Uri Alon

List of Publications by Year
in descending order

69	7,512	101543	106344
papers	citations	36 h-index	65 g-index

77	77	77	9677
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Controls for Phylogeny and Robust Analysis in Pareto Task Inference. Molecular Biology and Evolution, 2022, 39, .	8.9	7
2	Distinct extracellularâ€“matrix remodeling events precede symptoms of inflammation. Matrix Biology, 2021, 96, 47-68.	3.6	25
3	Senescent cell accumulation mechanisms inferred from parabiosis. GeroScience, 2021, 43, 329-341.	4.6	29
4	Hormone seasonality in medical records suggests circannual endocrine circuits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	55
5	Senescent cells and the incidence of ageâ€related diseases. Aging Cell, 2021, 20, e13314.	6.7	44
6	An opponent process for alcohol addiction based on changes in endocrine gland mass. IScience, 2021, 24, 102127.	4.1	10
7	Temporal fluctuations in chemotaxis gain implement a simulated-tempering strategy for efficient navigation in complex environments. IScience, 2021, 24, 102796.	4.1	5
8	Timescales of Human Hair Cortisol Dynamics. IScience, 2020, 23, 101501.	4.1	8
9	Endocrine Autoimmune Disease as a Fragility of Immune Surveillance against Hypersecreting Mutants. Immunity, 2020, 52, 872-884.e5.	14.3	27
10	Principles of Cell Circuits for Tissue Repair and Fibrosis. IScience, 2020, 23, 100841.	4.1	90
11	Cancer-associated fibroblast compositions change with breast cancer progression linking the ratio of S100A4+ and PDPN+ CAFs to clinical outcome. Nature Cancer, 2020, 1, 692-708.	13.2	159
12	Tumour heterogeneity and the evolutionary trade-offs of cancer. Nature Reviews Cancer, 2020, 20, 247-257.	28.4	111
13	A new model for the HPA axis explains dysregulation of stress hormones on the timescale of weeks. Molecular Systems Biology, 2020, 16, e9510.	7.2	74
14	Noise-precision tradeoff in predicting combinations of mutations and drugs. PLoS Computational Biology, 2019, 15, e1006956.	3.2	13
15	Identity domains capture individual differences from across the behavioral repertoire. Nature Neuroscience, 2019, 22, 2023-2028.	14.8	69
16	Prediction of ultra-high-order antibiotic combinations based on pairwise interactions. PLoS Computational Biology, 2019, 15, e1006774.	3.2	49
17	Tumor diversity and the trade-off between universal cancer tasks. Nature Communications, 2019, 10, 5423.	12.8	53
18	Senescent cell turnover slows with age providing an explanation for the Gompertz law. Nature Communications, 2019, 10, 5495.	12.8	94

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19	Central dogma rates and the trade-off between precision and economy in gene expression. Nature Communications, 2019, 10, 68.	12.8	140
20	Continuum of Gene-Expression Profiles Provides Spatial Division of Labor within a Differentiated Cell Type. Cell Systems, 2019, 8, 43-52.e5.	6.2	51
21	Evolutionary trade-offs and the structure of polymorphisms. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170105.	4.0	13
22	Circuit Design Features of a Stable Two-Cell System. Cell, 2018, 172, 744-757.e17.	28.9	276
23	Endocytosis as a stabilizing mechanism for tissue homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1926-E1935.	7.1	41
24	Peer power. EMBO Reports, 2018, 19, .	4.5	7
25	Fold-change Response of Photosynthesis to Step Increases of Light Level. IScience, 2018, 8, 126-137.	4.1	12
26	Programming cells and tissues. Science, 2018, 361, 1199-1200.	12.6	10
27	A Bacterial Growth Law out of Steady State. Cell Reports, 2018, 23, 2891-2900.	6.4	68
28	Optimal Regulatory Circuit Topologies for Fold-Change Detection. Cell Systems, 2017, 4, 171-181.e8.	6.2	66
29	Optimality and sub-optimality in a bacterial growth law. Nature Communications, 2017, 8, 14123.	12.8	102
30	An Endogenously Tagged Fluorescent Fusion Protein Library in Mouse Embryonic Stem Cells. Stem Cell Reports, 2017, 9, 1304-1314.	4.8	19
31	Biphasic response as a mechanism against mutant takeover in tissue homeostasis circuits. Molecular Systems Biology, 2017, 13, 933.	7.2	28
32	Dynamic Proteomics of Herpes Simplex Virus Infection. MBio, 2017, 8, .	4.1	25
33	Dynamic proteomics reveals bimodal protein dynamics of cancer cells in response to HSP90 inhibitor. BMC Systems Biology, 2017, 11, 33.	3.0	13
34	Prediction of drug cocktail effects when the number of measurements is limited. PLoS Biology, 2017, 15, e2002518.	5.6	32
35	A reduced-dimensionality approach to uncovering dyadic modes of body motion in conversations. PLoS ONE, 2017, 12, e0170786.	2.5	10
36	Exit from Synchrony in Joint Improvised Motion. PLoS ONE, 2016, 11, e0160747.	2.5	27

