Anna Niarakis

List of Publications by Year
in descending order

31 papers	1,030 citations	687363 13 h-index	477307 29 g-index
42 all docs	42 docs citations	42 times ranked	1567 citing authors

#	Article	IF	Citations
1	Curcumin-decorated nanoliposomes with very high affinity for amyloid-β1-42 peptide. Biomaterials, 2011, 32, 1635-1645.	11.4	198
2	Effect of curcumin-associated and lipid ligand-functionalized nanoliposomes on aggregation of the Alzheimer's Aβ peptide. Nanomedicine: Nanotechnology, Biology, and Medicine, 2011, 7, 541-550.	3.3	122
3	Uptake and permeability studies of BBB-targeting immunoliposomes using the hCMEC/D3 cell line. European Journal of Pharmaceutics and Biopharmaceutics, 2011, 77, 265-274.	4.3	108
4	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
5	Automated inference of Boolean models from molecular interaction maps using CaSQ. Bioinformatics, 2020, 36, 4473-4482.	4.1	57
6	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
7	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	6.5	48
8	Building digital twins of the human immune system: toward a roadmap. Npj Digital Medicine, 2022, 5, .	10.9	43
9	RA-map: building a state-of-the-art interactive knowledge base for rheumatoid arthritis. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	25
10	Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. Briefings in Bioinformatics, 2021, 22, 1848-1859.	6.5	25
11	Boolean modelling as a logic-based dynamic approach in systems medicine. Computational and Structural Biotechnology Journal, 2022, 20, 3161-3172.	4.1	23
12	Computational Modeling of the Main Signaling Pathways Involved in Mast Cell Activation. Current Topics in Microbiology and Immunology, 2014, 382, 69-93.	1.1	22
13	Computational Systems Biology Approach for the Study of Rheumatoid Arthritis: From a Molecular Map to a Dynamical Model. Genomics and Computational Biology, 2017, 4, 100050.	0.7	20
14	A practical guide to mechanistic systems modeling in biology using a logic-based approach. Briefings in Bioinformatics, 2021, 22, .	6.5	19
15	Metabolic Reprogramming of Fibroblasts as Therapeutic Target in Rheumatoid Arthritis and Cancer: Deciphering Key Mechanisms Using Computational Systems Biology Approaches. Cancers, 2021, 13, 35.	3.7	16
16	The status of causality in biological databases: data resources and data retrieval possibilities to support logical modeling. Briefings in Bioinformatics, 2021, 22, .	6.5	15
17	Antiovarian antibodies in primary Sjogren's syndrome. Rheumatology International, 2007, 27, 1149-1155.	3.0	14
18	Identification of putative master regulators in rheumatoid arthritis synovial fibroblasts using gene expression data and network inference. Scientific Reports, 2020, 10, 16236.	3.3	12

#	Article	IF	Citations
19	Proteomic Analysis of the SH2Domain-containing Leukocyte Protein of 76 kDa (SLP76) Interactome. Molecular and Cellular Proteomics, 2013, 12, 2874-2889.	3.8	11
20	Inference of an Integrative, Executable Network for Rheumatoid Arthritis Combining Data-Driven Machine Learning Approaches and a State-of-the-Art Mechanistic Disease Map. Journal of Personalized Medicine, 2021, 11, 785.	2.5	11
21	Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i>. Briefings in Bioinformatics, 2022, 23, .	6.5	10
22	Walker 256 cancer cells secrete tissue inhibitor of metalloproteinase-free metalloproteinase-9. Molecular and Cellular Biochemistry, 2009, 328, 189-199.	3.1	9
23	Detection of a latent soluble form of membrane typeÂ1 matrix metalloprotease bound with tissue inhibitor of matrix metalloproteinases-2 in periprosthetic tissues and fluids from loose arthroplasty endoprostheses. FEBS Journal, 2013, 280, 6541-6555.	4.7	9
24	Data integration in logic-based models of biological mechanisms. Current Opinion in Systems Biology, 2021, 28, 100386.	2.6	9
25	A Mechanistic Cellular Atlas of the Rheumatic Joint. Frontiers in Systems Biology, 0, 2, .	0.7	8
26	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	4.1	6
27	Effects of proteasome inhibitors on cytokines, metalloproteinases and their inhibitors and collagen type-I expression in periprosthetic tissues and fibroblasts from loose arthroplasty endoprostheses. Connective Tissue Research, 2019, 60, 555-570.	2.3	2
28	Activating and Inhibitory Receptors on Mast Cells. , 2014, , 1-10.		2
29	Toehold switch based biosensors for sensing the highly trafficked rosewood Dalbergia maritima. Synthetic and Systems Biotechnology, 2022, 7, 791-801.	3.7	2
30	ModÃ©lisation logique et analyse intÃ©grative des voies molÃ©culaires impliquÃ©es dans la polyarthrite rhumatoÃ¯de. Revue Du Rhumatisme (Edition Francaise), 2016, 83, A297.	0.0	0
31	Fc epsilon receptor (FCERI) signaling. Reactome - A Curated Knowledgebase of Biological Pathways, 0, 45, .	0.0	0