

# Michael Imelfort

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10567065/publications.pdf>

Version: 2024-02-01

15  
papers

10,181  
citations

567144

15  
h-index

940416

16  
g-index

20  
all docs

20  
docs citations

20  
times ranked

11563  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. <i>Genome Research</i> , 2015, 25, 1043-1055.  | 2.4  | 7,539     |
| 2  | Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <i>Nature</i> , 2013, 500, 567-570.  | 13.7 | 1,029     |
| 3  | An Expanded Genomic Representation of the Phylum Cyanobacteria. <i>Genome Biology and Evolution</i> , 2014, 6, 1031-1045.   | 1.1  | 326       |
| 4  | Fast, accurate error-correction of amplicon pyrosequences using Acacia. <i>Nature Methods</i> , 2012, 9, 425-426.   | 9.0  | 322       |
| 5  | GroopM: an automated tool for the recovery of population genomes from related metagenomes. <i>PeerJ</i> , 2014, 2, e603.  | 0.9  | 254       |
| 6  | Discovering genetic polymorphisms in next-generation sequencing data. <i>Plant Biotechnology Journal</i> , 2009, 7, 312-317.  | 4.1  | 118       |
| 7  | Sequencing and assembly of low copy and genic regions of isolated <i>Triticum aestivum</i> chromosome arm 7DS. <i>Plant Biotechnology Journal</i> , 2011, 9, 768-775.   | 4.1  | 105       |
| 8  | De novo sequencing of plant genomes using second-generation technologies. <i>Briefings in Bioinformatics</i> , 2009, 10, 609-618.   | 3.2  | 93        |
| 9  | AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants. <i>Nucleic Acids Research</i> , 2009, 37, D951-D953.   | 6.5  | 83        |
| 10 | Bioinformatics tools and databases for analysis of next-generation sequence data. <i>Briefings in Functional Genomics</i> , 2012, 11, 12-24.  | 1.3  | 73        |
| 11 | Single nucleotide polymorphism discovery in barley using autoSNPdb. <i>Plant Biotechnology Journal</i> , 2009, 7, 326-333.  | 4.1  | 56        |
| 12 | Future tools for association mapping in crop plants This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 1017-1023. | 0.9  | 46        |
| 13 | Spatial uniformity of microbial diversity in a continuous bioelectrochemical system. <i>Bioresource Technology</i> , 2013, 129, 599-605.  | 4.8  | 35        |
| 14 | Targeted identification of genomic regions using TAGdb. <i>Plant Methods</i> , 2010, 6, 19.   | 1.9  | 34        |
| 15 | Genome Sequencing Approaches and Successes. <i>Methods in Molecular Biology</i> , 2009, 513, 345-358.   | 0.4  | 24        |