

# T Roderick Docking

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8735783/publications.pdf>

Version: 2024-02-01

24  
papers

2,293  
citations

471509

17  
h-index

642732

23  
g-index

24  
all docs

24  
docs citations

24  
times ranked

5008  
citing authors

#	ARTICLE	IF	CITATIONS
1	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2474.	12.8	49
2	Assessing Limit of Detection in Clinical Sequencing. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 455-466.	2.8	7
3	Sample Tracking Using Unique Sequence Controls. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 141-146.	2.8	10
4	Loss of lenalidomide-induced megakaryocytic differentiation leads to therapy resistance in del(5q) myelodysplastic syndrome. <i>Nature Cell Biology</i> , 2020, 22, 526-533.	10.3	30
5	Altered microRNA expression links IL6 and TNF-induced inflammaging with myeloid malignancy in humans and mice. <i>Blood</i> , 2020, 135, 2235-2251.	1.4	35
6	Genomic testing in myeloid malignancy. <i>International Journal of Laboratory Hematology</i> , 2019, 41, 117-125.	1.3	7
7	Fixation Effects on Variant Calling in a Clinical Resequencing Panel. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 705-717.	2.8	5
8	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.	2.4	27
9	Applications of Bayesian network models in predicting types of hematological malignancies. <i>Scientific Reports</i> , 2018, 8, 6951.	3.3	48
10	Resistance to Lenalidomide in Del(5q) MDS Is Mediated By Inhibition of Drug-Induced Megakaryocytic Differentiation. <i>Blood</i> , 2018, 132, 176-176.	1.4	2
11	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES. , 2014, , .		14
12	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013, 14, R27.	9.6	260
13	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.	2.8	72
14	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.	2.8	29
15	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582
16	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013, 14, 550.	2.8	12
17	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, 525-536.	2.7	93
18	Concurrent <i>CIC</i> mutations, <i>IDH</i> mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012, 226, 7-16.	4.5	272

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19	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.	2.8	35
20	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
21	Gene discovery for the bark beetle-vectored fungal tree pathogen <i>Grosmannia clavigera</i> . <i>BMC Genomics</i> , 2010, 11, 536.	2.8	25
22	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, 16589-16594.	7.1	74
23	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009, 10, R94.	9.6	130
24	Retrotransposon Sequence Variation in Four Asexual Plant Species. <i>Journal of Molecular Evolution</i> , 2006, 62, 375-387.	1.8	32