

# Micha Bayer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7200841/publications.pdf>

Version: 2024-02-01

20  
papers

4,033  
citations

759233

12  
h-index

794594

19  
g-index

24  
all docs

24  
docs citations

24  
times ranked

6846  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Association Study for Resistance to Rhynchosporium in a Diverse Collection of Spring Barley Germplasm. <i>Agronomy</i> , 2022, 12, 782.	3.0	2
2	EORNA, a barley gene and transcript abundance database. <i>Scientific Data</i> , 2021, 8, 90.	5.3	20
3	Barley sodium content is regulated by natural variants of the Na <sup>+</sup> transporter HvHKT1;5. <i>Communications Biology</i> , 2020, 3, 258.	4.4	21
4	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. <i>BMC Genomics</i> , 2019, 20, 968.	2.8	50
5	Characterisation of barley resistance to rhynchosporium on chromosome 6HS. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1089-1107.	3.6	13
6	Exome Capture for Variant Discovery and Analysis in Barley. <i>Methods in Molecular Biology</i> , 2019, 1900, 283-310.	0.9	5
7	<i>ELIGULUM-A</i> Regulates Lateral Branch and Leaf Development in Barley. <i>Plant Physiology</i> , 2018, 176, 2750-2760.	4.8	22
8	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
9	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
10	Association Mapping of Diastatic Power in UK Winter and Spring Barley by Exome Sequencing of Phenotypically Contrasting Variety Sets. <i>Frontiers in Plant Science</i> , 2017, 8, 1566.	3.6	6
11	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	21.4	259
12	Tablet: Visualizing Next-Generation Sequence Assemblies and Mappings. <i>Methods in Molecular Biology</i> , 2016, 1374, 253-268.	0.9	48
13	The low recombining pericentromeric region of barley restricts gene diversity and evolution but not gene expression. <i>Plant Journal</i> , 2014, 79, 981-992.	5.7	30
14	An evaluation of genotyping by sequencing (GBS) to map the <i>Breviaristatum-e</i> (ari-e) locus in cultivated barley. <i>BMC Genomics</i> , 2014, 15, 104.	2.8	145
15	In silico identification and characterization of conserved plant microRNAs in barley. <i>Open Life Sciences</i> , 2014, 9, 841-852.	1.4	1
16	Using Tablet for visual exploration of second-generation sequencing data. <i>Briefings in Bioinformatics</i> , 2013, 14, 193-202.	6.5	836
17	Natural variation in a homolog of <i>Antirrhinum CENTRORADIALIS</i> contributed to spring growth habit and environmental adaptation in cultivated barley. <i>Nature Genetics</i> , 2012, 44, 1388-1392.	21.4	477
18	Tablet – next generation sequence assembly visualization. <i>Bioinformatics</i> , 2010, 26, 401-402.	4.1	590

#	ARTICLE	IF	CITATIONS
19	CONTROLLING THE CHAOS: DEVELOPING POST-GENOMIC GRID INFRASTRUCTURES. , 2006, , .		1
20	Development of a Grid Infrastructure for Functional Genomics. Lecture Notes in Computer Science, 2005, , 125-139.	1.3	3