

# Rachid Ounit

## List of Publications by Year in Descending Order

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

16  
papers

1,794  
citations

11  
h-index

21  
g-index

21  
ext. papers

2,576  
ext. citations

10.2  
avg, IF

4.33  
L-index

#	Paper	IF	Citations
16	Characterization of Spacesuit Associated Microbial Communities and Their Implications for NASA Missions. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 608478	5.7	1
15	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , <b>2019</b> , 98, 767-782	6.9	128
14	1154. Comparison of Five Testing Modalities for the Assessment of Patient Environment Cleanliness. <i>Open Forum Infectious Diseases</i> , <b>2018</b> , 5, S347-S347	1	78
13	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , <b>2017</b> , 544, 427-433	33.4	822
12	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L. <i>Scientific Data</i> , <b>2017</b> , 4, 170044	8.2	93
11	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , <b>2017</b> , 18, 182	18.3	152
10	Metagenomic characterization of ambulances across the USA. <i>Microbiome</i> , <b>2017</b> , 5, 125	16.6	17
9	Higher classification sensitivity of short metagenomic reads with CLARK-S. <i>Bioinformatics</i> , <b>2016</b> , 32, 3823-3825	38.4	71
8	rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005107	5	26
7	BRAT-nova: fast and accurate mapping of bisulfite-treated reads. <i>Bioinformatics</i> , <b>2016</b> , 32, 2696-8	7.2	11
6	CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. <i>BMC Genomics</i> , <b>2015</b> , 16, 236	4.5	347
5	Sequencing of 15622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , <b>2015</b> , 84, 216-27	6.9	31
4	Higher Classification Accuracy of Short Metagenomic Reads by Discriminative Spaced k-mers. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 286-295	0.9	8
3	Comprehensive Benchmarking and Ensemble Approaches for Metagenomic Classifiers		3
2	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.)		2
1	Higher classification sensitivity of short metagenomic reads with CLARK-S		3