Roland Arnold

List of Publications by Year
in descending order

52 papers	5,618 citations	159585 30 h-index	197818 49 g-index
56 all docs	56 docs citations	56 times ranked	13109 citing authors

#	Article	IF	Citations
1	COVID-19 mortality in patients with cancer on chemotherapy or other anticancer treatments: a prospective cohort study. Lancet, The, 2020, 395, 1919-1926.	13.7	908
2	Gepard: a rapid and sensitive tool for creating dotplots on genome scale. Bioinformatics, 2007, 23, 1026-1028.	4.1	639
3	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. Nucleic Acids Research, 2012, 40, D284-D289.	14.5	490
4	COVID-19 prevalence and mortality in patients with cancer and the effect of primary tumour subtype and patient demographics: a prospective cohort study. Lancet Oncology, The, 2020, 21, 1309-1316.	10.7	473
5	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. Nature Genetics, 2015, 47, 257-262.	21.4	306
6	Sequence-Based Prediction of Type III Secreted Proteins. PLoS Pathogens, 2009, 5, e1000376.	4.7	230
7	The binary protein-protein interaction landscape of Escherichia coli. Nature Biotechnology, 2014, 32, 285-290.	17.5	218
8	EffectiveDBâ€"updates and novel features for a better annotation of bacterial secreted proteins and Type III, IV, VI secretion systems. Nucleic Acids Research, 2016, 44, D669-D674.	14.5	172
9	probeCheck â€" a central resource for evaluating oligonucleotide probe coverage and specificity. Environmental Microbiology, 2008, 10, 2894-2898.	3.8	170
10	MIPS Arabidopsisthaliana Database (MAtDB): an integrated biological knowledge resource based on the first complete plant genome. Nucleic Acids Research, 2002, 30, 91-93.	14.5	159
11	A Transcriptionally Distinct CXCL13+CD103+CD8+ T-cell Population Is Associated with B-cell Recruitment and Neoantigen Load in Human Cancer. Cancer Immunology Research, 2019, 7, 784-796.	3.4	141
12	The Genome of the Amoeba Symbiont â€œ<i>Candidatus</i> Amoebophilus asiaticusâ€·Reveals Common Mechanisms for Host Cell Interaction among Amoeba-Associated Bacteria. Journal of Bacteriology, 2010, 192, 1045-1057.	2.2	138
13	B2G-FAR, a species-centered GO annotation repository. Bioinformatics, 2011, 27, 919-924.	4.1	137
14	Large-scale interaction profiling of PDZ domains through proteomic peptide-phage display using human and viral phage peptidomes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2542-2547.	7.1	124
15	Effective--a database of predicted secreted bacterial proteins. Nucleic Acids Research, 2011, 39, D591-D595.	14.5	102
16	The evolutionary landscape of colorectal tumorigenesis. Nature Ecology and Evolution, 2018, 2, 1661-1672.	7.8	99
17	PEDANT covers all complete RefSeq genomes. Nucleic Acids Research, 2009, 37, D408-D411.	14.5	97
18	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in Escherichia coli. PLoS Genetics, 2014, 10, e1004120.	3.5	96