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37	Manipulating the Placebo Response in Experimental Pain by Altering Doctorâ€™s Performance Style. Frontiers in Psychology, 2016, 7, 874.	2.1	41
38	Dynamical compensation in physiological circuits. Molecular Systems Biology, 2016, 12, 886.	7.2	67
39	Prediction of multidimensional drug dose responses based on measurements of drug pairs. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10442-10447.	7.1	139
40	Massively Parallel Interrogation of the Effects of Gene Expression Levels on Fitness. Cell, 2016, 166, 1282-1294.e18.	28.9	168
41	Glucose becomes one of the worst carbon sources for E.coli on poor nitrogen sources due to suboptimal levels of cAMP. Scientific Reports, 2016, 6, 24834.	3.3	110
42	A Tunable Mechanism Determines the Duration of the Transgenerational Small RNA Inheritance in C.Âelegans. Cell, 2016, 165, 88-99.	28.9	129
43	The Mass-Longevity Triangle: Pareto Optimality and the Geometry of Life-History Trait Space. PLoS Computational Biology, 2015, 11, e1004524.	3.2	35
44	Geometry of the Gene Expression Space of Individual Cells. PLoS Computational Biology, 2015, 11, e1004224.	3.2	65
45	A cellular and regulatory map of the cholinergic nervous system of C. elegans. ELife, 2015, 4, .	6.0	279
46	Inferring biological tasks using Pareto analysis of high-dimensional data. Nature Methods, 2015, 12, 233-235.	19.0	145
47	Evolution of Bow-Tie Architectures in Biology. PLoS Computational Biology, 2015, 11, e1004055.	3.2	101
48	Evolutionary tradeoffs, Pareto optimality and the morphology of ammonite shells. BMC Systems Biology, 2015, 9, 12.	3.0	86
49	Individuality and Togetherness in Joint Improvised Motion. PLoS ONE, 2014, 9, e87213.	2.5	70
50	Logarithmic and Power Law Input-Output Relations in Sensory Systems with Fold-Change Detection. PLoS Computational Biology, 2014, 10, e1003781.	3.2	49
51	Noise Genetics: Inferring Protein Function by Correlating Phenotype with Protein Levels and Localization in Individual Human Cells. PLoS Genetics, 2014, 10, e1004176.	3.5	20
52	Linear Superposition and Prediction of Bacterial Promoter Activity Dynamics in Complex Conditions. PLoS Computational Biology, 2014, 10, e1003602.	3.2	16
53	Paradoxical Signaling by a Secreted Molecule Leads to Homeostasis of Cell Levels. Cell, 2014, 158, 1022-1032.	28.9	86
54	Developmental bias in the evolution of phalanges. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18190-18195.	7.1	83

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55	Promoter activity dynamics in the lag phase of Escherichia coli. BMC Systems Biology, 2013, 7, 136.	3.0	72
56	The geometry of the <scp>P</scp>areto front in biological phenotype space. Ecology and Evolution, 2013, 3, 1471-1483.	1.9	66
57	Mutation Rules and the Evolution of Sparseness and Modularity in Biological Systems. PLoS ONE, 2013, 8, e70444.	2.5	29
58	Input symmetry invariance, and applications to biological systems. , 2011, , .		0
59	How to Build a Motivated Research Group. Molecular Cell, 2010, 37, 151-152.	9.7	21
60	How To Choose a Good Scientific Problem. Molecular Cell, 2009, 35, 726-728.	9.7	51
61	How To Give a Good Talk. Molecular Cell, 2009, 36, 165-167.	9.7	6
62	DEFINED ORDER OF EVOLUTIONARY ADAPTATIONS: EXPERIMENTAL EVIDENCE. Evolution; International Journal of Organic Evolution, 2008, 62, 1547-1554.	2.3	33
63	Understanding Hydrogen-Bond Patterns in Proteins using a Novel Statistical Model. Nature Precedings, 2008, , .	0.1	0
64	Simplicity in biology. Nature, 2007, 446, 497-497.	27.8	98
65	Network motifs: theory and experimental approaches. Nature Reviews Genetics, 2007, 8, 450-461.	16.3	2,789
66	Optimality and evolutionary tuning of the expression level of a protein. Nature, 2005, 436, 588-592.	27.8	712
67	Response to Comment on "Network Motifs: Simple Building Blocks of Complex Networks" and "Superfamilies of Evolved and Designed Networks". Science, 2004, 305, 1107d-1107d.	12.6	45
68	Correlation profiles and motifs in complex networks. , 2004, , 168-198.		34
69	Architecture and Dynamics of Transcriptional Networks. , 0, , 17-30.		0