

T Roderick Docking

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8735783/t-roderick-docking-publications-by-year.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

24
papers

1,788
citations

15
h-index

24
g-index

24
ext. papers

2,103
ext. citations

7.6
avg, IF

3.13
L-index

#	Paper	IF	Citations
24	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021 , 12, 2474	17.4	10
23	Assessing Limit of Detection in Clinical Sequencing. <i>Journal of Molecular Diagnostics</i> , 2021 , 23, 455-466	5.1	0
22	Loss of lenalidomide-induced megakaryocytic differentiation leads to therapy resistance in del(5q) myelodysplastic syndrome. <i>Nature Cell Biology</i> , 2020 , 22, 526-533	23.4	16
21	Altered microRNA expression links IL6 and TNF-induced inflammaging with myeloid malignancy in humans and mice. <i>Blood</i> , 2020 , 135, 2235-2251	2.2	15
20	Sample Tracking Using Unique Sequence Controls. <i>Journal of Molecular Diagnostics</i> , 2020 , 22, 141-146	5.1	3
19	Genomic testing in myeloid malignancy. <i>International Journal of Laboratory Hematology</i> , 2019 , 41 Suppl 1, 117-125	2.5	5
18	Fixation Effects on Variant Calling in a Clinical Resequencing Panel. <i>Journal of Molecular Diagnostics</i> , 2019 , 21, 705-717	5.1	2
17	Data sharing as a national quality improvement program: reporting on BRCA1 and BRCA2 variant-interpretation comparisons through the Canadian Open Genetics Repository (COGR). <i>Genetics in Medicine</i> , 2018 , 20, 294-302	8.1	20
16	Applications of Bayesian network models in predicting types of hematological malignancies. <i>Scientific Reports</i> , 2018 , 8, 6951	4.9	22
15	Resistance to Lenalidomide in Del(5q) MDS Is Mediated By Inhibition of Drug-Induced Megakaryocytic Differentiation. <i>Blood</i> , 2018 , 132, 176-176	2.2	1
14	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES 2014 ,		5
13	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013 , 14, R27	18.3	212
12	The genome and transcriptome of the pine saprophyte <i>Ophiostoma piceae</i> , and a comparison with the bark beetle-associated pine pathogen <i>Grosmannia clavigera</i> . <i>BMC Genomics</i> , 2013 , 14, 373	4.5	54
11	A clinically validated diagnostic second-generation sequencing assay for detection of hereditary BRCA1 and BRCA2 mutations. <i>Journal of Molecular Diagnostics</i> , 2013 , 15, 796-809	5.1	27
10	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
9	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013 , 14, 550	4.5	10
8	Transcriptome and full-length cDNA resources for the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major insect pest of pine forests. <i>Insect Biochemistry and Molecular Biology</i> , 2012 , 42, 525-36	4.5	79

7	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012 , 226, 7-16	9.4	226
6	Updated genome assembly and annotation of <i>Paenibacillus</i> larvae, the agent of American foulbrood disease of honey bees. <i>BMC Genomics</i> , 2011 , 12, 450	4.5	31
5	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
4	A regulatory toolbox of MiniPromoters to drive selective expression in the brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 16589-94	11.5	62
3	Gene discovery for the bark beetle-vectored fungal tree pathogen <i>Grosmannia clavigera</i> . <i>BMC Genomics</i> , 2010 , 11, 536	4.5	23
2	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009 , 10, R94	18.3	119
1	Retrotransposon sequence variation in four asexual plant species. <i>Journal of Molecular Evolution</i> , 2006 , 62, 375-87	3.1	21