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19	Genetic Interaction Maps in Escherichia coli Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. PLoS Genetics, 2011, 7, e1002377.	3.5	95
20	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. Molecular Systems Biology, 2013, 9, 696.	7.2	90
21	Severity of COVID-19 in children with cancer: Report from the United Kingdom Paediatric Coronavirus Cancer Monitoring Project. British Journal of Cancer, 2021, 124, 754-759.	6.4	72
22	Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. Molecular Microbiology, 2010, 78, 1539-1555.	2.5	57
23	The UK Coronavirus Cancer Monitoring Project: protecting patients with cancer in the era of COVID-19. Lancet Oncology, The, 2020, 21, 622-624.	10.7	53
24	Computational analysis of interactomes: Current and future perspectives for bioinformatics approaches to model the host–pathogen interaction space. Methods, 2012, 57, 508-518.	3.8	49
25	Proteome‐wide analysis of phospho‐regulated <scp>PDZ</scp> domain interactions. Molecular Systems Biology, 2018, 14, e8129.	7.2	48
26	SIMAP: the similarity matrix of proteins. Nucleic Acids Research, 2006, 34, D252-D256.	14.5	44
27	SIMAP—a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. Nucleic Acids Research, 2010, 38, D223-D226.	14.5	40
28	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i>. Bioinformatics, 2015, 31, 306-310.	4.1	38
29	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	6.4	36
30	SIMAP--The similarity matrix of proteins. Bioinformatics, 2005, 21, ii42-ii46.	4.1	35
31	Mortality Among Adults With Cancer Undergoing Chemotherapy or Immunotherapy and Infected With COVID-19. JAMA Network Open, 2022, 5, e220130.	5.9	34
32	SIMAP structuring the network of protein similarities. Nucleic Acids Research, 2007, 36, D289-D292.	14.5	24
33	SIMAP—the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. Nucleic Acids Research, 2014, 42, D279-D284.	14.5	24
34	Proteomic peptide phage display uncovers novel interactions of the PDZ1‐2 supramodule of syntenin. FEBS Letters, 2016, 590, 3-12.	2.8	24
35	Targeting effectors: the molecular recognition of Type III secreted proteins. Microbes and Infection, 2010, 12, 346-358.	1.9	23
36	Key findings from the UKCCMP cohort of 877 patients with haematological malignancy and COVID‐19: disease control as an important factor relative to recent chemotherapy or anti‐CD20 therapy. British Journal of Haematology, 2022, 196, 892-901.	2.5	23

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37	Srrm234, but not canonical SR and hnRNP proteins, drive inclusion of <i>Dscam</i> exon 9 variable exons. Rna, 2019, 25, 1353-1365.	3.5	16
38	COVID-19 in children with haematological malignancies. Archives of Disease in Childhood, 2022, 107, 186-188.	1.9	14
39	Dynamically expressed single ELAV/Hu orthologue elavl2 of bees is required for learning and memory. Communications Biology, 2021, 4, 1234.	4.4	12
40	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. Nature Communications, 2017, 8, 2109.	12.8	11
41	Back-Splicing Transcript Isoforms (Circular RNAs) Affect Biologically Relevant Pathways and Offer an Additional Layer of Information to Stratify NMIBC Patients. Frontiers in Oncology, 2020, 10, 812.	2.8	11
42	Non-Coding Mutations in Urothelial Bladder Cancer: Biological and Clinical Relevance and Potential Utility as Biomarkers. Bladder Cancer, 2019, 5, 263-272.	0.4	10
43	Tropomyosins: Potential Biomarkers for Urothelial Bladder Cancer. International Journal of Molecular Sciences, 2019, 20, 1102.	4.1	7
44	Trends in urine biomarker discovery for urothelial bladder cancer: DNA, RNA, or protein?. Translational Andrology and Urology, 2021, 10, 2787-2808.	1.4	7
45	Functional analysis of the finO distal region of plasmid R1. Plasmid, 2011, 65, 159-168.	1.4	6
46	Molecular Subtypes of T1 Bladder Cancer: Biomolecular Characteristics Versus Clinical Utility. European Urology, 2020, 78, 538-539.	1.9	4
47	Urine DNA for monitoring chemoradiotherapy response in muscleâ€invasive bladder cancer: a pilot study. BJU International, 2021, , .	2.5	3
48	STAG2 Protein Expression in Nonâ€"muscle-invasive Bladder Cancer: Associations with Sex, Genomic and Transcriptomic Changes, and Clinical Outcomes. European Urology Open Science, 2022, 38, 88-95.	0.4	3
49	Establishing the Bladder Cancer Research Centre at the University of Birmingham. Nature Reviews Urology, 2021, 18, 318-320.	3.8	1
50	PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. BMC Bioinformatics, 2016, 17, 150.	2.6	0
51	Abstract B09: DNA polymerase mutations trigger rapid onset of ultra-hypermutant malignant brain tumors in children with biallelic mismatch repair deficiency. , 2015, , .		0
52	Metastatic disease representation: An analysis of 148 paired colorectal cancer lymph node metastatic tumour deposits.. Journal of Clinical Oncology, 2018, 36, e15595-e15595.	1.6	0