Sol Efroni

List of Publications by Year
in descending order

76	3,371	186265 28	155660 55
papers	citations	h-index	g-index

85	85	85	6268
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Global Transcription in Pluripotent Embryonic Stem Cells. Cell Stem Cell, 2008, 2, 437-447.	11.1	603
2	IL-27 acts on DCs to suppress the T cell response and autoimmunity by inducing expression of the immunoregulatory molecule CD39. Nature Immunology, 2013, 14, 1054-1063.	14.5	294
3	Repâ€Seq: uncovering the immunological repertoire through nextâ€generation sequencing. Immunology, 2012, 135, 183-191.	4.4	252
4	The linker histone H1.0 generates epigenetic and functional intratumor heterogeneity. Science, 2016, 353, .	12.6	147
5	Genetic variations at loci involved in the immune response are risk factors for hepatocellular carcinoma. Hepatology, 2010, 52, 2034-2043.	7.3	124
6	Toward Rigorous Comprehension of Biological Complexity: Modeling, Execution, and Visualization of Thymic T-Cell Maturation. Genome Research, 2003, 13, 2485-2497.	5.5	122
7	The Immune System Computes the State of the Body: Crowd Wisdom, Machine Learning, and Immune Cell Reference Repertoires Help Manage Inflammation. Frontiers in Immunology, 2019, 10, 10.	4.8	120
8	Identification of Key Processes Underlying Cancer Phenotypes Using Biologic Pathway Analysis. PLoS ONE, 2007, 2, e425.	2.5	108
9	Tamoxifen-resistant breast cancer cells are resistant to DNA-damaging chemotherapy because of upregulated BARD1 and BRCA1. Nature Communications, 2018, 9, 1595.	12.8	89
10	Fmrp Interacts with Adar and Regulates RNA Editing, Synaptic Density and Locomotor Activity in Zebrafish. PLoS Genetics, 2015, 11, e1005702.	3.5	76
11	Reciprocal Regulation between SIRT6 and miR-122 Controls Liver Metabolism and Predicts Hepatocarcinoma Prognosis. Cell Reports, 2016, 14, 234-242.	6.4	73
12	Altered immune pathway activity under exercise challenge in Gulf War Illness: An exploratory analysis. Brain, Behavior, and Immunity, 2013, 28, 159-169.	4.1	70
13	System-wide Analysis of the T Cell Response. Cell Reports, 2016, 14, 2733-2744.	6.4	67
14	Emergent Dynamics of Thymocyte Development and Lineage Determination. PLoS Computational Biology, 2007, 3, e13.	3.2	64
15	Reactive animation: realistic modeling of complex dynamic systems. Computer, 2005, 38, 38-47.	1.1	59
16	Predicting and affecting response to cancer therapy based on pathway-level biomarkers. Nature Communications, 2020, 11, 3296.	12.8	55
17	Synaptojanin 2 is a druggable mediator of metastasis and the gene is overexpressed and amplified in breast cancer. Science Signaling, 2015, 8, ra7.	3.6	53
18	MicroRNA regulation of molecular pathways as a generic mechanism and as a core disease phenotype. Oncotarget, 2015, 6, 1594-1604.	1.8	50

