Arnold Kuzniar

List of Publications by Year
in descending order

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

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