

Natali Gulbahce

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11020069/publications.pdf>

Version: 2024-02-01

26
papers

6,396
citations

361045

20
h-index

642321

23
g-index

27
all docs

27
docs citations

27
times ranked

10711
citing authors

#	ARTICLE	IF	CITATIONS
1	Network medicine: a network-based approach to human disease. <i>Nature Reviews Genetics</i> , 2011, 12, 56-68.	7.7	3,987
2	Global landscape of HIV-human protein complexes. <i>Nature</i> , 2012, 481, 365-370.	13.7	651
3	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	13.7	349
4	Network-based methods for human disease gene prediction. <i>Briefings in Functional Genomics</i> , 2011, 10, 280-293.	1.3	214
5	Global Mapping of the Inc-Human Interactome Reveals that Retromer Restricts Chlamydia Infection. <i>Cell Host and Microbe</i> , 2015, 18, 109-121.	5.1	174
6	A disease module in the interactome explains disease heterogeneity, drug response and captures novel pathways and genes in asthma. <i>Human Molecular Genetics</i> , 2015, 24, 3005-3020.	1.4	162
7	Predicting synthetic rescues in metabolic networks. <i>Molecular Systems Biology</i> , 2008, 4, 168.	3.2	123
8	Viral Perturbations of Host Networks Reflect Disease Etiology. <i>PLoS Computational Biology</i> , 2012, 8, e1002531.	1.5	102
9	The art of community detection. <i>BioEssays</i> , 2008, 30, 934-938.	1.2	87
10	Local Structure of Directed Networks. <i>Physical Review Letters</i> , 2008, 100, 118701.	2.9	61
11	Mapping the Evolution of Scientific Fields. <i>PLoS ONE</i> , 2010, 5, e10355.	1.1	61
12	Scoring Large-Scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.19.1-8.19.16.	25.8	58
13	Purification and characterization of HIV-human protein complexes. <i>Methods</i> , 2011, 53, 13-19.	1.9	56
14	Detection and phasing of single base de novo mutations in biopsies from human in vitro fertilized embryos by advanced whole-genome sequencing. <i>Genome Research</i> , 2015, 25, 426-434.	2.4	49
15	Comparison of an expanded ataxia interactome with patient medical records reveals a relationship between macular degeneration and ataxia. <i>Human Molecular Genetics</i> , 2011, 20, 510-527.	1.4	45
16	Quantitative Whole Genome Sequencing of Circulating Tumor Cells Enables Personalized Combination Therapy of Metastatic Cancer. <i>Cancer Research</i> , 2017, 77, 4530-4541.	0.4	44
17	Emergent Criticality through Adaptive Information Processing in Boolean Networks. <i>Physical Review Letters</i> , 2012, 108, 128702.	2.9	39
18	Damage Spreading and Criticality in Finite Random Dynamical Networks. <i>Physical Review Letters</i> , 2007, 99, 248701.	2.9	36

#	ARTICLE	IF	CITATIONS
19	Spontaneous Reaction Silencing in Metabolic Optimization. PLoS Computational Biology, 2008, 4, e1000236.	1.5	36
20	Network-based Analysis of Genome Wide Association Data Provides Novel Candidate Genes for Lipid and Lipoprotein Traits. Molecular and Cellular Proteomics, 2013, 12, 3398-3408.	2.5	28
21	An Assessment of Random Dynamical Network Automata for Nanoelectronics. International Journal of Nanotechnology and Molecular Computation, 2009, 1, 58-76.	0.3	12
22	Advanced Whole-Genome Sequencing and Analysis of Fetal Genomes from Amniotic Fluid. Clinical Chemistry, 2018, 64, 715-725.	1.5	10
23	Assessing random dynamical network architectures for nanoelectronics. , 2008, , .		8
24	Whole genome sequence analysis of BT-474 using complete Genomicsâ€™ standard and long fragment read technologies. GigaScience, 2016, 5, 8.	3.3	4
25	Random Dynamical Network Automata for Nanoelectronics. , 0, , 1699-1718.		0
26	Random Dynamical Network Automata for Nanoelectronics. , 0, , 295-314.		0