

Brian J Haas

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5558664/publications.pdf>

Version: 2024-02-01

11
papers

26,072
citations

1039406

9
h-index

1372195

10
g-index

13
all docs

13
docs citations

13
times ranked

34557
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Fusions Create Partner and Collateral Dependencies Essential to Cancer Cell Survival. <i>Cancer Research</i> , 2021, 81, 3971-3984.	0.4	11
2	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021, 12, 827-838.e5.	2.9	15
3	Cover Image: Volume 22, Issue 4. <i>Evolution & Development</i> , 2020, 22, i.	1.1	0
4	von Willebrand factor D and EGF domains is an evolutionarily conserved and required feature of blastemas capable of multitissue appendage regeneration. <i>Evolution & Development</i> , 2020, 22, 297-311.	1.1	25
5	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. <i>Genome Biology</i> , 2019, 20, 213.	3.8	379
6	Transcriptomic landscape of the blastema niche in regenerating adult axolotl limbs at single-cell resolution. <i>Nature Communications</i> , 2018, 9, 5153.	5.8	133
7	A Tissue-Mapped Axolotl De Novo Transcriptome Enables Identification of Limb Regeneration Factors. <i>Cell Reports</i> , 2017, 18, 762-776.	2.9	752
8	Advances in Decoding Axolotl Limb Regeneration. <i>Trends in Genetics</i> , 2017, 33, 553-565.	2.9	74
9	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	5.5	7,054
10	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
11	Advancing RNA-Seq analysis. <i>Nature Biotechnology</i> , 2010, 28, 421-423.	9.4	192