

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

126708

33
h-index

149479

56
g-index

73
all docs

73
docs citations

73
times ranked

22436
citing authors

#	ARTICLE	IF	CITATIONS
1	Response to: "Tofacitinib for the treatment of polyarteritis nodosa: a literature review"™. Correspondence on "Tofacitinib for polyarteritis nodosa: a tailored therapy"™ by Rimar<i>et al</i>. Annals of the Rheumatic Diseases, 2022, 81, e205-e205.	0.5	0
2	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.	0.6	15
3	Mature neutrophils and a NFκB-to-IFN transition determine the unifying disease recovery dynamics in COVID-19. Cell Reports Medicine, 2022, , 100652.	3.3	9
4	Phenotypic Models of CAR T-Cell Activation Elucidate the Pivotal Regulatory Role of CAR Downmodulation. Molecular Cancer Therapeutics, 2021, 20, 946-957.	1.9	8
5	Shaping Functional Avidity of CAR T Cells: Affinity, Avidity, and Antigen Density That Regulate Response. Molecular Cancer Therapeutics, 2021, 20, 872-884.	1.9	26
6	IL-6 contributes to metastatic switch via the differentiation of monocytic-dendritic progenitors into prometastatic immune cells. , 2021, 9, e002856.		19
7	An inflammatory aging clock (iAge) based on deep learning tracks multimorbidity, immunosenescence, frailty and cardiovascular aging. Nature Aging, 2021, 1, 598-615.	5.3	202
8	Alignment of single-cell trajectories by tuMap enables high-resolution quantitative comparison of cancer samples. Cell Systems, 2021, , .	2.9	3
9	IL-31 induces antitumor immunity in breast carcinoma. , 2020, 8, e001010.		9
10	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.	0.6	0
11	Autologous Hematological Stem Cell Transplantation for Systemic Sclerosis in Israel. Israel Medical Association Journal, 2020, 22, 104-110.	0.1	2
12	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. Frontiers in Immunology, 2019, 10, 2469.	2.2	36
13	UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. Cell, 2019, 179, 219-235.e21.	13.5	270
14	Infliximab's Tumor Necrosis Factor Complexes Elicit Formation of Anti-Drug Antibodies. Gastroenterology, 2019, 157, 1338-1351.e8.	0.6	24
15	Batch correction evaluation framework using a-priori gene-gene associations: applied to the GTEx dataset. BMC Bioinformatics, 2019, 20, 268.	1.2	24
16	Simulation of single-protein nanopore sensing shows feasibility for whole-proteome identification. PLoS Computational Biology, 2019, 15, e1007067.	1.5	46
17	A clinically meaningful metric of immune age derived from high-dimensional longitudinal monitoring. Nature Medicine, 2019, 25, 487-495.	15.2	317
18	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. Nature Communications, 2019, 10, 38.	5.8	215

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19	CTLA-4 Genetic Variants Predict Survival in Patients with Sepsis. <i>Journal of Clinical Medicine</i> , 2019, 8, 70.	1.0	13
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.	6.1	153
21	A Unique Crosstalk between Tumor Cells and Hematopoietic Stem Cells Reveals a Myeloid Differentiation Pattern Signature Contributing to Metastasis. <i>Blood</i> , 2019, 134, 2465-2465.	0.6	0
22	ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. <i>Scientific Data</i> , 2018, 5, 180015.	2.4	529
23	Alignment of single-cell trajectories to compare cellular expression dynamics. <i>Nature Methods</i> , 2018, 15, 267-270.	9.0	78
24	Found In Translation: a machine learning model for mouse-to-human inference. <i>Nature Methods</i> , 2018, 15, 1067-1073.	9.0	60
25	UV-Protection Timer Controls Linkage between Stress and Pigmentation Skin Protection Systems. <i>Molecular Cell</i> , 2018, 72, 444-456.e7.	4.5	34
26	The CTLA-4 rs231775 GG genotype is associated with favorable 90-day survival in Caucasian patients with sepsis. <i>Scientific Reports</i> , 2018, 8, 15140.	1.6	13
27	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.	2.9	39
28	Immune-centric network of cytokines and cells in disease context identified by computational mining of PubMed. <i>Nature Biotechnology</i> , 2018, 36, 651-659.	9.4	58
29	Inflammatory macrophage-associated 3-gene signature predicts subclinical allograft injury and graft survival. <i>JCI Insight</i> , 2018, 3, .	2.3	27
30	Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology</i> , 2017, 18, 583-593.	7.0	296
31	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. <i>Science Immunology</i> , 2017, 2, .	5.6	122
32	Activation of the reward system boosts innate and adaptive immunity. <i>Nature Medicine</i> , 2016, 22, 940-944.	15.2	168
33	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.	2.9	45
34	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.	2.9	107
35	Tofacitinib for polyarteritis nodosa: a tailored therapy. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 2214-2216.	0.5	36
36	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.	2.9	1,098

