

# 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  | COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.   | 14.5 | 441       |
| 2  | BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , 2017, 33, 2580-2582.  | 4.1  | 205       |
| 3  | TPMCalculator: one-step software to quantify mRNA abundance of genomic features. <i>Bioinformatics</i> , 2019, 35, 1960-1962.  | 4.1  | 149       |
| 4  | MutaBind2: Predicting the Impacts of Single and Multiple Mutations on Protein-Protein Interactions. <i>IScience</i> , 2020, 23, 100939.  | 4.1  | 109       |
| 5  | Census of solo LuxR genes in prokaryotic genomes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 20.   | 3.9  | 82        |
| 6  | BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks. <i>Epigenetics and Chromatin</i> , 2020, 13, 21.  | 3.9  | 40        |
| 7  | ComQXPA Quorum Sensing Systems May Not Be Unique to <i>Bacillus subtilis</i> : A Census in Prokaryotic Genomes. <i>PLoS ONE</i> , 2014, 9, e96122.   | 2.5  | 39        |
| 8  | LitSense: making sense of biomedical literature at sentence level. <i>Nucleic Acids Research</i> , 2019, 47, W594-W599.  | 14.5 | 37        |
| 9  | 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        |
| 10 | 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        |
| 11 | BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. <i>Journal of Proteome Research</i> , 2021, 20, 2056-2061.  | 3.7  | 19        |
| 12 | Quantifying deleterious effects of regulatory variants. <i>Nucleic Acids Research</i> , 2016, 45, gkw1263.   | 14.5 | 14        |
| 13 | Nonessential Ribosomal Proteins in Bacteria and Archaea Identified Using Clusters of Orthologous Genes. <i>Journal of Bacteriology</i> , 2021, 203, .  | 2.2  | 14        |
| 14 | SNPDeScore: combining multiple methods to score deleterious effects of noncoding mutations in the human genome. <i>Bioinformatics</i> , 2018, 34, 289-291.   | 4.1  | 11        |
| 15 | 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. <i>Analytical Chemistry</i> , 2010, 82, 8492-8501. | 6.5  | 10        |
| 16 | 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        |
| 17 | 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         |
| 18 | Transcriptome annotation in the cloud: complexity, best practices, and cost. <i>GigaScience</i> , 2021, 10, .  | 6.4  | 9         |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | Workflow and web application for annotating NCBI BioProject transcriptome data. Database: the Journal of Biological Databases and Curation, 2017, 2017, . | 3.0 | 6         |
| 20 | PM4NGS, a project management framework for next-generation sequencing data analysis. GigaScience, 2021, 10, .   | 6.4 | 0         |