

# Sophia Tsoka

## List of Publications by Year in descending order

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Version: 2024-02-01

83  
papers

4,612  
citations

147801

31  
h-index

106344

65  
g-index

84  
all docs

84  
docs citations

84  
times ranked

10057  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-based identification of novel endotypes in adult atopic dermatitis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 1486-1498.	5.7	8
2	Novel drug-target interactions via link prediction and network embedding. <i>BMC Bioinformatics</i> , 2022, 23, 121.	2.6	6
3	INFLUENCE OF FLG LOSS-OF-FUNCTION MUTATIONS IN HOST-MICROBE INTERACTIONS DURING ATOPIC SKIN INFLAMMATION. <i>Journal of Dermatological Science</i> , 2022, , .	1.9	0
4	Microbial and transcriptional differences elucidate atopic dermatitis heterogeneity across skin sites. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1173-1187.	5.7	16
5	Translational aspects of biologicals: monoclonal antibodies and antibody-drug conjugates as examples. , 2021, , 329-350.		0
6	Combined anti-PD-1 and anti-CTLA-4 checkpoint blockade: Treatment of melanoma and immune mechanisms of action. <i>European Journal of Immunology</i> , 2021, 51, 544-556.	2.9	71
7	Cancer Grade Model: a multi-gene machine learning-based risk classification for improving prognosis in breast cancer. <i>British Journal of Cancer</i> , 2021, 125, 748-758.	6.4	15
8	Tumor-Infiltrating B Lymphocyte Profiling Identifies IgG-Biased, Clonally Expanded Prognostic Phenotypes in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2021, 81, 4290-4304.	0.9	40
9	Sparse Regression in Cancer Genomics: Comparing Variable Selection and Predictions in Real World Data. <i>Cancer Informatics</i> , 2021, 20, 117693512110562.	1.9	2
10	IgE Activates Monocytes from Cancer Patients to Acquire a Pro-Inflammatory Phenotype. <i>Cancers</i> , 2020, 12, 3376.	3.7	15
11	B Cells in Patients With Melanoma: Implications for Treatment With Checkpoint Inhibitor Antibodies. <i>Frontiers in Immunology</i> , 2020, 11, 622442.	4.8	39
12	Identification of Important Biological Pathways for Ischemic Stroke Prediction through a Mathematical Programming Optimisation Model-DIGS. , 2020, , .		1
13	Microbe-host interplay in atopic dermatitis and psoriasis. <i>Nature Communications</i> , 2019, 10, 4703.	12.8	217
14	Network-based piecewise linear regression for QSAR modelling. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 831-844.	2.9	13
15	Immune mediator expression signatures are associated with improved outcome in ovarian carcinoma. <i>Oncology</i> , 2019, 8, e1593811.	4.6	20
16	Optimal Piecewise Linear Regression Algorithm for QSAR Modelling. <i>Molecular Informatics</i> , 2019, 38, e1800028.	2.5	19
17	IgE re-programs alternatively-activated human macrophages towards pro-inflammatory anti-tumoural states. <i>EBioMedicine</i> , 2019, 43, 67-81.	6.1	49
18	PHI-Nets: A Network Resource for Ascomycete Fungal Pathogens to Annotate and Identify Putative Virulence Interacting Proteins and siRNA Targets. <i>Frontiers in Microbiology</i> , 2019, 10, 2721.	3.5	8

