Kazuhiro Takemoto

List of Publications by Year in Descending Order

62 papers	906 citations	17 h-index	28 g-index
67 ext. papers	1,198 ext. citations	3.4 avg, IF	4.94 L-index

#	Paper	IF	Citations
62	Natural Images Allow Universal Adversarial Attacks on Medical Image Classification Using Deep Neural Networks with Transfer Learning.. *Journal of Imaging*, **2022**, 8,	3.1	2
61	Simple Black-Box Universal Adversarial Attacks on Deep Neural Networks for Medical Image Classification. *Algorithms*, **2022**, 15, 144	1.8	0
60	Backdoor Attacks to Deep Neural Network-Based System for COVID-19 Detection from Chest X-ray Images. *Applied Sciences (Switzerland)*, **2021**, 11, 9556	2.6	1
59	Universal adversarial attacks on deep neural networks for medical image classification. *BMC Medical Imaging*, **2021**, 21, 9	2.9	23
58	Diversity of Dominant Soil Bacteria Increases with Warming Velocity at the Global Scale. *Diversity*, **2021**, 13, 120	2.5	1
57	Simple Iterative Method for Generating Targeted Universal Adversarial Perturbations. *Algorithms*, **2020**, 13, 268	1.8	12
56	Vulnerability of deep neural networks for detecting COVID-19 cases from chest X-ray images to universal adversarial attacks. *PLoS ONE*, **2020**, 15, e0243963	3.7	14
55	The brain-derived neurotrophic factor Val66Met polymorphism increases segregation of structural correlation networks in healthy adult brains. *PeerJ*, **2020**, 8, e9632	3.1	3
54	Revisiting the hypothesis of an energetic barrier to genome complexity between eukaryotes and prokaryotes. *Royal Society Open Science*, **2020**, 7, 191859	3.3	4
53	Ecological Networks **2019**, 1131-1141		1
52	Difficulty in inferring microbial community structure based on co-occurrence network approaches. *BMC Bioinformatics*, **2019**, 20, 329	3.6	53
51	PREvaIL, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. *Journal of Theoretical Biology*, **2018**, 443, 125-137	2.3	106
50	Large-scale aggregation analysis of eukaryotic proteins reveals an involvement of intrinsically disordered regions in protein folding. *Scientific Reports*, **2018**, 8, 678	4.9	17
49	Decomposing the effects of ocean environments on predator-prey body-size relationships in food webs. *Royal Society Open Science*, **2018**, 5, 180707	3.3	5
48	Network resilience of mutualistic ecosystems and environmental changes: an empirical study. *Royal Society Open Science*, **2018**, 5, 180706	3.3	6
47	Brain structural connectivity and neuroticism in healthy adults. *Scientific Reports*, **2018**, 8, 16491	4.9	11
46	MAPLE 2.3.0: an improved system for evaluating the functionomes of genomes and metagenomes. *Bioscience, Biotechnology and Biochemistry*, **2018**, 82, 1515-1517	2.1	28

45	A network biology-based approach to evaluating the effect of environmental contaminants on human interactome and diseases. *Ecotoxicology and Environmental Safety*, **2018**, 160, 316-327	7	11
44	Exosomes in mammals with greater habitat variability contain more proteins and RNAs. *Royal Society Open Science*, **2017**, 4, 170162	3.3	3
43	Data integration aids understanding of butterfly-host plant networks. *Scientific Reports*, **2017**, 7, 43368	4.9	12
42	Limitations of a metabolic network-based reverse ecology method for inferring host-pathogen interactions. *BMC Bioinformatics*, **2017**, 18, 278	3.6	3
41	Importance of metabolic rate to the relationship between the number of genes in a functional category and body size in Peto's paradox for cancer. *Royal Society Open Science*, **2016**, 3, 160267	3.3	4
40	Habitat variability does not generally promote metabolic network modularity in flies and mammals. *BioSystems*, **2016**, 139, 46-54	1.9	3
39	Systematic Protein Level Regulation via Degradation Machinery Induced by Genotoxic Drugs. *Journal of Proteome Research*, **2016**, 15, 205-15	5.6	2
38	Human Impacts and Climate Change Influence Nestedness and Modularity in Food-Web and Mutualistic Networks. *PLoS ONE*, **2016**, 11, e0157929	3.7	22
37	An automated system for evaluation of the potential functionome: MAPLE version 2.1.0. *DNA Research*, **2016**, 23, 467-475	4.5	40
36	Analysis of the Effect of Degree Correlation on the Size of Minimum Dominating Sets in Complex Networks. *PLoS ONE*, **2016**, 11, e0157868	3.7	8
35	The proportion of genes in a functional category is linked to mass-specific metabolic rate and lifespan. *Scientific Reports*, **2015**, 5, 10008	4.9	5
34	Heterogeneity of cells may explain allometric scaling of metabolic rate. *BioSystems*, **2015**, 130, 11-6	1.9	3
33	Functional Classification of Uncultured "Candidatus Caldiarchaeum subterraneum" Using the Maple System. *PLoS ONE*, **2015**, 10, e0132994	3.7	16
32	Climatic seasonality may affect ecological network structure: food webs and mutualistic networks. *BioSystems*, **2014**, 121, 29-37	1.9	17
31	Metabolic networks are almost nonfractal: a comprehensive evaluation. *Physical Review E*, **2014**, 90, 022802	2.4	9
30	Heterogeneity in ecological mutualistic networks dominantly determines community stability. *Scientific Reports*, **2014**, 4, 5912	4.9	21
29	Theoretical estimation of metabolic network robustness against multiple reaction knockouts using branching process approximation. *Physica A: Statistical Mechanics and Its Applications*, **2013**, 392, 5525-5535	2.3	4
28	Modular organization of cancer signaling networks is associated with patient survivability. *BioSystems*, **2013**, 113, 149-54	1.9	17

