

Benjamin J Ainscough

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1600427/publications.pdf>

Version: 2024-02-01

16
papers

2,276
citations

567281

15
h-index

888059

17
g-index

21
all docs

21
docs citations

21
times ranked

6560
citing authors

#	ARTICLE	IF	CITATIONS
1	Convergent loss of PTEN leads to clinical resistance to a PI(3)K± inhibitor. <i>Nature</i> , 2015, 518, 240-244.	27.8	486
2	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017, 49, 170-174.	21.4	460
3	DGIdb 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016, 44, D1036-D1044.	14.5	359
4	High-performance web services for querying gene and variant annotation. <i>Genome Biology</i> , 2016, 17, 91.	8.8	166
5	Genome-Wide Association Study of CSF Levels of 59 Alzheimer's Disease Candidate Proteins: Significant Associations with Proteins Involved in Amyloid Processing and Inflammation. <i>PLoS Genetics</i> , 2014, 10, e1004758.	3.5	109
6	DoCM: a database of curated mutations in cancer. <i>Nature Methods</i> , 2016, 13, 806-807.	19.0	96
7	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.	12.8	89
8	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	3.2	83
9	Organizing knowledge to enable personalization of medicine in cancer. <i>Genome Biology</i> , 2014, 15, 438.	8.8	81
10	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. <i>PLoS Computational Biology</i> , 2015, 11, e1004393.	3.2	74
11	Phosphorylated Tau-A ²⁴² Ratio as a Continuous Trait for Biomarker Discovery for Early-Stage Alzheimer's Disease in Multiplex Immunoassay Panels of Cerebrospinal Fluid. <i>Biological Psychiatry</i> , 2014, 75, 723-731.	1.3	72
12	Standard operating procedure for somatic variant refinement of sequencing data with paired tumor and normal samples. <i>Genetics in Medicine</i> , 2019, 21, 972-981.	2.4	67
13	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. <i>Nature Genetics</i> , 2018, 50, 1735-1743.	21.4	62
14	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. <i>Experimental Hematology</i> , 2016, 44, 603-613.	0.4	44
15	Molecular phylogenetics of the burrowing crayfish genus <i>Fallicambarus</i> (Decapoda:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	1.7	15
16	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022, 3, 522-525.	18.2	3