single nucleotide variants from transcriptome sequencing data. Nucleic Acids Research, 2014, 42, e172-e172.	14.5	33
63	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. BMC Bioinformatics, 2014, 15, 224.	2.6	284
64	HiChIP: a high-throughput pipeline for integrative analysis of ChIP-Seq data. BMC Bioinformatics, 2014, 15, 280.	2.6	55
65	PatternCNV: a versatile tool for detecting copy number changes from exome sequencing data. Bioinformatics, 2014, 30, 2678-2680.	4.1	43
66	From Days to Hours: Reporting Clinically Actionable Variants from Whole Genome Sequencing. PLoS ONE, 2014, 9, e86803.	2.5	4
67	Genome-Wide Analysis of Loss of Heterozygosity in Breast Infiltrating Ductal Carcinoma Distant Normal Tissue Highlights Arm Specific Enrichment and Expansion across Tumor Stages. PLoS ONE, 2014, 9, e95783.	2.5	3
68	CPAT: Coding-Potential Assessment Tool using an alignment-free logistic regression model. Nucleic Acids Research, 2013, 41, e74-e74.	14.5	1,574
69	SoftSearch: Integration of Multiple Sequence Features to Identify Breakpoints of Structural Variations. PLoS ONE, 2013, 8, e83356.	2.5	37
70	Learning on Weighted Hypergraphs to Integrate Protein Interactions and Gene Expressions for Cancer Outcome Prediction. , 2008, , .		46