

Shai S Shen-Orr

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

17,222
citations

126907

33
h-index

149698

56
g-index

73
all docs

73
docs citations

73
times ranked

22436
citing authors

#	ARTICLE	IF	CITATIONS
1	Network Motifs: Simple Building Blocks of Complex Networks. <i>Science</i> , 2002, 298, 824-827.	12.6	5,915
2	Network motifs in the transcriptional regulation network of <i>Escherichia coli</i> . <i>Nature Genetics</i> , 2002, 31, 64-68.	21.4	2,603
3	Superfamilies of Evolved and Designed Networks. <i>Science</i> , 2004, 303, 1538-1542.	12.6	1,182
4	A Single-Cell Transcriptomic Map of the Human and Mouse Pancreas Reveals Inter- and Intra-cell Population Structure. <i>Cell Systems</i> , 2016, 3, 346-360.e4.	6.2	1,098
5	Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. <i>Cell</i> , 2015, 160, 37-47.	28.9	828
6	Glycolysis-Mediated Changes in Acetyl-CoA and Histone Acetylation Control the Early Differentiation of Embryonic Stem Cells. <i>Cell Metabolism</i> , 2015, 21, 392-402.	16.2	541
7	ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. <i>Scientific Data</i> , 2018, 5, 180015.	5.3	529
8	Cell type-specific gene expression differences in complex tissues. <i>Nature Methods</i> , 2010, 7, 287-289.	19.0	460
9	A clinically meaningful metric of immune age derived from high-dimensional longitudinal monitoring. <i>Nature Medicine</i> , 2019, 25, 487-495.	30.7	317
10	Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology</i> , 2017, 18, 583-593.	14.5	296
11	Systems Analysis of Immunity to Influenza Vaccination across Multiple Years and in Diverse Populations Reveals Shared Molecular Signatures. <i>Immunity</i> , 2015, 43, 1186-1198.	14.3	286
12	Cytomegalovirus infection enhances the immune response to influenza. <i>Science Translational Medicine</i> , 2015, 7, 281ra43.	12.4	277
13	Computational deconvolution: extracting cell type-specific information from heterogeneous samples. <i>Current Opinion in Immunology</i> , 2013, 25, 571-578.	5.5	270
14	UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. <i>Cell</i> , 2019, 179, 219-235.e21.	28.9	270
15	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. <i>Nature Communications</i> , 2019, 10, 38.	12.8	215
16	An inflammatory aging clock (iAge) based on deep learning tracks multimorbidity, immunosenescence, frailty and cardiovascular aging. <i>Nature Aging</i> , 2021, 1, 598-615.	11.6	202
17	GeneCards TM 2002: towards a complete, object-oriented, human gene compendium. <i>Bioinformatics</i> , 2002, 18, 1542-1543.	4.1	185
18	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. <i>Molecular Systems Biology</i> , 2013, 9, 659.	7.2	173

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19	Activation of the reward system boosts innate and adaptive immunity. <i>Nature Medicine</i> , 2016, 22, 940-944.	30.7	168
20	Cell-centred meta-analysis reveals baseline predictors of anti-TNF \pm non-response in biopsy and blood of patients with IBD. <i>Gut</i> , 2019, 68, 604-614.	12.1	153
21	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. <i>Science Immunology</i> , 2017, 2, .	11.9	122
22	Defective Signaling in the JAK-STAT Pathway Tracks with Chronic Inflammation and Cardiovascular Risk in Aging Humans. <i>Cell Systems</i> , 2016, 3, 374-384.e4.	6.2	107
23	New tools for classification and monitoring of autoimmune diseases. <i>Nature Reviews Rheumatology</i> , 2012, 8, 317-328.	8.0	81
24	Alignment of single-cell trajectories to compare cellular expression dynamics. <i>Nature Methods</i> , 2018, 15, 267-270.	19.0	78
25	Found In Translation: a machine learning model for mouse-to-human inference. <i>Nature Methods</i> , 2018, 15, 1067-1073.	19.0	60
26	Immune-centric network of cytokines and cells in disease context identified by computational mining of PubMed. <i>Nature Biotechnology</i> , 2018, 36, 651-659.	17.5	58
27	Simulation of single-protein nanopore sensing shows feasibility for whole-proteome identification. <i>PLoS Computational Biology</i> , 2019, 15, e1007067.	3.2	46
28	Variability in the immune system: of vaccine responses and immune states. <i>Current Opinion in Immunology</i> , 2013, 25, 542-547.	5.5	45
29	A c-Myc/miR17-92/Pten Axis Controls PI3K-Mediated Positive and Negative Selection in B Cell Development and Reconstitutes CD19 Deficiency. <i>Cell Reports</i> , 2016, 16, 419-431.	6.4	45
30	Reconstructing the Genomic Content of Microbiome Taxa through Shotgun Metagenomic Deconvolution. <i>PLoS Computational Biology</i> , 2013, 9, e1003292.	3.2	41
31	Regulation of S100A8 Stability by RNF5 in Intestinal Epithelial Cells Determines Intestinal Inflammation and Severity of Colitis. <i>Cell Reports</i> , 2018, 24, 3296-3311.e6.	6.4	39
32	Tofacitinib for polyarteritis nodosa: a tailored therapy. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 2214-2216.	0.9	36
33	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. <i>Frontiers in Immunology</i> , 2019, 10, 2469.	4.8	36
34	Systems Immunology Reveals Markers of Susceptibility to West Nile Virus Infection. <i>Vaccine Journal</i> , 2015, 22, 6-16.	3.1	35
35	UV-Protection Timer Controls Linkage between Stress and Pigmentation Skin Protection Systems. <i>Molecular Cell</i> , 2018, 72, 444-456.e7.	9.7	34
36	A relational schema for both array-based and SAGE gene expression experiments. <i>Bioinformatics</i> , 2001, 17, 300-308.	4.1	33

