

# Sadegh Azimzadeh Jamalkandi

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

749  
citations

516215

16  
h-index

580395

25  
g-index

40  
all docs

40  
docs citations

40  
times ranked

1081  
citing authors

#	ARTICLE	IF	CITATIONS
1	Therapeutic face of RNAi: <i>in vivo</i> challenges. Expert Opinion on Biological Therapy, 2015, 15, 269-285.	1.4	51
2	A multimodal deep learning-based drug repurposing approach for treatment of COVID-19. Molecular Diversity, 2021, 25, 1717-1730.	2.1	44
3	Reconstruction of Arabidopsis thaliana fully integrated small RNA pathway. Functional and Integrative Genomics, 2009, 9, 419-432.	1.4	42
4	Worldwide prevalence of viral infection in AECOPD patients: A meta-analysis. Microbial Pathogenesis, 2017, 113, 190-196.	1.3	42
5	Isolation of Novel Probiotic Lactobacillus and Enterococcus Strains From Human Salivary and Fecal Sources. Frontiers in Microbiology, 2020, 11, 597946.	1.5	40
6	Bacterial infections in acute exacerbation of chronic obstructive pulmonary disease: a systematic review and meta-analysis. Infection, 2020, 48, 19-35.	2.3	37
7	Human endogenous retrovirus env genes: Potential blood biomarkers in lung cancer. Microbial Pathogenesis, 2018, 115, 189-193.	1.3	34
8	Detection of novel biomarkers for early detection of Non-Muscle-Invasive Bladder Cancer using Competing Endogenous RNA network analysis. Scientific Reports, 2019, 9, 8434.	1.6	34
9	Identification of biomarkers in common chronic lung diseases by co-expression networks and drug-target interactions analysis. Molecular Medicine, 2020, 26, 9.	1.9	34
10	A logic-based dynamic modeling approach to explicate the evolution of the central dogma of molecular biology. PLoS ONE, 2017, 12, e0189922.	1.1	33
11	The composition of lung microbiome in lung cancer: a systematic review and meta-analysis. BMC Microbiology, 2021, 21, 315.	1.3	28
12	Identification of Novel Genes in Human Airway Epithelial Cells associated with Chronic Obstructive Pulmonary Disease (COPD) using Machine-Based Learning Algorithms. Scientific Reports, 2018, 8, 15775.	1.6	27
13	Oral and nasal probiotic administration for the prevention and alleviation of allergic diseases, asthma and chronic obstructive pulmonary disease. Nutrition Research Reviews, 2021, 34, 1-16.	2.1	27
14	Involvement of microRNAs in physiological and pathological processes in asthma. Journal of Cellular Physiology, 2019, 234, 21547-21559.	2.0	26
15	Systems Biomedicine of Rabies Delineates the Affected Signaling Pathways. Frontiers in Microbiology, 2016, 7, 1688.	1.5	21
16	Pneumococcal Disease and the Effectiveness of the PPV23 Vaccine in Adults: A Two-Stage Bayesian Meta-Analysis of Observational and RCT Reports. Scientific Reports, 2018, 8, 11051.	1.6	21
17	An efficient hybrid feature selection method to identify potential biomarkers in common chronic lung inflammatory diseases. Genomics, 2020, 112, 3284-3293.	1.3	17
18	Human RNAi pathway: crosstalk with organelles and cells. Functional and Integrative Genomics, 2014, 14, 31-46.	1.4	16

#	ARTICLE	IF	CITATIONS
19	Atopic dermatitis-associated protein interaction network lead to new insights in chronic sulfur mustard skin lesion mechanisms. <i>Expert Review of Proteomics</i> , 2013, 10, 449-460.	1.3	14
20	<scp>PI3K</scp> signalling in chronic obstructive pulmonary disease and opportunities for therapy. <i>Journal of Pathology</i> , 2021, 254, 505-518.	2.1	14
21	Immunology of Chronic Obstructive Pulmonary Disease and Sulfur Mustard Induced Airway Injuries: Implications for Immunotherapeutic Interventions. <i>Current Pharmaceutical Design</i> , 2016, 22, 2975-2996.	0.9	14
22	Cellular and molecular mechanisms of acute exposure to sulfur mustard: a systematic review. <i>Journal of Receptor and Signal Transduction Research</i> , 2017, 37, 200-216.	1.3	13
23	Distinguishing drug/non-drug-like small molecules in drug discovery using deep belief network. <i>Molecular Diversity</i> , 2021, 25, 827-838.	2.1	13
24	Th17/Treg immunoregulation and implications in treatment of sulfur mustard gas-induced lung diseases. <i>Expert Review of Clinical Immunology</i> , 2017, 13, 1173-1188.	1.3	12
25	Association between chronic obstructive pulmonary disease and interleukins gene variants: A systematic review and meta-analysis. <i>Cytokine</i> , 2019, 117, 65-71.	1.4	12
26	MiR-486-5p enhances cisplatin sensitivity of human muscle-invasive bladder cancer cells by induction of apoptosis and down-regulation of metastatic genes. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2020, 38, 738.e9-738.e21.	0.8	12
27	Small regulatory noncoding RNAs in <i>Drosophila melanogaster</i> : biogenesis and biological functions. <i>Briefings in Functional Genomics</i> , 2020, 19, 309-323.	1.3	12
28	RNAi pathway integration in <i>Caenorhabditis elegans</i> development. <i>Functional and Integrative Genomics</i> , 2011, 11, 389-405.	1.4	11
29	Laboratory methods to decipher epigenetic signatures: a comparative review. <i>Cellular and Molecular Biology Letters</i> , 2021, 26, 46.	2.7	11
30	Involvement of immune system and Epithelial-Mesenchymal-Transition in increased invasiveness of clustered circulatory tumor cells in breast cancer. <i>BMC Medical Genomics</i> , 2021, 14, 273.	0.7	10
31	Atopic dermatitis: molecular, cellular, and clinical aspects. <i>Molecular Biology Reports</i> , 2022, 49, 3333-3348.	1.0	10
32	TNF- $\alpha$ $\gamma$ 308 G/A variant and susceptibility to chronic obstructive pulmonary disease: A systematic review and meta-analysis. <i>Cytokine</i> , 2019, 123, 154763.	1.4	7
33	Re-wiring and gene expression changes of AC025034.1 and ATP2B1 play complex roles in early-to-late breast cancer progression. <i>BMC Genomic Data</i> , 2022, 23, 6.	0.7	6
34	Airway remodeling: Systems biology approach, from bench to bedside. <i>Technology and Health Care</i> , 2016, 24, 811-819.	0.5	1
35	Causal Path of COPD Progression-Associated Genes in Different Biological Samples. <i>COPD: Journal of Chronic Obstructive Pulmonary Disease</i> , 2022, 19, 290-299.	0.7	1
36	The identification of co-expressed gene modules in <i>Streptococcus pneumoniae</i> from colonization to infection to predict novel potential virulence genes. <i>BMC Microbiology</i> , 2020, 20, 376.	1.3	0