

Roland Arnold

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5982823/publications.pdf>

Version: 2024-02-01

52
papers

5,618
citations

182225

30
h-index

223390

49
g-index

56
all docs

56
docs citations

56
times ranked

14314
citing authors

#	ARTICLE	IF	CITATIONS
1	COVID-19 in children with haematological malignancies. Archives of Disease in Childhood, 2022, 107, 186-188.	1.0	14
2	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.	1.2	23
3	Mortality Among Adults With Cancer Undergoing Chemotherapy or Immunotherapy and Infected With COVID-19. JAMA Network Open, 2022, 5, e220130.	2.8	34
4	STAG2 Protein Expression in Non-muscle-invasive Bladder Cancer: Associations with Sex, Genomic and Transcriptomic Changes, and Clinical Outcomes. European Urology Open Science, 2022, 38, 88-95.	0.2	3
5	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.	2.9	72
6	Establishing the Bladder Cancer Research Centre at the University of Birmingham. Nature Reviews Urology, 2021, 18, 318-320.	1.9	1
7	Trends in urine biomarker discovery for urothelial bladder cancer: DNA, RNA, or protein?. Translational Andrology and Urology, 2021, 10, 2787-2808.	0.6	7
8	Urine DNA for monitoring chemoradiotherapy response in muscle-invasive bladder cancer: a pilot study. BJU International, 2021, , .	1.3	3
9	Dynamically expressed single ELAV/Hu orthologue elavl2 of bees is required for learning and memory. Communications Biology, 2021, 4, 1234.	2.0	12
10	Molecular Subtypes of T1 Bladder Cancer: Biomolecular Characteristics Versus Clinical Utility. European Urology, 2020, 78, 538-539.	0.9	4
11	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.	5.1	473
12	COVID-19 mortality in patients with cancer on chemotherapy or other anticancer treatments: a prospective cohort study. Lancet, The, 2020, 395, 1919-1926.	6.3	908
13	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.	1.3	11
14	The UK Coronavirus Cancer Monitoring Project: protecting patients with cancer in the era of COVID-19. Lancet Oncology, The, 2020, 21, 622-624.	5.1	53
15	Srrm234, but not canonical SR and hnRNP proteins, drive inclusion of Dscam exon 9 variable exons. Rna, 2019, 25, 1353-1365.	1.6	16
16	Tropomyosins: Potential Biomarkers for Urothelial Bladder Cancer. International Journal of Molecular Sciences, 2019, 20, 1102.	1.8	7
17	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.	1.6	141
18	Non-Coding Mutations in Urothelial Bladder Cancer: Biological and Clinical Relevance and Potential Utility as Biomarkers. Bladder Cancer, 2019, 5, 263-272.	0.2	10

#	ARTICLE	IF	CITATIONS
19	The evolutionary landscape of colorectal tumorigenesis. <i>Nature Ecology and Evolution</i> , 2018, 2, 1661-1672.	3.4	99
20	Proteome-wide analysis of phospho-regulated PDZ domain interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8129.	3.2	48
21	Metastatic disease representation: An analysis of 148 paired colorectal cancer lymph node metastatic tumour deposits. <i>Journal of Clinical Oncology</i> , 2018, 36, e15595-e15595.	0.8	0
22	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. <i>Nature Communications</i> , 2017, 8, 2109.	5.8	11
23	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , 2016, 16, 2032-2046.	2.9	36
24	PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. <i>BMC Bioinformatics</i> , 2016, 17, 150.	1.2	0
25	Proteomic peptide phage display uncovers novel interactions of the PDZ1 supramodule of syntenin. <i>FEBS Letters</i> , 2016, 590, 3-12.	1.3	24
26	EffectiveDB updates and novel features for a better annotation of bacterial secreted proteins and Type III, IV, VI secretion systems. <i>Nucleic Acids Research</i> , 2016, 44, D669-D674.	6.5	172
27	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermuted cancers. <i>Nature Genetics</i> , 2015, 47, 257-262.	9.4	306
28	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015, 31, 306-310.	1.8	38
29	Abstract B09: DNA polymerase mutations trigger rapid onset of ultra-hypermuted malignant brain tumors in children with biallelic mismatch repair deficiency. , 2015, , .		0
30	Large-scale interaction profiling of PDZ domains through proteomic peptide-phage display using human and viral phage peptidomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2542-2547.	3.3	124
31	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2014, 10, e1004120.	1.5	96
32	SIMAP—the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. <i>Nucleic Acids Research</i> , 2014, 42, D279-D284.	6.5	24
33	The binary protein-protein interaction landscape of <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2014, 32, 285-290.	9.4	218
34	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013, 9, 696.	3.2	90
35	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	6.5	490
36	Computational analysis of interactomes: Current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. <i>Methods</i> , 2012, 57, 508-518.	1.9	49

#	ARTICLE	IF	CITATIONS
37	Genetic Interaction Maps in <i>Escherichia coli</i> Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. <i>PLoS Genetics</i> , 2011, 7, e1002377.	1.5	95
38	Functional analysis of the <i>finO</i> distal region of plasmid R1. <i>Plasmid</i> , 2011, 65, 159-168.	0.4	6
39	B2C-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924.	1.8	137
40	Effective-a database of predicted secreted bacterial proteins. <i>Nucleic Acids Research</i> , 2011, 39, D591-D595.	6.5	102
41	Targeting effectors: the molecular recognition of Type III secreted proteins. <i>Microbes and Infection</i> , 2010, 12, 346-358.	1.0	23
42	Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. <i>Molecular Microbiology</i> , 2010, 78, 1539-1555.	1.2	57
43	SIMAP—a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. <i>Nucleic Acids Research</i> , 2010, 38, D223-D226.	6.5	40
44	The Genome of the <i>Amoeba Symbiont</i> <i>Candidatus</i> <i>Amoebophilus asiaticus</i> Reveals Common Mechanisms for Host Cell Interaction among <i>Amoeba</i> -Associated Bacteria. <i>Journal of Bacteriology</i> , 2010, 192, 1045-1057.	1.0	138
45	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	6.5	97
46	Sequence-Based Prediction of Type III Secreted Proteins. <i>PLoS Pathogens</i> , 2009, 5, e1000376.	2.1	230
47	probeCheck—a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , 2008, 10, 2894-2898.	1.8	170
48	SIMAP structuring the network of protein similarities. <i>Nucleic Acids Research</i> , 2007, 36, D289-D292.	6.5	24
49	Gepard: a rapid and sensitive tool for creating dotplots on genome scale. <i>Bioinformatics</i> , 2007, 23, 1026-1028.	1.8	639
50	SIMAP: the similarity matrix of proteins. <i>Nucleic Acids Research</i> , 2006, 34, D252-D256.	6.5	44
51	SIMAP—The similarity matrix of proteins. <i>Bioinformatics</i> , 2005, 21, ii42-ii46.	1.8	35
52	MIPS <i>Arabidopsis thaliana</i> Database (MATDB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002, 30, 91-93.	6.5	159