# Arnold Kuzniar

List of Publications by Year
in descending order

| 14 papers | 1,000 citations | 1163117<br>8 h-index | 1199594<br>12 g-index |
|---|---|---|---|
| 14 all docs | 14 docs citations | 14 times ranked | 1861 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Linked Data Platform for Solanaceae Species. Applied Sciences (Switzerland), 2020, 10, 6813. | 2.5 | 5 |
| 2 | sv-callers: a highly portable parallel workflow for structural variant detection in whole-genome sequence data. PeerJ, 2020, 8, e8214. | 2.0 | 17 |
| 3 | A portable and scalable workflow for detecting structural variants in whole-genome sequencing data. , 2018, , . | | 1 |
| 4 | QTLTableMiner++: semantic mining of QTL tables in scientific articles. BMC Bioinformatics, 2018, 19, 183. | 2.6 | 8 |
| 5 | Semi-quantitative proteomics of mammalian cells upon short-term exposure to non-ionizing electromagnetic fields. PLoS ONE, 2017, 12, e0170762. | 2.5 | 13 |
| 6 | PIQMIe: a web server for semi-quantitative proteomics data management and analysis. Nucleic Acids Research, 2014, 42, W100-W106. | 14.5 | 8 |
| 7 | Selectome update: quality control and computational improvements to a database of positive selection. Nucleic Acids Research, 2014, 42, D917-D921. | 14.5 | 65 |
| 8 | gcodeml: a Grid-enabled tool for detecting positive selection in biological evolution. Studies in Health Technology and Informatics, 2012, 175, 59-68. | 0.3 | 5 |
| 9 | Finished Genome of the Fungal Wheat Pathogen Mycosphaerella graminicola Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. PLoS Genetics, 2011, 7, e1002070. | 3.5 | 532 |
| 10 | Evidence for RNA recombination between distinct isolates of Pepino mosaic virus. Acta Biochimica Polonica, 2010, 57, 385-8. | 0.5 | 5 |
| 11 | ProGMap: an integrated annotation resource for protein orthology. Nucleic Acids Research, 2009, 37, W428-W434. | 14.5 | 12 |
| 12 | The quest for orthologs: finding the corresponding gene across genomes. Trends in Genetics, 2008, 24, 539-551. | 6.7 | 258 |
| 13 | Benchmarking protein classification algorithms via supervised cross-validation. Journal of Proteomics, 2008, 70, 1215-1223. | 2.4 | 13 |
| 14 | Interoperability and FAIRness through a novel combination of Web technologies. PeerJ Computer Science, 0, 3, e110. | 4.5 | 58 |