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	CPAT: Coding-Potential Assessment Tool using an alignment-free logistic regression model. Nucleic Acids Research, 2013, 41, e74-e74.	14.5	1,574
2	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
3	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
4	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. BMC Bioinformatics, 2014, 15, 224.	2.6	284
5	Measure transcript integrity using RNA-seq data. BMC Bioinformatics, 2016, 17, 58.	2.6	187
6	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
7	Circular RNAs and their associations with breast cancer subtypes. Oncotarget, 2016, 7, 80967-80979.	1.8	140
8	A comprehensive analysis of breast cancer microbiota and host gene expression. PLoS ONE, 2017, 12, e0188873.	2.5	111
9	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. PLoS ONE, 2014, 9, e114804.	2.5	110
10	Linnorm: improved statistical analysis for single cell RNA-seq expression data. Nucleic Acids Research, 2017, 45, e179-e179.	14.5	100
11	Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. Epigenomics, 2015, 7, 813-828.	2.1	97
12	MACE: model based analysis of ChIP-exo. Nucleic Acids Research, 2014, 42, e156-e156.	14.5	84
13	The Biological Reference Repository (BioR): a rapid and flexible system for genomics annotation. Bioinformatics, 2014, 30, 1920-1922.	4.1	67
14	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	61
15	Aberrant signature methylome by DNMT1 hot spot mutation in hereditary sensory and autonomic neuropathy 1E. Epigenetics, 2014, 9, 1184-1193.	2.7	55
16	HiChIP: a high-throughput pipeline for integrative analysis of ChIP-Seq data. BMC Bioinformatics, 2014, 15, 280.	2.6	55
17	Experience with precision genomics and tumor board, indicates frequent target identification, but barriers to delivery. Oncotarget, 2017, 8, 27145-27154.	1.8	55
18	Recurrent MSCE116K mutations in ALK-negative anaplastic large cell lymphoma. Blood, 2019, 133, 2776-2789.	1.4	55

#	Article	IF	Citations
19	Ccne1 Overexpression Causes Chromosome Instability in Liver Cells and Liver Tumor Development in Mice. Gastroenterology, 2019, 157, 210-226.e12.	1.3	50
20	Transcriptional atlas of cardiogenesis maps congenital heart disease interactome. Physiological Genomics, 2014, 46, 482-495.	2.3	47
21	Learning on Weighted Hypergraphs to Integrate Protein Interactions and Gene Expressions for Cancer Outcome Prediction. , 2008, , .		46
22	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
23	Application of whole exome sequencing in undiagnosed inherited polyneuropathies. Journal of Neurology, Neurosurgery and Psychiatry, 2014, 85, 1265-1272.	1.9	43
24	PatternCNV: a versatile tool for detecting copy number changes from exome sequencing data. Bioinformatics, 2014, 30, 2678-2680.	4.1	43
25	Predicting regulatory variants with composite statistic. Bioinformatics, 2016, 32, 2729-2736.	4.1	40
26	Exploring genetic associations with ceRNA regulation in the human genome. Nucleic Acids Research, 2017, 45, 5653-5665.	14.5	39
27	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
28	SoftSearch: Integration of Multiple Sequence Features to Identify Breakpoints of Structural Variations. PLoS ONE, 2013, 8, e83356.	2.5	37
29	Murine Leukemia Virus Uses NXF1 for Nuclear Export of Spliced and Unspliced Viral Transcripts. Journal of Virology, 2014, 88, 4069-4082.	3.4	36
30	Prognostic subclass of intrahepatic cholangiocarcinoma by integrative molecularâ€“clinical analysis and potential targeted approach. Hepatology International, 2019, 13, 490-500.	4.2	36
31	Predict drug sensitivity of cancer cells with pathway activity inference. BMC Medical Genomics, 2019, 12, 15.	1.5	36
32	RVboost: RNA-seq variants prioritization using a boosting method. Bioinformatics, 2014, 30, 3414-3416.	4.1	34
33	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
34	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. Genome Biology, 2017, 18, 52.	8.8	33
35	Comprehensive Assessment of Genetic Variants WithinTCF4in Fuchs' Endothelial Corneal Dystrophy. , 2014, 55, 6101.		31
36	UClncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. Scientific Reports, 2017, 7, 14196.	3.3	29

