

Roberto Vera Alvarez

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4363036/publications.pdf>

Version: 2024-02-01

20
papers

1,262
citations

759233

12
h-index

794594

19
g-index

26
all docs

26
docs citations

26
times ranked

1890
citing authors

#	ARTICLE	IF	CITATIONS
1	Conservation and Evolution of the Sporulation Gene Set in Diverse Members of the <i>Firmicutes</i> . <i>Journal of Bacteriology</i> , 2022, 204, .	2.2	20
2	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.	14.5	441
3	PM4NGS, a project management framework for next-generation sequencing data analysis. <i>GigaScience</i> , 2021, 10, .	6.4	0
4	Transcriptome annotation in the cloud: complexity, best practices, and cost. <i>GigaScience</i> , 2021, 10, .	6.4	9
5	BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. <i>Journal of Proteome Research</i> , 2021, 20, 2056-2061.	3.7	19
6	Nonessential Ribosomal Proteins in Bacteria and Archaea Identified Using Clusters of Orthologous Genes. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	14
7	MutaBind2: Predicting the Impacts of Single and Multiple Mutations on Protein-Protein Interactions. <i>IScience</i> , 2020, 23, 100939.	4.1	109
8	BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks. <i>Epigenetics and Chromatin</i> , 2020, 13, 21.	3.9	40
9	LitSense: making sense of biomedical literature at sentence level. <i>Nucleic Acids Research</i> , 2019, 47, W594-W599.	14.5	37
10	Banana (<i>Musa acuminata</i>) transcriptome profiling in response to rhizobacteria: <i>Bacillus amyloliquefaciens</i> Bs006 and <i>Pseudomonas fluorescens</i> Ps006. <i>BMC Genomics</i> , 2019, 20, 378.	2.8	31
11	TPMCalculator: one-step software to quantify mRNA abundance of genomic features. <i>Bioinformatics</i> , 2019, 35, 1960-1962.	4.1	149
12	SNPDelScore: combining multiple methods to score deleterious effects of noncoding mutations in the human genome. <i>Bioinformatics</i> , 2018, 34, 289-291.	4.1	11
13	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , 2017, 33, 2580-2582.	4.1	205
14	Workflow and web application for annotating NCBI BioProject transcriptome data. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	6
15	Quantifying deleterious effects of regulatory variants. <i>Nucleic Acids Research</i> , 2016, 45, gkw1263.	14.5	14
16	Census of solo LuxR genes in prokaryotic genomes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 20.	3.9	82
17	A Network-Based Target Overlap Score for Characterizing Drug Combinations: High Correlation with Cancer Clinical Trial Results. <i>PLoS ONE</i> , 2015, 10, e0129267.	2.5	10
18	Fast and Sensitive Alignment of Microbial Whole Genome Sequencing Reads to Large Sequence Datasets on a Desktop PC: Application to Metagenomic Datasets and Pathogen Identification. <i>PLoS ONE</i> , 2014, 9, e103441.	2.5	9

#	ARTICLE	IF	CITATIONS
19	ComQXPA Quorum Sensing Systems May Not Be Unique to <i>Bacillus subtilis</i> : A Census in Prokaryotic Genomes. PLoS ONE, 2014, 9, e96122.	2.5	39
20	Evaluation of Phenylthiocarbamoyl-Derivatized Peptides by Electrospray Ionization Mass Spectrometry: Selective Isolation and Analysis of Modified Multiply Charged Peptides for Liquid Chromatography-Tandem Mass Spectrometry Experiments. Analytical Chemistry, 2010, 82, 8492-8501.	6.5	10