

# Dong-Yeon Cho

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4512644/publications.pdf>

Version: 2024-02-01

18  
papers

888  
citations

759233

12  
h-index

1058476

14  
g-index

23  
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23  
docs citations

23  
times ranked

1614  
citing authors

#	ARTICLE	IF	CITATIONS
1	A central role for PI3K-AKT signaling pathway in linking SAMHD1-deficiency to the type I interferon signature. <i>Scientific Reports</i> , 2018, 8, 84.	3.3	29
2	Dosage-Dependent Expression Variation Suppressed on the <i>Drosophila</i> Male X Chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 587-598.	1.8	9
3	Reprogramming of regulatory network using expression uncovers sex-specific gene regulation in <i>Drosophila</i> . <i>Nature Communications</i> , 2018, 9, 4061.	12.8	23
4	Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. <i>PLoS Computational Biology</i> , 2016, 12, e1004747.	3.2	51
5	Effects of Gene Dose, Chromatin, and Network Topology on Expression in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2016, 12, e1006295.	3.5	38
6	MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. <i>Bioinformatics</i> , 2015, 31, i284-i292.	4.1	87
7	Transcription Factor Networks in <i>Drosophila melanogaster</i> . <i>Cell Reports</i> , 2014, 8, 2031-2043.	6.4	83
8	DNA copy number evolution in <i>Drosophila</i> cell lines. <i>Genome Biology</i> , 2014, 15, R70.	8.8	96
9	Dissecting cancer heterogeneity with a probabilistic genotype-phenotype model. <i>Nucleic Acids Research</i> , 2013, 41, 8011-8020.	14.5	17
10	Chapter 5: Network Biology Approach to Complex Diseases. <i>PLoS Computational Biology</i> , 2012, 8, e1002820.	3.2	239
11	Mediation of <i>Drosophila</i> autosomal dosage effects and compensation by network interactions. <i>Genome Biology</i> , 2012, 13, R28.	9.6	98
12	Finding Cancer-Related Gene Combinations Using a Molecular Evolutionary Algorithm. , 2007, , .		2
13	Identification of biochemical networks by S-tree based genetic programming. <i>Bioinformatics</i> , 2006, 22, 1631-1640.	4.1	87
14	System identification using evolutionary Markov chain Monte Carlo. <i>Journal of Systems Architecture</i> , 2001, 47, 587-599.	4.3	18
15	Evolving complex group behaviors using genetic programming with fitness switching. <i>Artificial Life and Robotics</i> , 2000, 4, 103-108.	1.2	3
16	Evolving neural trees for time series prediction using Bayesian evolutionary algorithms. , 0, , .		6
17	Bayesian evolutionary algorithms for evolving neural tree models of time series data. , 0, , .		1
18	Evolutionary optimization by distribution estimation with mixtures of factor analyzers. , 0, , .		1