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37	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.	6.6	286
38	Systems Immunology Reveals Markers of Susceptibility to West Nile Virus Infection. <i>Vaccine Journal</i> , 2015, 22, 6-16.	3.2	35
39	Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. <i>Cell</i> , 2015, 160, 37-47.	13.5	828
40	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.	7.2	541
41	Cytomegalovirus infection enhances the immune response to influenza. <i>Science Translational Medicine</i> , 2015, 7, 281ra43.	5.8	277
42	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. <i>Molecular Systems Biology</i> , 2014, 10, .	3.2	2
43	Antigen-Dependent Integration of Opposing Proximal TCR-Signaling Cascades Determines the Functional Fate of T Lymphocytes. <i>Journal of Immunology</i> , 2014, 192, 2109-2119.	0.4	27
44	Sensitivity analysis for inference with partially identifiable covariance matrices. <i>Computational Statistics</i> , 2014, 29, 529-546.	0.8	1
45	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. <i>Molecular Systems Biology</i> , 2013, 9, 659.	3.2	173
46	Variability in the immune system: of vaccine responses and immune states. <i>Current Opinion in Immunology</i> , 2013, 25, 542-547.	2.4	45
47	Computational deconvolution: extracting cell type-specific information from heterogeneous samples. <i>Current Opinion in Immunology</i> , 2013, 25, 571-578.	2.4	270
48	<i>Systems Immunology</i> . , 2013, , 481-497.		0
49	Reconstructing the Genomic Content of Microbiome Taxa through Shotgun Metagenomic Deconvolution. <i>PLoS Computational Biology</i> , 2013, 9, e1003292.	1.5	41
50	Significance analysis of xMap cytokine bead arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2848-2853.	3.3	30
51	Challenges and Promise for the Development of Human Immune Monitoring. <i>Rambam Maimonides Medical Journal</i> , 2012, 3, e0023.	0.4	4
52	Gene expression deconvolution in linear space. <i>Nature Methods</i> , 2012, 9, 9-9.	9.0	8
53	New tools for classification and monitoring of autoimmune diseases. <i>Nature Reviews Rheumatology</i> , 2012, 8, 317-328.	3.5	81
54	Cell type-specific gene expression differences in complex tissues. <i>Nature Methods</i> , 2010, 7, 287-289.	9.0	460

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55	Immunological response in normal healthy twins across age. , 2010, , .		0
56	Composition and regulation of maternal and zygotic transcriptomes reflects species-specific reproductive mode. Genome Biology, 2010, 11, R58.	13.9	18
57	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
58	TOWARDS A CYTOKINE-CELL INTERACTION KNOWLEDGEBASE OF THE ADAPTIVE IMMUNE SYSTEM. , 2008, , .		10
59	Pairing of competitive and topologically distinct regulatory modules enhances patterned gene expression. Molecular Systems Biology, 2008, 4, 163.	3.2	28
60	Superfamilies of Evolved and Designed Networks. Science, 2004, 303, 1538-1542.	6.0	1,182
61	GeneCards TM 2002: towards a complete, object-oriented, human gene compendium. Bioinformatics, 2002, 18, 1542-1543.	1.8	185
62	Network Motifs: Simple Building Blocks of Complex Networks. Science, 2002, 298, 824-827.	6.0	5,915
63	Network motifs in the transcriptional regulation network of Escherichia coli. Nature Genetics, 2002, 31, 64-68.	9.4	2,603
64	A relational schema for both array-based and SAGE gene expression experiments. Bioinformatics, 2001, 17, 300-308.	1.8	33
65	GeneCards/spl trade/ 2002: an evolving human gene compendium. , 0, , .		1