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19	Reactome Pengine: a web-logic API to the Homo sapiens reactome. <i>Bioinformatics</i> , 2018, 34, 2856-2858.	4.1	5
20	An immunologically relevant rodent model demonstrates safety of therapy using a tumour-specific IgE. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2018, 73, 2328-2341.	5.7	24
21	Anti-Folate Receptor-1 IgE but not IgG Recruits Macrophages to Attack Tumors via TNF/MCP-1 Signaling. <i>Cancer Research</i> , 2017, 77, 1127-1141.	0.9	58
22	A regression tree approach using mathematical programming. <i>Expert Systems With Applications</i> , 2017, 78, 347-357.	7.6	89
23	Chondroitin Sulfate Proteoglycan 4 and Its Potential As an Antibody Immunotherapy Target across Different Tumor Types. <i>Frontiers in Immunology</i> , 2017, 8, 1911.	4.8	87
24	Community Structure Detection for Directed Networks through Modularity Optimisation. <i>Algorithms</i> , 2016, 9, 73.	2.1	11
25	Organizational principles of the Reactome human BioPAX model using graph theory methods. <i>Journal of Complex Networks</i> , 2016, , cnw003.	1.8	1
26	The pruritus- and TH2-associated cytokine IL-31 promotes growth of sensory nerves. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 500-508.e24.	2.9	201
27	A mathematical programming approach for sequential clustering of dynamic networks. <i>European Physical Journal B</i> , 2016, 89, 1.	1.5	9
28	Mathematical programming for piecewise linear regression analysis. <i>Expert Systems With Applications</i> , 2016, 44, 156-167.	7.6	85
29	Using ILP to Identify Pathway Activation Patterns in Systems Biology. <i>Lecture Notes in Computer Science</i> , 2016, 9575, 137-151.	1.3	2
30	Detection of Composite Communities in Multiplex Biological Networks. <i>Scientific Reports</i> , 2015, 5, 10345.	3.3	37
31	Link Prediction Methods and Their Accuracy for Different Social Networks and Network Metrics. <i>Scientific Programming</i> , 2015, 2015, 1-13.	0.7	44
32	CytoASP: a Cytoscape app for qualitative consistency reasoning, prediction and repair in biological networks. <i>BMC Systems Biology</i> , 2015, 9, 34.	3.0	3
33	Sample re-weighting hyper box classifier for multi-class data classification. <i>Computers and Industrial Engineering</i> , 2015, 85, 44-56.	6.3	13
34	Pathway-level disease data mining through hyper-box principles. <i>Mathematical Biosciences</i> , 2015, 260, 25-34.	1.9	5
35	DyCoNet: A Gephi Plugin for Community Detection in Dynamic Complex Networks. <i>PLoS ONE</i> , 2014, 9, e101357.	2.5	41
36	Community Structure Detection for Overlapping Modules through Mathematical Programming in Protein Interaction Networks. <i>PLoS ONE</i> , 2014, 9, e112821.	2.5	18

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37	Integrative Biology Approach Identifies Cytokine Targeting Strategies for Psoriasis. <i>Science Translational Medicine</i> , 2014, 6, 223ra22.	12.4	41
38	Pathway activity inference for multiclass disease classification through a mathematical programming optimisation framework. <i>BMC Bioinformatics</i> , 2014, 15, 390.	2.6	6
39	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013, 93, 876-890.	6.2	330
40	Gene Network and Proteomic Analyses of Cardiac Responses to Pathological and Physiological Stress. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 588-597.	5.1	21
41	Network-Based Data Integration for Selecting Candidate Virulence Associated Proteins in the Cereal Infecting Fungus <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2013, 8, e67926.	2.5	18
42	A Mathematical Programming Approach to Community Structure Detection in Complex Networks. <i>Computer Aided Chemical Engineering</i> , 2012, 30, 1387-1391.	0.5	2
43	DETECTION OF DISJOINT AND OVERLAPPING MODULES IN WEIGHTED COMPLEX NETWORKS. <i>International Journal of Modeling, Simulation, and Scientific Computing</i> , 2012, 15, 1150023.	1.4	9
44	Transcriptome classification reveals molecular subtypes in psoriasis. <i>BMC Genomics</i> , 2012, 13, 472.	2.8	55
45	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	21.4	701
46	Functional and Topological Properties in Hepatocellular Carcinoma Transcriptome. <i>PLoS ONE</i> , 2012, 7, e35510.	2.5	24
47	Toward Prediction of Immune Mechanisms and Design of Immunotherapies in Melanoma. <i>Critical Reviews in Biomedical Engineering</i> , 2012, 40, 279-294.	0.9	8
48	Detection of Multi-clustered Genes and Community Structure for the Plant Pathogenic Fungus <i>Fusarium graminearum</i> . <i>Lecture Notes in Computer Science</i> , 2012, , 69-86.	1.3	8
49	Metabolic homeostasis is maintained in myocardial hibernation by adaptive changes in the transcriptome and proteome. <i>Journal of Molecular and Cellular Cardiology</i> , 2011, 50, 982-990.	1.9	24
50	Disease Classification through Integer Optimisation. <i>Computer Aided Chemical Engineering</i> , 2011, 29, 1548-1552.	0.5	1
51	Functional Genomics Assistant (FUGA): a toolbox for the analysis of complex biological networks. <i>BMC Research Notes</i> , 2011, 4, 462.	1.4	17
52	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. <i>BMC Evolutionary Biology</i> , 2011, 11, 142.	3.2	3
53	Genome-wide expression patterns in physiological cardiac hypertrophy. <i>BMC Genomics</i> , 2010, 11, 557.	2.8	17
54	A Systems Model for Immune Cell Interactions Unravels the Mechanism of Inflammation in Human Skin. <i>PLoS Computational Biology</i> , 2010, 6, e1001024.	3.2	51

