# Shai S Shen-Orr

List of Publications by Year
in descending order

| 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 | Network Motifs: Simple Building Blocks of Complex Networks. Science, 2002, 298, 824-827. | 6.0 | 5,915 |
| 2 | Network motifs in the transcriptional regulation network of Escherichia coli. Nature Genetics, 2002, 31, 64-68. | 9.4 | 2,603 |
| 3 | Superfamilies of Evolved and Designed Networks. Science, 2004, 303, 1538-1542. | 6.0 | 1,182 |
| 4 | A Single-Cell Transcriptomic Map of the Human and Mouse Pancreas Reveals Inter- and Intra-cell Population Structure. Cell Systems, 2016, 3, 346-360.e4. | 2.9 | 1,098 |
| 5 | Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. Cell, 2015, 160, 37-47. | 13.5 | 828 |
| 6 | Glycolysis-Mediated Changes in Acetyl-CoA and Histone Acetylation Control the Early Differentiation of Embryonic Stem Cells. Cell Metabolism, 2015, 21, 392-402. | 7.2 | 541 |
| 7 | ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. Scientific Data, 2018, 5, 180015. | 2.4 | 529 |
| 8 | Cell type–specific gene expression differences in complex tissues. Nature Methods, 2010, 7, 287-289. | 9.0 | 460 |
| 9 | A clinically meaningful metric of immune age derived from high-dimensional longitudinal monitoring. Nature Medicine, 2019, 25, 487-495. | 15.2 | 317 |
| 10 | Social network architecture of human immune cells unveiled by quantitative proteomics. Nature Immunology, 2017, 18, 583-593. | 7.0 | 296 |
| 11 | Systems Analysis of Immunity to Influenza Vaccination across Multiple Years and in Diverse Populations Reveals Shared Molecular Signatures. Immunity, 2015, 43, 1186-1198. | 6.6 | 286 |
| 12 | Cytomegalovirus infection enhances the immune response to influenza. Science Translational Medicine, 2015, 7, 281ra43. | 5.8 | 277 |
| 13 | Computational deconvolution: extracting cell type-specific information from heterogeneous samples. Current Opinion in Immunology, 2013, 25, 571-578. | 2.4 | 270 |
| 14 | UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. Cell, 2019, 179, 219-235.e21. | 13.5 | 270 |
| 15 | Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. Nature Communications, 2019, 10, 38. | 5.8 | 215 |
| 16 | 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 |
| 17 | GeneCardsTM 2002: towards a complete, object-oriented, human gene compendium. Bioinformatics, 2002, 18, 1542-1543. | 1.8 | 185 |
| 18 | Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. Molecular Systems Biology, 2013, 9, 659. | 3.2 | 173 |

