Artem Lysenko

List of Publications by Year
in descending order

22 papers	743 citations	759233 12 h-index	713466 21 g-index
24 all docs	24 docs citations	24 times ranked	1147 citing authors

#	Article	IF	Citations
1	Immune subtypes and neoantigen-related immune evasion in advanced colorectal cancer. IScience, 2022, 25, 103740.	4.1	4
2	DeepFeature: feature selection in nonimage data using convolutional neural network. Briefings in Bioinformatics, 2021, 22, .	6.5	31
3	Navigating the disease landscape: knowledge representations for contextualizing molecular signatures. Briefings in Bioinformatics, 2019, 20, 609-623.	6.5	16
4	PHI-Nets: A Network Resource for Ascomycete Fungal Pathogens to Annotate and Identify Putative Virulence Interacting Proteins and siRNA Targets. Frontiers in Microbiology, 2019, 10, 2721.	3.5	8
5	An integrative machine learning approach for prediction of toxicity-related drug safety. Life Science Alliance, 2018, 1, e201800098.	2.8	44
6	Recon2Neo4j: applying graph database technologies for managing comprehensive genome-scale networks. Bioinformatics, 2017, 33, 1096-1098.	4.1	25
7	EpiGeNet: A Graph Database of Interdependencies Between Genetic and Epigenetic Events in Colorectal Cancer. Journal of Computational Biology, 2017, 24, 969-980.	1.6	16
8	Developing integrated crop knowledge networks to advance candidate gene discovery. Applied & Translational Genomics, 2016, 11, 18-26.	2.1	66
9	Representing and querying disease networks using graph databases. BioData Mining, 2016, 9, 23.	4.0	75
10	Transcriptome and Metabolite Profiling of the Infection Cycle of *Zymoseptoria tritici* on Wheat Reveals a Biphasic Interaction with Plant Immunity Involving Differential Pathogen Chromosomal Contributions and a Variation on the Hemibiotrophic Lifestyle Definition Â. Plant Physiology, 2015, 167, 1158-1185.	4.8	301
11	A novel approach to identify genes that determine grain protein deviation in cereals. Plant Biotechnology Journal, 2015, 13, 625-635.	8.3	28
12	Discovering Study-Specific Gene Regulatory Networks. PLoS ONE, 2014, 9, e106524.	2.5	8
13	Interactive exploration of integrated biological datasets using context-sensitive workflows. Frontiers in Genetics, 2014, 5, 21.	2.3	4
14	Genetical and Comparative Genomics of *Brassica* under Altered Ca Supply Identifies *Arabidopsis* Ca-Transporter Orthologs Â. Plant Cell, 2014, 26, 2818-2830.	6.6	40
15	A Framework for Mining Life Sciences Data on the Semantic Web in an Interactive, Graph-Based Environment. Lecture Notes in Computer Science, 2014, , 225-237.	1.3	0
16	Network-Based Data Integration for Selecting Candidate Virulence Associated Proteins in the Cereal Infecting Fungus Fusarium graminearum. PLoS ONE, 2013, 8, e67926.	2.5	18
17	Integrating Multiple Studies of Wheat Microarray Data to Identify Treatment-Specific Regulatory Networks. Lecture Notes in Computer Science, 2013, , 104-115.	1.3	1
18	Detection of Multi-clustered Genes and Community Structure for the Plant Pathogenic Fungus Fusarium graminearum. Lecture Notes in Computer Science, 2012, , 69-86.	1.3	8

#	Article	IF	Citations
19	Assessing the functional coherence of modules found in multiple-evidence networks from Arabidopsis. BMC Bioinformatics, 2011, 12, 203.	2.6	14
20	AIGO: Towards a unified framework for the Analysis and the Inter-comparison of GO functional annotations. BMC Bioinformatics, 2011, 12, 431.	2.6	12
21	Analysis and visualisation of RDF resources in Ondex. Nature Precedings, 2010, , .	0.1	1
22	Data integration for plant genomics--exemplars from the integration of Arabidopsis thaliana databases. Briefings in Bioinformatics, 2009, 10, 676-693.	6.5	21