# Bruno A Gaëta

List of Publications by Year
in descending order

| 41 papers | 1,797 citations | 361413<br>20 h-index | 345221<br>36 g-index |
|---|---|---|---|
| 41 all docs | 41 docs citations | 41 times ranked | 2734 citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Undergraduate Education in Bioinformaticsâ€"Progress and Lessons Learnt from an Engineering Degree. , 2021, , 73-77. | | 0 |
| 2 | Pairwise alignment of nucleotide sequences using maximal exact matches. BMC Bioinformatics, 2019, 20, 261. | 2.6 | 4 |
| 3 | Chlorogenic acid attenuates virulence factors and pathogenicity of Pseudomonas aeruginosa by regulating quorum sensing. Applied Microbiology and Biotechnology, 2019, 103, 903-915. | 3.6 | 60 |
| 4 | Cache Friendly Optimisation of de Bruijn Graph based Local Re-assembly in Variant Calling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1. | 3.0 | 1 |
| 5 | Art in Science Competition invites artworks to the annual exhibition on ISMB 2018 in Chicago. PLoS Computational Biology, 2018, 14, e1006139. | 3.2 | 0 |
| 6 | The development and application of bioinformatics core competencies to improve bioinformatics training and education. PLoS Computational Biology, 2018, 14, e1005772. | 3.2 | 84 |
| 7 | Art in Science Competition invites artworks to the annual exhibition on ISMB 2018 in Chicago. F1000Research, 2018, 7, 337. | 1.6 | 0 |
| 8 | Improved VCF normalization for accurate VCF comparison. Bioinformatics, 2017, 33, 964-970. | 4.1 | 11 |
| 9 | ISCBâ€™s initial reaction to <i>New England Journal of Medicine</i> editorial on data sharing. Bioinformatics, 2017, 33, 2968-2968. | 4.1 | 1 |
| 10 | Ten simple rules for forming a scientific professional society. PLoS Computational Biology, 2017, 13, e1005226. | 3.2 | 7 |
| 11 | Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) Tj ETQq1 1 0.784314 rgBT /Ov | 3.2 | 24 |
| 12 | ISCBâ€™s initial reaction to New England Journal of Medicine editorial on data sharing. F1000Research, 2016, 5, 157. | 1.6 | 1 |
| 13 | ISCBâ€™s Initial Reaction to The New England Journal of Medicine Editorial on Data Sharing. PLoS Computational Biology, 2016, 12, e1004816. | 3.2 | 12 |
| 14 | The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. Bioinformatics, 2015, 31, 140-142. | 4.1 | 34 |
| 15 | GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. PLoS Computational Biology, 2015, 11, e1004143. | 3.2 | 52 |
| 16 | IgE-Associated IGHV Genes from Venom and Peanut Allergic Individuals Lack Mutational Evidence of Antigen Selection. PLoS ONE, 2014, 9, e89730. | 2.5 | 13 |
| 17 | Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. PLoS Computational Biology, 2014, 10, e1003496. | 3.2 | 102 |
| 18 | Candidate disease gene prediction using <i>Gentrepid</i>: application to a genomeâ€wide association study on coronary artery disease. Molecular Genetics &amp; Genomic Medicine, 2014, 2, 44-57. | 1.2 | 11 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | Combining spatial and chemical information for clustering pharmacophores. BMC Bioinformatics, 2014, 15, S5. | 2.6 | 7 |
| 20 | GentrepidV2.0: a web server for candidate disease gene prediction. BMC Bioinformatics, 2013, 14, 249. | 2.6 | 6 |
| 21 | The Inference of Phased Haplotypes for the Immunoglobulin H Chain V Region Gene Loci by Analysis of VDJ Gene Rearrangements. Journal of Immunology, 2012, 188, 1333-1340. | 0.8 | 102 |
| 22 | Divergent human populations show extensive shared IGK rearrangements in peripheral blood B cells. Immunogenetics, 2012, 64, 3-14. | 2.4 | 46 |
| 23 | IgE Sequences in Individuals Living in an Area of Endemic Parasitism Show Little Mutational Evidence of Antigen Selection. Scandinavian Journal of Immunology, 2011, 73, 496-504. | 2.7 | 38 |
| 24 | Genomic screening by 454 pyrosequencing identifies a new human IGHV gene and sixteen other new IGHV allelic variants. Immunogenetics, 2011, 63, 259-265. | 2.4 | 62 |
| 25 | Analysis of genome-wide association study data using the protein knowledge base. BMC Genetics, 2011, 12, 98. | 2.7 | 10 |
| 26 | Clustering-based identification of clonally-related immunoglobulin gene sequence sets. Immunome Research, 2010, 6, S4. | 0.1 | 34 |
| 27 | Individual Variation in the Germline Ig Gene Repertoire Inferred from Variable Region Gene Rearrangements. Journal of Immunology, 2010, 184, 6986-6992. | 0.8 | 261 |
| 28 | Benchmarking the performance of human antibody gene alignment utilities using a 454 sequence dataset. Bioinformatics, 2010, 26, 3129-3130. | 4.1 | 22 |
| 29 | MINER: exploratory analysis of gene interaction networks by machine learning from expression data. BMC Genomics, 2009, 10, S17. | 2.8 | 5 |
| 30 | Parallelizing Optimal Multiple Sequence Alignment by Dynamic Programming. , 2008, , . | | 4 |
| 31 | Fld1p, a functional homologue of human seipin, regulates the size of lipid droplets in yeast. Journal of Cell Biology, 2008, 180, 473-482. | 5.2 | 411 |
| 32 | iHMMune-align: hidden Markov model-based alignment and identification of germline genes in rearranged immunoglobulin gene sequences. Bioinformatics, 2007, 23, 1580-1587. | 4.1 | 117 |
| 33 | Identifying highly mutated IGHD genes in the junctions of rearranged human immunoglobulin heavy chain genes. Journal of Immunological Methods, 2007, 324, 26-37. | 1.4 | 10 |
| 34 | Reconsidering the human immunoglobulin heavy-chain locus:. Immunogenetics, 2006, 57, 917-925. | 2.4 | 23 |
| 35 | Partitioning of Rearranged Ig Genes by Mutation Analysis Demonstrates D-D Fusion and V Gene Replacement in the Expressed Human Repertoire. Journal of Immunology, 2004, 172, 340-348. | 0.8 | 25 |
| 36 | Exonuclease activity and P nucleotide addition in the generation of the expressed immunoglobulin repertoire. BMC Immunology, 2004, 5, 19. | 2.2 | 29 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 37 | Identification of vaccine candidate antigens from a genomic analysis of Porphyromonas gingivalis. Vaccine, 2001, 19, 4135-4142. | 3.8 | 127 |
| 38 | BLAST on the Web. BioTechniques, 2000, 28, 436-439. | 1.8 | 8 |
| 39 | BLAST...What Next?. BioTechniques, 2000, 28, 874-876. | 1.8 | 0 |
| 40 | The 5â€²-flanking region of the Î±2MR/LRP gene contains an enhancer-like cluster of Sp1 binding sites. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1994, 1219, 307-313. | 2.4 | 22 |
| 41 | Saturation mutagenesis of theDrosophilatRNAArggene B-Box intragenic promoter element: requirements for transcription activation and stable complex formation. Nucleic Acids Research, 1990, 18, 1541-1548. | 14.5 | 11 |