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19	Using cellular automata modeling of the emergence of innovations. Technological Forecasting and Social Change, 2001, 68, 293-308.	11.6	45
20	A novel mitosis-associated lncRNA, MA-linc1, is required for cell cycle progression and sensitizes cancer cells to Paclitaxel. Oncotarget, 2015, 6, 27880-27890.	1.8	43
21	RBM38 Is a Direct Transcriptional Target of E2F1 that Limits E2F1-Induced Proliferation. Molecular Cancer Research, 2012, 10, 1169-1177.	3.4	41
22	Shift in GATA3 functions, and GATA3 mutations, control progression and clinical presentation in breast cancer. Breast Cancer Research, 2014, 16, 464.	5.0	40
23	Gene expression profile of empirically delineated classes of unexplained chronic fatigue. Pharmacogenomics, 2006, 7, 375-386.	1.3	37
24	Immunological analysis of phase II glioblastoma dendritic cell vaccine (Audencel) trial: immune system characteristics influence outcome and Audencel up-regulates Th1-related immunovariables. Acta Neuropathologica Communications, 2018, 6, 135.	5.2	37
25	Immune-Induced Evolutionary Selection Focused on a Single Reading Frame in Overlapping Hepatitis B Virus Proteins. Journal of Virology, 2011, 85, 4558-4566.	3.4	34
26	SENP5 mediates breast cancer invasion via a TGFÎ²RI SUMOylation cascade. Oncotarget, 2014, 5, 1071-1082.	1.8	34
27	Gene expression and network-based analysis reveals a novel role for hsa-miR-9 and drug control over the p38 network in glioblastoma multiforme progression. Genome Medicine, 2011, 3, 77.	8.2	33
28	The PathOlogist: an automated tool for pathway-centric analysis. BMC Bioinformatics, 2011, 12, 133.	2.6	33
29	The whole-organism heavy chain B cell repertoire from Zebrafish self-organizes into distinct network features. BMC Systems Biology, 2011, 5, 27.	3.0	32
30	Biomarker robustness reveals the PDGF network as driving disease outcome in ovarian cancer patients in multiple studies. BMC Systems Biology, 2012, 6, 3.	3.0	28
31	Age-related loss of gene-to-gene transcriptional coordination among single cells. Nature Metabolism, 2020, 2, 1305-1315.	11.9	27
32	Simplicity belies a complex system: a response to the minimal model of immunity of Langman and Cohn. Cellular Immunology, 2002, 216, 23-30.	3.0	24
33	Detecting Cancer Gene Networks Characterized by Recurrent Genomic Alterations in a Population. PLoS ONE, 2011, 6, e14437.	2.5	24
34	Resistance to paclitaxel is associated with a variant of the gene BCL2 in multiple tumor types. Npj Precision Oncology, 2019, 3, 12.	5.4	21
35	Stem cells do play with dice: A statistical physics view of transcription. Cell Cycle, 2009, 8, 43-48.	2.6	20
36	De novo transcriptome assembly databases for the central nervous system of the medicinal leech. Scientific Data, 2015, 2, 150015.	5.3	20

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37	Distinct inhibitory effects on mTOR signaling by ethanol and INK128 in diffuse large B-cell lymphoma. Cell Communication and Signaling, 2015, 13, 15.	6.5	20
38	The immune system and other cognitive systems. Complexity, 2001, 6, 14-21.	1.6	18
39	Astrocyteâ€specific transcriptome analysis using the ALDH1L1 bacTRAP mouse reveals novel biomarkers of astrogliosis in response to neurotoxicity. Journal of Neurochemistry, 2019, 150, 420-440.	3.9	18
40	hsa-miR-9 controls the mobility behavior of glioblastoma cellsviaregulation of MAPK14 signaling elements. Oncotarget, 2016, 7, 23170-23181.	1.8	18
41	Heat acclimation memory: do the kinetics of the deacclimated transcriptome predispose to rapid reacclimation and cytoprotection?. Journal of Applied Physiology, 2014, 117, 1262-1277.	2.5	17
42	PhenoNet: identification of key networks associated with disease phenotype. Bioinformatics, 2014, 30, 2399-2405.	4.1	17
43	MicroRNA-Gene Association As a Prognostic Biomarker in Cancer Exposes Disease Mechanisms. PLoS Computational Biology, 2013, 9, e1003351.	3.2	15
44	Network as biomarker. Systems Biomedicine (Austin, Tex), 2013, 1, 35-41.	0.7	15
45	Network Representation of T-Cell Repertoireâ€" A Novel Tool to Analyze Immune Response to Cancer Formation. Frontiers in Immunology, 2018, 9, 2913.	4.8	15
46	Comparing Transcriptome Profiles of Neurons Interfacing Adjacent Cells and Nanopatterned Substrates Reveals Fundamental Neuronal Interactions. Nano Letters, 2019, 19, 1451-1459.	9.1	15
47	The heuristics of biologic theory: the case of selfâ€"nonself discrimination. Cellular Immunology, 2003, 223, 87-89.	3.0	14
48	Autotaxinâ€"Lysophosphatidic Acid Axis Acts Downstream of Apoprotein B Lipoproteins in Endothelial Cells. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 2058-2067.	2.4	14
49	Dendritic Cells in the Context of Human Tumors: Biology and Experimental Tools. International Reviews of Immunology, 2016, 35, 116-135.	3.3	14
50	Superposition of Transcriptional Behaviors Determines Gene State. PLoS ONE, 2008, 3, e2901.	2.5	14
51	Reactive Animation. Lecture Notes in Computer Science, 2003, , 136-153.	1.3	13
52	IntroducingÂSystems Biomedicine. Systems Biomedicine (Austin, Tex), 2013, 1, 1-1.	0.7	11
53	Design principles of biologically fabricated avian nests. Scientific Reports, 2019, 9, 4792.	3.3	11
54	Breast cancer is marked by specific, Public T-cell receptor CDR3 regions shared by mice and humans. PLoS Computational Biology, 2021, 17, e1008486.	3.2	11

