## Istvan U Albert

List of Publications by Year in descending order

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109321 114465 9,406 64 35 63 citations h-index g-index papers 66 66 66 14258 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5 <b>.</b> 5	1,795
2	Structural vulnerability of the North American power grid. Physical Review E, 2004, 69, 025103.	2.1	1,046
3	Nucleosome organization in the Drosophila genome. Nature, 2008, 453, 358-362.	27.8	636
4	Translational and rotational settings of H2A.Z nucleosomes across the Saccharomyces cerevisiae genome. Nature, 2007, 446, 572-576.	27.8	610
5	A barrier nucleosome model for statistical positioning of nucleosomes throughout the yeast genome. Genome Research, 2008, 18, 1073-1083.	5.5	591
6	Microbiome remodelling leads to inhibition of intestinal farnesoid X receptor signalling and decreased obesity. Nature Communications, 2013, 4, 2384.	12.8	549
7	Intestinal farnesoid X receptor signaling promotes nonalcoholic fatty liver disease. Journal of Clinical Investigation, 2015, 125, 386-402.	8.2	517
8	Nucleosome positions predicted through comparative genomics. Nature Genetics, 2006, 38, 1210-1215.	21.4	283
9	Boolean network simulations for life scientists. Source Code for Biology and Medicine, 2008, 3, 16.	1.7	280
10	What keeps sandcastles standing?. Nature, 1997, 387, 765-765.	27.8	273
11	Persistent Organic Pollutants Modify Gut Microbiota–Host Metabolic Homeostasis in Mice Through Aryl Hydrocarbon Receptor Activation. Environmental Health Perspectives, 2015, 123, 679-688.	6.0	262
12	Rapid magnetic isolation of extracellular vesicles via lipid-based nanoprobes. Nature Biomedical Engineering, 2017, $1$ , .	22.5	188
13	Conserved network motifs allow protein-protein interaction prediction. Bioinformatics, 2004, 20, 3346-3352.	4.1	179
14	Attractor analysis of asynchronous Boolean models of signal transduction networks. Journal of Theoretical Biology, 2010, 266, 641-656.	1.7	163
15	Dynamical and Structural Analysis of a T Cell Survival Network Identifies Novel Candidate Therapeutic Targets for Large Granular Lymphocyte Leukemia. PLoS Computational Biology, 2011, 7, e1002267.	3.2	162
16	A rapid and label-free platform for virus capture and identification from clinical samples. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 895-901.	7.1	157
17	Jamming and Fluctuations in Granular Drag. Physical Review Letters, 2000, 84, 5122-5125.	7.8	139
18	Maximum angle of stability in wet and dry spherical granular media. Physical Review E, 1997, 56, R6271-R6274.	2.1	133

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19	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	5.5	122
20	Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. BMC Genomics, 2015, 16, 620.	2.8	107
21	GeneTrack—a genomic data processing and visualization framework. Bioinformatics, 2008, 24, 1305-1306.	4.1	94
22	BioStar: An Online Question & Description of the Bioinformatics Community. PLoS Computational Biology, 2011, 7, e1002216.	3.2	82
23	Tunable and label-free virus enrichment for ultrasensitive virus detection using carbon nanotube arrays. Science Advances, 2016, 2, e1601026.	10.3	73
24	Genome-wide real-time in vivo transcriptional dynamics during Plasmodium falciparum blood-stage development. Nature Communications, 2018, 9, 2656.	12.8	73
25	Testing the kinship theory of intragenomic conflict in honey bees ( <i>Apis mellifera</i> ). Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1020-1025.	7.1	69
26	NusA-dependent transcription termination prevents misregulation of global gene expression. Nature Microbiology, 2016, 1, 15007.	13.3	68
27	Molecular tandem repeat strategy for elucidating mechanical properties of high-strength proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6478-6483.	7.1	63
28	Selection on Aedes aegypti alters Wolbachia-mediated dengue virus blocking and fitness. Nature Microbiology, 2019, 4, 1832-1839.	13.3	62
29	Impact of Helminth Infections and Nutritional Constraints on the Small Intestine Microbiota. PLoS ONE, 2016, 11, e0159770.	2.5	60
30	A critical role of RBM8a in proliferation and differentiation of embryonic neural progenitors. Neural Development, 2015, 10, 18.	2.4	52
31	Rapid and asymmetric divergence of duplicate genes in the human gene coexpression network. BMC Bioinformatics, 2006, 7, 46.	2.6	45
32	Materials Fabrication from Native and Recombinant Thermoplastic Squid Proteins. Advanced Functional Materials, 2014, 24, 7401-7409.	14.9	44
33	Dominant Effects of the Diet on the Microbiome and the Local and Systemic Immune Response in Mice. PLoS ONE, 2014, 9, e86366.	2.5	41
34	Regulating life or death: Potential role of microRNA in rescue of the corpus luteum. Molecular and Cellular Endocrinology, 2014, 398, 78-88.	3.2	37
35	Comparative Analysis of Super-Shedder Strains of Escherichia coli O157:H7 Reveals Distinctive Genomic Features and a Strongly Aggregative Adherent Phenotype on Bovine Rectoanal Junction Squamous Epithelial Cells. PLoS ONE, 2015, 10, e0116743.	2.5	36
36	Disease dynamics in a dynamic social network. Physica A: Statistical Mechanics and Its Applications, 2010, 389, 2663-2674.	2.6	31