#	Article	IF	Citations
37	CpGFilter: model-based CpG probe filtering with replicates for epigenome-wide association studies. Bioinformatics, 2016, 32, 469-471.	4.1	27
38	Detection and visualization of complex structural variants from long reads. BMC Bioinformatics, 2018, 19, 508.	2.6	25
39	Text mining facilitates database curation - extraction of mutation-disease associations from Bio-medical literature. BMC Bioinformatics, 2015, 16, 185.	2.6	23
40	glmgraph: an R package for variable selection and predictive modeling of structured genomic data. Bioinformatics, 2015, 31, 3991-3993.	4.1	23
41	Early genetic aberrations in patients with sporadic colorectal cancer. Molecular Carcinogenesis, 2018, 57, 114-124.	2.7	23
42	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
43	CpGtools: a python package for DNA methylation analysis. Bioinformatics, 2021, 37, 1598-1599.	4.1	19
44	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
45	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
46	Chromosome X genomic and epigenomic aberrations and clinical implications in breast cancer by base resolution profiling. Epigenomics, 2015, 7, 1099-1110.	2.1	12
47	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
48	Epidaurus: aggregation and integration analysis of prostate cancer epigenome. Nucleic Acids Research, 2015, 43, e7-e7.	14.5	10
49	Adipose tissue DNA methylome changes in development of new-onset diabetes after kidney transplantation. Epigenomics, 2017, 9, 1423-1435.	2.1	8
50	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. Rare Tumors, 2017, 9, 50-53.	0.6	8
51	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
52	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
53	CircularLogo: A lightweight web application to visualize intra-motif dependencies. BMC Bioinformatics, 2017, 18, 269.	2.6	5
54	Indel sensitive and comprehensive variant/mutation detection from RNA sequencing data for precision medicine. BMC Medical Genomics, 2018, 11, 67.	1.5	5

#	Article	IF	Citations
55	Re-Evaluate Fusion Genes in Prostate Cancer. Cancer Informatics, 2021, 20, 117693512110275.	1.9	5
56	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
57	From Days to Hours: Reporting Clinically Actionable Variants from Whole Genome Sequencing. PLoS ONE, 2014, 9, e86803.	2.5	4
58	PVAAS: identify variants associated with aberrant splicing from RNA-seq. Bioinformatics, 2015, 31, 1668-1670.	4.1	3
59	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
60	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
61	The impact of pharmacokinetic gene profiles across human cancers. BMC Cancer, 2018, 18, 577.	2.6	3
62	Exogene: A performant workflow for detecting viral integrations from paired-end next-generation sequencing data. PLoS ONE, 2021, 16, e0250915.	2.5	3
63	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
64	PANDA: pathway and annotation explorer for visualizing and interpreting gene-centric data. PeerJ, 2015, 3, e970.	2.0	3
65	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
66	Telogator: a method for reporting chromosome-specific telomere lengths from long reads. Bioinformatics, 2022, 38, 1788-1793.	4.1	2
67	A data science approach for the classification of low-grade and high-grade ovarian serous carcinomas. BMC Genomics, 2018, 19, 841.	2.8	1
68	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
69	Elevated expression of plasminogen activator inhibitor (PAI-1/SERPINE1) is independent from rs1799889 genotypes in arthrofibrosis. Meta Gene, 2021, 28, 100877.	0.6	1
70	P2T2: Protein Panoramic annoTation Tool for the interpretation of protein coding genetic variants. JAMIA Open, 2021, 4, ooab065.	2.0	1