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37	Significance analysis of xMap cytokine bead arrays. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2848-2853.	7.1	30
38	Pairing of competitive and topologically distinct regulatory modules enhances patterned gene expression. Molecular Systems Biology, 2008, 4, 163.	7.2	28
39	Antigen-Dependent Integration of Opposing Proximal TCR-Signaling Cascades Determines the Functional Fate of T Lymphocytes. Journal of Immunology, 2014, 192, 2109-2119.	0.8	27
40	Inflammatory macrophage-associated 3-gene signature predicts subclinical allograft injury and graft survival. JCI Insight, 2018, 3, .	5.0	27
41	Shaping Functional Avidity of CAR T Cells: Affinity, Avidity, and Antigen Density That Regulate Response. Molecular Cancer Therapeutics, 2021, 20, 872-884.	4.1	26
42	Infliximab-Tumor Necrosis Factor Complexes Elicit Formation of Anti-Drug Antibodies. Gastroenterology, 2019, 157, 1338-1351.e8.	1.3	24
43	Batch correction evaluation framework using a-priori gene-gene associations: applied to the GTEx dataset. BMC Bioinformatics, 2019, 20, 268.	2.6	24
44	IL-6 contributes to metastatic switch via the differentiation of monocytic-dendritic progenitors into prometastatic immune cells. , 2021, 9, e002856.		19
45	Composition and regulation of maternal and zygotic transcriptomes reflects species-specific reproductive mode. Genome Biology, 2010, 11, R58.	9.6	18
46	Identification of Gene Expression Profiles Associated with an Increased Risk of Post-Operative Recurrence in Crohn's Disease. Journal of Crohn's and Colitis, 2022, 16, 1269-1280.	1.3	15
47	The CTLA-4 rs231775 GG genotype is associated with favorable 90-day survival in Caucasian patients with sepsis. Scientific Reports, 2018, 8, 15140.	3.3	13
48	CTLA-4 Genetic Variants Predict Survival in Patients with Sepsis. Journal of Clinical Medicine, 2019, 8, 70.	2.4	13
49	TOWARDS A CYTOKINE-CELL INTERACTION KNOWLEDGEBASE OF THE ADAPTIVE IMMUNE SYSTEM. , 2008, , .		10
50	Towards a cytokine-cell interaction knowledgebase of the adaptive immune system. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 439-50.	0.7	10
51	IL-31 induces antitumor immunity in breast carcinoma. , 2020, 8, e001010.		9
52	Mature neutrophils and a NFkB-to-IFN transition determine the unifying disease recovery dynamics in COVID-19. Cell Reports Medicine, 2022, , 100652.	6.5	9
53	Gene expression deconvolution in linear space. Nature Methods, 2012, 9, 9-9.	19.0	8
54	Phenotypic Models of CAR T-Cell Activation Elucidate the Pivotal Regulatory Role of CAR Downmodulation. Molecular Cancer Therapeutics, 2021, 20, 946-957.	4.1	8

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55	Challenges and Promise for the Development of Human Immune Monitoring. Rambam Maimonides Medical Journal, 2012, 3, e0023.	1.0	4
56	Alignment of single-cell trajectories by tuMap enables high-resolution quantitative comparison of cancer samples. Cell Systems, 2021, , .	6.2	3
57	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. Molecular Systems Biology, 2014, 10, .	7.2	2
58	Autologous Hematological Stem Cell Transplantation for Systemic Sclerosis in Israel. Israel Medical Association Journal, 2020, 22, 104-110.	0.1	2
59	GeneCards/spl trade/ 2002: an evolving human gene compendium. , 0, , .		1
60	Sensitivity analysis for inference with partially identifiable covariance matrices. Computational Statistics, 2014, 29, 529-546.	1.5	1
61	Immunological response in normal healthy twins across age. , 2010, , .		0
62	Systems Immunology. , 2013, , 481-497.		0
63	Response to: â€ˆTofacitinib for the treatment of polyarteritis nodosa: a literature reviewâ€™™. Correspondence on â€ˆTofacitinib for polyarteritis nodosa: a tailored therapyâ€™™ by Rimar<i>et al</i>. Annals of the Rheumatic Diseases, 2022, 81, e205-e205.	0.9	0
64	OP33 Multi-omics analysis reveals specific bio-geographical and functional characteristics in inflammatory bowel disease intestinal mucosa. Journal of Crohn's and Colitis, 2020, 14, S031-S034.	1.3	0
65	A Unique Crosstalk between Tumor Cells and Hematopoietic Stem Cells Reveals a Myeloid Differentiation Pattern Signature Contributing to Metastasis. Blood, 2019, 134, 2465-2465.	1.4	0