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55	Concurrency in Biological Modeling: Behavior, Execution and Visualization. Electronic Notes in Theoretical Computer Science, 2008, 194, 119-131.	0.9	9
56	Classification of lung adenocarcinoma and squamous cell carcinoma samples based on their gene expression profile in the sbv IMPROVER Diagnostic Signature Challenge. Systems Biomedicine (Austin,) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.7	8
57	A TÂcell repertoire timestamp is at the core of responsiveness to CTLA-4 blockade. IScience, 2021, 24, 102100.	4.1	8
58	Digitizable therapeutics for decentralized mitigation of global pandemics. Scientific Reports, 2019, 9, 14345.	3.3	7
59	Reactive animation: From piecemeal experimentation to reactive biological systems. Autoimmunity, 2011, 44, 271-281.	2.6	6
60	Spatial regulation dominates gene function in the ganglia chain. Bioinformatics, 2014, 30, 310-316.	4.1	6
61	A modeling algorithm for exploring the architecture and construction of bird nests. Scientific Reports, 2019, 9, 14772.	3.3	6
62	CDR3 and V genes show distinct reconstitution patterns in T cell repertoire post-allogeneic bone marrow transplantation. Immunogenetics, 2021, 73, 163-173.	2.4	6
63	17 A theory for complex systems: reactive animation. Studies in Multidisciplinarity, 2005, , 309-324.	0.0	5
64	Systems analysis utilising pathway interactions identifies sonic hedgehog pathway as a primary biomarker and oncogenic target in hepatocellular carcinoma. IET Systems Biology, 2013, 7, 243-251.	1.5	5
65	Cell studio: A platform for interactive, 3D graphical simulation of immunological processes. APL Bioengineering, 2018, 2, 026107.	6.2	5
66	T cell repertoire sequencing as a cancer's liquid biopsyâ€"can we decode what the immune system is coding?. Current Opinion in Systems Biology, 2020, 24, 135-141.	2.6	4
67	A single nucleotide variant of human PARP1 determines response to PARP inhibitors. Npj Precision Oncology, 2020, 4, 10.	5.4	3
68	Distribution equality as an optimal epidemic mitigation strategy. Scientific Reports, 2022, 12, .	3.3	2
69	Experimental Support for the Ecoimmunity Theory: Distinct Phenotypes of Nonlymphocytic Cells in SCID and Wild-Type Mice. Cell Transplantation, 2016, 25, 1575-1588.	2.5	1
70	Immune Computation and COVID-19 Mortality: A Rationale for IVIg. Critical Reviews in Immunology, 2020, 40, 195-203.	0.5	1
71	hsa-miR-9 and drug control over the P38 network as driving disease outcome in GBM patients. Systems Biomedicine (Austin, Tex), 2013, 1, 76-83.	0.7	0
72	IL-27 acts on DCs to suppress CNS autoimmunity by inducing CD39 expression. Journal of Neuroimmunology, 2014, 275, 88.	2.3	0

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73	Quantification of read species behavior within whole genome sequencing of cancer genomes for the stratification and visualization of genomic variation. Nucleic Acids Research, 2016, 44, e81-e81.	14.5	0
74	Emergent Dynamics of Thymocyte Development and Lineage Determination. PLoS Computational Biology, 2005, preprint, e13.	3.2	0
75	10.1063/1.5039473.1. , 2018, , .		0
76	Abstract B39: The T-cell repertoire as a biomarker for response to anti PD-1 immunotherapy. , 2020, , .		0