27	Does habitat variability really promote metabolic network modularity?. *PLoS ONE*, **2013**, 8, e61348	3.7	13
26	Limited influence of oxygen on the evolution of chemical diversity in metabolic networks. *Metabolites*, **2013**, 3, 979-92	5.6	7
25	Analysis of the impact degree distribution in metabolic networks using branching process approximation. *Physica A: Statistical Mechanics and Its Applications*, **2012**, 391, 379-387	3.3	3
24	Metabolic network modularity arising from simple growth processes. *Physical Review E*, **2012**, 86, 036107	2.4	11
23	An integrative computational framework based on a two-step random forest algorithm improves prediction of zinc-binding sites in proteins. *PLoS ONE*, **2012**, 7, e49716	3.7	23
22	Identification of chemogenomic features from drug-target interaction networks using interpretable classifiers. *Bioinformatics*, **2012**, 28, i487-i494	7.2	61
21	Introduction to Complex Networks: Measures, Statistical Properties, and Models **2012**, 45-75		8
20	Current understanding of the formation and adaptation of metabolic systems based on network theory. *Metabolites*, **2012**, 2, 429-57	5.6	12
19	FunSAV: predicting the functional effect of single amino acid variants using a two-stage random forest model. *PLoS ONE*, **2012**, 7, e43847	3.7	36
18	Metabolic network modularity in archaea depends on growth conditions. *PLoS ONE*, **2011**, 6, e25874	3.7	17
17	Difference in the distribution pattern of substrate enzymes in the metabolic network of Escherichia coli, according to chaperonin requirement. *BMC Systems Biology*, **2011**, 5, 98	3.5	11
16	Finding Minimum Reaction Cuts of Metabolic Networks Under a Boolean Model Using Integer Programming and Feedback Vertex Sets. *International Journal of Knowledge Discovery in Bioinformatics*, **2010**, 1, 14-31		35
15	Prediction of Protein Folding Rates from Structural Topology and Complex Network Properties. *IPSJ Transactions on Bioinformatics*, **2010**, 3, 40-53	1.3	8
14	Nested structure acquired through simple evolutionary process. *Journal of Theoretical Biology*, **2010**, 264, 782-6	2.3	11
13	Global architecture of metabolite distributions across species and its formation mechanisms. *BioSystems*, **2010**, 100, 8-13	1.9	4
12	Measuring Structural Robustness of Metabolic Networks under a Boolean Model Using Integer Programming and Feedback Vertex Sets **2009**,		6
11	Heterogeneous distribution of metabolites across plant species. *Physica A: Statistical Mechanics and Its Applications*, **2009**, 388, 2771-2780	3.3	9
10	Origin of structural difference in metabolic networks with respect to temperature. *BMC Systems Biology*, **2008**, 2, 82	3.5	11

9	HSEpred: predict half-sphere exposure from protein sequences. *Bioinformatics*, **2008**, 24, 1489-97	7.2	42
8	Structure of n-clique networks embedded in a complex network. *Physica A: Statistical Mechanics and Its Applications*, **2007**, 380, 665-672	3.3	11
7	Correlation between structure and temperature in prokaryotic metabolic networks. *BMC Bioinformatics*, **2007**, 8, 303	3.6	30
6	Modeling for evolving biological networks with scale-free connectivity, hierarchical modularity, and disassortativity. *Mathematical Biosciences*, **2007**, 208, 454-68	3.9	16
5	Evolving networks by merging cliques. *Physical Review E*, **2005**, 72, 046116	2.4	14
4	Finding Minimum Reaction Cuts of Metabolic Networks Under a Boolean Model Using Integer Programming and Feedback Vertex Sets774-791		
3	Finding Minimum Reaction Cuts of Metabolic Networks Under a Boolean Model240-258		1
2	Global COVID-19 transmission rate is influenced by precipitation seasonality and the speed of climate temperature warming		18
1	Modeling for Evolving Biological Networks77-108		1