

# Natali Gulbahce

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

6,396  
citations

361296

20  
h-index

642610

23  
g-index

27  
all docs

27  
docs citations

27  
times ranked

10711  
citing authors

#	ARTICLE	IF	CITATIONS
1	Advanced Whole-Genome Sequencing and Analysis of Fetal Genomes from Amniotic Fluid. <i>Clinical Chemistry</i> , 2018, 64, 715-725.	1.5	10
2	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
3	Whole genome sequence analysis of BT-474 using complete Genomics™ standard and long fragment read technologies. <i>GigaScience</i> , 2016, 5, 8.	3.3	4
4	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
5	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
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	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
8	Network-based Analysis of Genome Wide Association Data Provides Novel Candidate Genes for Lipid and Lipoprotein Traits. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3398-3408.	2.5	28
9	Viral Perturbations of Host Networks Reflect Disease Etiology. <i>PLoS Computational Biology</i> , 2012, 8, e1002531.	1.5	102
10	Emergent Criticality through Adaptive Information Processing in Boolean Networks. <i>Physical Review Letters</i> , 2012, 108, 128702.	2.9	39
11	Global landscape of HIV-human protein complexes. <i>Nature</i> , 2012, 481, 365-370.	13.7	651
12	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	13.7	349
13	Purification and characterization of HIV-human protein complexes. <i>Methods</i> , 2011, 53, 13-19.	1.9	56
14	Network medicine: a network-based approach to human disease. <i>Nature Reviews Genetics</i> , 2011, 12, 56-68.	7.7	3,987
15	Network-based methods for human disease gene prediction. <i>Briefings in Functional Genomics</i> , 2011, 10, 280-293.	1.3	214
16	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
17	Mapping the Evolution of Scientific Fields. <i>PLoS ONE</i> , 2010, 5, e10355.	1.1	61
18	An Assessment of Random Dynamical Network Automata for Nanoelectronics. <i>International Journal of Nanotechnology and Molecular Computation</i> , 2009, 1, 58-76.	0.3	12

#	ARTICLE	IF	CITATIONS
19	The art of community detection. BioEssays, 2008, 30, 934-938.	1.2	87
20	Assessing random dynamical network architectures for nanoelectronics. , 2008, , .		8
21	Spontaneous Reaction Silencing in Metabolic Optimization. PLoS Computational Biology, 2008, 4, e1000236.	1.5	36
22	Predicting synthetic rescues in metabolic networks. Molecular Systems Biology, 2008, 4, 168.	3.2	123
23	Local Structure of Directed Networks. Physical Review Letters, 2008, 100, 118701.	2.9	61
24	Damage Spreading and Criticality in Finite Random Dynamical Networks. Physical Review Letters, 2007, 99, 248701.	2.9	36
25	Random Dynamical Network Automata for Nanoelectronics. , 0, , 1699-1718.		0
26	Random Dynamical Network Automata for Nanoelectronics. , 0, , 295-314.		0