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55	Promoter Complexity and Tissue-Specific Expression of Stress Response Components in <i>Mytilus galloprovincialis</i> , a Sessile Marine Invertebrate Species. <i>PLoS Computational Biology</i> , 2010, 6, e1000847.	3.2	9
56	Module detection in complex networks using integer optimisation. <i>Algorithms for Molecular Biology</i> , 2010, 5, 36.	1.2	23
57	Stratification of co-evolving genomic groups using ranked phylogenetic profiles. <i>BMC Bioinformatics</i> , 2009, 10, 355.	2.6	8
58	MINLP Models for the Synthesis of Optimal Peptide Tags and Downstream Protein Processing. <i>Biotechnology Progress</i> , 2008, 21, 875-884.	2.6	23
59	Computational methodologies for genome evolution and functional association. <i>Computers and Chemical Engineering</i> , 2007, 31, 943-949.	3.8	1
60	Finding community structures in complex networks using mixed integer optimisation. <i>European Physical Journal B</i> , 2007, 60, 231-239.	1.5	67
61	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. <i>Nucleic Acids Research</i> , 2005, 33, 6083-6089.	14.5	570
62	CoGenT++: an extensive and extensible data environment for computational genomics. <i>Bioinformatics</i> , 2005, 21, 3806-3810.	4.1	22
63	Percolation of annotation errors through hierarchically structured protein sequence databases. <i>Mathematical Biosciences</i> , 2005, 193, 223-234.	1.9	67
64	Robustness of the p53 network and biological hackers. <i>FEBS Letters</i> , 2005, 579, 3037-3042.	2.8	38
65	Automated metabolic reconstruction for <i>Methanococcus jannaschii</i> . <i>Archaea</i> , 2004, 1, 223-229.	2.3	37
66	Computational Analysis of <i>Plasmodium falciparum</i> Metabolism: Organizing Genomic Information to Facilitate Drug Discovery. <i>Genome Research</i> , 2004, 14, 917-924.	5.5	206
67	Metabolic database systems for the analysis of genome-wide function. <i>Biotechnology and Bioengineering</i> , 2003, 84, 750-755.	3.3	7
68	Beyond 100 genomes. <i>Genome Biology</i> , 2003, 4, 402.	9.6	23
69	Genome evolution reveals biochemical networks and functional modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15428-15433.	7.1	140
70	The Phylogenetic Extent of Metabolic Enzymes and Pathways. <i>Genome Research</i> , 2003, 13, 422-427.	5.5	91
71	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	4.1	65
72	Automated Genome Functional Annotation for Structural Genomics. , 2003, , 349-368.		0

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73	Modeling the percolation of annotation errors in a database of protein sequences. <i>Bioinformatics</i> , 2002, 18, 1641-1649.	4.1	153
74	Functional Versatility and Molecular Diversity of the Metabolic Map of <i>Escherichia coli</i> . <i>Genome Research</i> , 2001, 11, 1503-1510.	5.5	29
75	Prediction of protein interactions: metabolic enzymes are frequently involved in gene fusion. <i>Nature Genetics</i> , 2000, 26, 141-142.	21.4	91
76	Selective Flocculation and Precipitation for the Improvement of Virus-Like Particle Recovery from Yeast Homogenate. <i>Biotechnology Progress</i> , 2000, 16, 661-667.	2.6	18
77	CAST: an iterative algorithm for the complexity analysis of sequence tracts. <i>Bioinformatics</i> , 2000, 16, 915-922.	4.1	165
78	Recent developments and future directions in computational genomics. <i>FEBS Letters</i> , 2000, 480, 42-48.	2.8	49
79	Genome sequences and great expectations. <i>Genome Biology</i> , 2000, 2, interactions0001.1.	9.6	40
80	Virus-like particle analysis in yeast homogenate using a laser light-scattering assay. , 1999, 63, 290-297.		5
81	Reproducibility in genome sequence annotation: the <i>Plasmodium falciparum</i> chromosome 2 case. <i>FEBS Letters</i> , 1999, 451, 354-355.	2.8	14
82	Rapid monitoring of virus-like particles using an optical biosensor: A feasibility study. <i>Journal of Biotechnology</i> , 1998, 63, 147-153.	3.8	20
83	Selection of Chromatographic Protein Purification Operations Based on Physicochemical Properties. <i>Annals of the New York Academy of Sciences</i> , 1994, 721, 348-364.	3.8	23