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|---|---------|-----|-----------|
| 19 | Activation of the reward system boosts innate and adaptive immunity. Nature Medicine, 2016, 22, 940-944. | 15.2 | 168 |
| 20 | Cell-centred meta-analysis reveals baseline predictors of anti-TNFÎ± non-response in biopsy and blood of patients with IBD. Gut, 2019, 68, 604-614. | 6.1 | 153 |
| 21 | Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. Science Immunology, 2017, 2, . | 5.6 | 122 |
| 22 | Defective Signaling in the JAK-STAT Pathway Tracks with Chronic Inflammation and Cardiovascular Risk in Aging Humans. Cell Systems, 2016, 3, 374-384.e4. | 2.9 | 107 |
| 23 | New tools for classification and monitoring of autoimmune diseases. Nature Reviews Rheumatology, 2012, 8, 317-328. | 3.5 | 81 |
| 24 | Alignment of single-cell trajectories to compare cellular expression dynamics. Nature Methods, 2018, 15, 267-270. | 9.0 | 78 |
| 25 | Found In Translation: a machine learning model for mouse-to-human inference. Nature Methods, 2018, 15, 1067-1073. | 9.0 | 60 |
| 26 | Immune-centric network of cytokines and cells in disease context identified by computational mining of PubMed. Nature Biotechnology, 2018, 36, 651-659. | 9.4 | 58 |
| 27 | Simulation of single-protein nanopore sensing shows feasibility for whole-proteome identification. PLoS Computational Biology, 2019, 15, e1007067. | 1.5 | 46 |
| 28 | Variability in the immune system: of vaccine responses and immune states. Current Opinion in Immunology, 2013, 25, 542-547. | 2.4 | 45 |
| 29 | A c-Myc/miR17-92/Pten Axis Controls PI3K-Mediated Positive and Negative Selection in B Cell Development and Reconstitutes CD19 Deficiency. Cell Reports, 2016, 16, 419-431. | 2.9 | 45 |
| 30 | Reconstructing the Genomic Content of Microbiome Taxa through Shotgun Metagenomic Deconvolution. PLoS Computational Biology, 2013, 9, e1003292. | 1.5 | 41 |
| 31 | Regulation of S100A8 Stability by RNF5 in Intestinal Epithelial Cells Determines Intestinal Inflammation and Severity of Colitis. Cell Reports, 2018, 24, 3296-3311.e6. | 2.9 | 39 |
| 32 | Tofacitinib for polyarteritis nodosa: a tailored therapy. Annals of the Rheumatic Diseases, 2016, 75, 2214-2216. | 0.5 | 36 |
| 33 | Pregnancy-Induced Alterations in NK Cell Phenotype and Function. Frontiers in Immunology, 2019, 10, 2469. | 2.2 | 36 |
| 34 | Systems Immunology Reveals Markers of Susceptibility to West Nile Virus Infection. Vaccine Journal, 2015, 22, 6-16. | 3.2 | 35 |
| 35 | UV-Protection Timer Controls Linkage between Stress and Pigmentation Skin Protection Systems. Molecular Cell, 2018, 72, 444-456.e7. | 4.5 | 34 |
| 36 | A relational schema for both array-based and SAGE gene expression experiments. Bioinformatics, 2001, 17, 300-308. | 1.8 | 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. | 3.3 | 30 |
| 38 | Pairing of competitive and topologically distinct regulatory modules enhances patterned gene expression. Molecular Systems Biology, 2008, 4, 163. | 3.2 | 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. | 0.4 | 27 |
| 40 | Inflammatory macrophage–associated 3-gene signature predicts subclinical allograft injury and graft survival. JCI Insight, 2018, 3, . | 2.3 | 27 |
| 41 | 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 |
| 42 | Infliximab–Tumor Necrosis Factor Complexes Elicit Formation of Anti-Drug Antibodies. Gastroenterology, 2019, 157, 1338-1351.e8. | 0.6 | 24 |
| 43 | Batch correction evaluation framework using a-priori gene-gene associations: applied to the GTEx dataset. BMC Bioinformatics, 2019, 20, 268. | 1.2 | 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. | 13.9 | 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. | 0.6 | 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. | 1.6 | 13 |
| 48 | CTLA-4 Genetic Variants Predict Survival in Patients with Sepsis. Journal of Clinical Medicine, 2019, 8, 70. | 1.0 | 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 NFκB-to-IFN transition determine the unifying disease recovery dynamics in COVID-19. Cell Reports Medicine, 2022, , 100652. | 3.3 | 9 |
| 53 | Gene expression deconvolution in linear space. Nature Methods, 2012, 9, 9-9. | 9.0 | 8 |
| 54 | Phenotypic Models of CAR T-Cell Activation Elucidate the Pivotal Regulatory Role of CAR Downmodulation. Molecular Cancer Therapeutics, 2021, 20, 946-957. | 1.9 | 8 |

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|---|---------|-----|-----------|
| 55 | Challenges and Promise for the Development of Human Immune Monitoring. Rambam Maimonides Medical Journal, 2012, 3, e0023. | 0.4 | 4 |
| 56 | Alignment of single-cell trajectories by tuMap enables high-resolution quantitative comparison of cancer samples. Cell Systems, 2021, , . | 2.9 | 3 |
| 57 | Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. Molecular Systems Biology, 2014, 10, . | 3.2 | 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. | 0.8 | 1 |
| 61 | Immunological response in normal healthy twins across age. , 2010, , . | | 0 |
| 62 | Systems Immunology. , 2013, , 481-497. | | 0 |
| 63 | Response to: â€˜Tofacitinib for the treatment of polyarteritis nodosa: a literature reviewâ€™. Correspondence on â€˜Tofacitinib for polyarteritis nodosa: a tailored therapyâ€™ by Rimar<i>et al</i>. Annals of the Rheumatic Diseases, 2022, 81, e205-e205. | 0.5 | 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. | 0.6 | 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. | 0.6 | 0 |