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37	VirAmp: a galaxy-based viral genome assembly pipeline. GigaScience, 2015, 4, 19.	6.4	30
38	In vivo genome-wide binding interactions of mouse and human constitutive androstane receptors reveal novel gene targets. Nucleic Acids Research, 2018, 46, 8385-8403.	14.5	27
39	White Button Mushrooms Increase Microbial Diversity and Accelerate the Resolution of Citrobacter rodentium Infection in Mice. Journal of Nutrition, 2013, 143, 526-532.	2.9	26
40	Genomic characterization of a turkey reovirus field strain by Next-Generation Sequencing. Infection, Genetics and Evolution, 2015, 32, 313-321.	2.3	21
41	Spatial distribution of bacterial communities on volumetric and planar anodes in single hamber air athode microbial fuel cells. Biotechnology and Bioengineering, 2013, 110, 3059-3062.	3.3	19
42	Paternal nicotine enhances fear memory, reduces nicotine administration, and alters hippocampal genetic and neural function in offspring. Addiction Biology, 2021, 26, e12859.	2.6	19
43	Caldichromatium japonicum gen. nov., sp. nov., a novel thermophilic phototrophic purple sulphur bacterium of the Chromatiaceae isolated from Nakabusa hot springs, Japan. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5701-5710.	1.7	17
44	Transcriptome Analyses of Heart and Liver Reveal Novel Pathways for Regulating Songbird Migration. Scientific Reports, 2019, 9, 6058.	3.3	16
45	Artificial Selection Finds New Hypotheses for the Mechanism of Wolbachia-Mediated Dengue Blocking in Mosquitoes. Frontiers in Microbiology, 2020, 11, 1456.	3.5	15
46	Relating Microbial Community Structure and Geochemistry in Deep Regolith Developed on Volcaniclastic Rock in the Luquillo Mountains, Puerto Rico. Geomicrobiology Journal, 2015, 32, 494-510.	2.0	12
47	Bioinformatic analysis of microRNA networks following the activation of the constitutive androstane receptor (CAR) in mouse liver. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1228-1237.	1.9	10
48	Puf3 participates in ribosomal biogenesis in malaria parasites. Journal of Cell Science, 2018, 131, .	2.0	8
49	Whole-Genome Sequence of Infectious Pancreatic Necrosis Virus Isolated from Farmed Brook Trout (Salvelinus fontinalis) in Pennsylvania. Genome Announcements, 2018, 6, .	0.8	7
50	Whole-genome sequence analysis reveals unique SNP profiles to distinguish vaccine and wild-type strains of bovine herpesvirus-1 (BoHV-1). Virology, 2018, 522, 27-36.	2.4	7
51	Effects of Spent Mushroom Compost (SMC) as an Ingredient in Phase I Compost on Production of <i>Agaricus bisporus </i> i>. Compost Science and Utilization, 2016, 24, 246-258.	1.2	6
52	The influence of adolescent nicotine exposure on ethanol intake and brain gene expression. PLoS ONE, 2018, 13, e0198935.	2.5	6
53	Advantageous microbial community development and improved performance of pilot-scale field systems treating high-risk acid mine drainage with crab shell. Journal of Hazardous Materials, 2021, 420, 126665.	12.4	6
54	Complete Genome Sequences of Three Related Avian Avulavirus $1$ Isolates from Poultry Farmers in Pakistan. Genome Announcements, $2018, 6, \ldots$	0.8	5

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55	Adolescent Stress Reduces Adult Morphine-Induced Behavioral Sensitization in C57BL/6J Mice. Frontiers in Behavioral Neuroscience, 2021, 15, 678102.	2.0	5
56	Metformin Affects the Transcriptomic Profile of Chicken Ovarian Cancer Cells. Genes, 2022, 13, 30.	2.4	5
57	Complete Genome Sequence of Mycobacterium orygis Strain 51145. Microbiology Resource Announcements, 2021, 10, .	0.6	4
58	RNAseq studies reveal distinct transcriptional response to vitamin A deficiency in small intestine versus colon, uncovering novel vitamin A-regulated genes. Journal of Nutritional Biochemistry, 2021, 98, 108814.	4.2	4
59	Genomic and Phenotypic Characterization of Chloracidobacterium Isolates Provides Evidence for Multiple Species. Frontiers in Microbiology, 2021, 12, 704168.	3.5	3
60	Transcriptional Profiling of the Small Intestine and the Colon Reveals Modulation of Gut Infection with Citrobacter rodentium According to the Vitamin A Status. Nutrients, 2022, 14, 1563.	4.1	2
61	Bioinformatics recipes: creating, executing and distributing reproducible data analysis workflows. BMC Bioinformatics, 2020, 21, 292.	2.6	1
62	Elioraea tepida, sp. nov., a Moderately Thermophilic Aerobic Anoxygenic Phototrophic Bacterium Isolated from the Mat Community of an Alkaline Siliceous Hot Spring in Yellowstone National Park, WY, USA. Microorganisms, 2022, 10, 80.	3.6	1
63	Whole-Genome Sequences of $18$ Bovine Alphaherpesvirus $1$ Field Isolates from Pennsylvania and Minnesota. Genome Announcements, $2018,6,.$	0.8	0
64	Addendum: Transcriptomics and proteomics reveal two waves of translational repression during the maturation of malaria parasite sporozoites. Nature Communications, 2022, 13, 283.	12.8	0