Alan Christoffels

List of Publications by Year
in descending order

99 papers	**6,789** citations

159585
30 h-index

62596
80 g-index

105 all docs	**105** docs citations

105 times ranked

10848 citing authors

#	Article	IF	Citations
1	New INN nomenclature for monoclonal antibodies. Lancet, The, 2022, 399, 24.	13.7	11
2	Repurposing Based Identification of Novel Inhibitors against MmpS5-MmpL5 Efflux Pump of Mycobacterium smegmatis: A Combined In Silico and In Vitro Study. Biomedicines, 2022, 10, 333.	3.2	0
3	The COMBAT-TB Workbench: Making Powerful Mycobacterium tuberculosis Bioinformatics Accessible. MSphere, 2022, 7, e0099121.	2.9	4
4	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. GigaScience, 2022, 11, .	6.4	18
5	Software Tools for Biobanking in LMICs. , 2022, , 137-146.		0
6	Current Status of Next-Generation Sequencing Approaches for Candidate Gene Discovery in Familial ParkinsonÂ´s Disease. Frontiers in Genetics, 2022, 13, 781816.	2.3	3
7	microRNA profile of Hermetia illucens (black soldier fly) and its implications on mass rearing. PLoS ONE, 2022, 17, e0265492.	2.5	1
8	The developmentally dynamic microRNA transcriptome of <i>Glossina pallidipes</i> tsetse flies, vectors of animal trypanosomiasis. Bioinformatics Advances, 2022, 2, .	2.4	1
9	International nonproprietary names for monoclonal antibodies: an evolving nomenclature system. MAbs, 2022, 14, 2075078.	5.2	10
10	Computational drug repurposing strategy predicted peptide-based drugs that can potentially inhibit the interaction of SARS-CoV-2 spike protein with its target (humanACE2). PLoS ONE, 2021, 16, e0245258.	2.5	19
11	Prioritization of candidate genes for a South African family with Parkinsonâ€™s disease using in-silico tools. PLoS ONE, 2021, 16, e0249324.	2.5	9
12	Cheminformatics techniques in antimalarial drug discovery and development from natural products 2: Molecular scaffold and machine learning approaches. ChemistrySelect, 2021, 6, .	1.5	0
13	Antennal Enriched Odorant Binding Proteins Are Required for Odor Communication in Glossina f. fuscipes. Biomolecules, 2021, 11, 541.	4.0	10
14	Evaluation of Protein Purification Techniques and Effects of Storage Duration on LC-MS/MS Analysis of Archived FFPE Human CRC Tissues. Pathology and Oncology Research, 2021, 27, 622855.	1.9	6
15	POPIA Code of Conduct for Research (with corrigendum). South African Journal of Science, 2021, 117, .	0.7	8
16	Cheminformatic Characterization of Natural Antimicrobial Products for the Development of New Lead Compounds. Molecules, 2021, 26, 3970.	3.8	11
17	Cheminformatic Profiling and Hit Prioritization of Natural Products with Activities against Methicillin-Resistant Staphylococcus aureus (MRSA). Molecules, 2021, 26, 3674.	3.8	8
18	Transcriptomic Profile of Mycobacterium smegmatis in Response to an Imidazo[1,2-b][1,2,4,5]tetrazine Reveals Its Possible Impact on Iron Metabolism. Frontiers in Microbiology, 2021, 12, 724042.	3.5	1

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19	In silico repurposing of a Novobiocin derivative for activity against latency associated Mycobacterium tuberculosis drug target nicotinate-nucleotide adenylyl transferase (Rv2421c). PLoS ONE, 2021, 16, e0259348.	2.5	3
20	Effect of polyethylene glycol 20 000 on protein extraction efficiency of formalin-fixed paraffin-embedded tissues in South Africa. African Journal of Laboratory Medicine, 2021, 10, 1122.	0.6	1
21	Title is missing!. , 2021, 16, e0245258.		0
22	Title is missing!. , 2021, 16, e0245258.		0
23	Title is missing!. , 2021, 16, e0245258.		0
24	Title is missing!. , 2021, 16, e0245258.		0
25	COMBAT-TB-NeoDB: fostering tuberculosis research through integrative analysis using graph database technologies. Bioinformatics, 2020, 36, 982-983.	4.1	8
26	Careful governance of African biobanks. Lancet, The, 2020, 395, 29-30.	13.7	4
27	Inhibiting CDK6 Activity by Quercetin Is an Attractive Strategy for Cancer Therapy. ACS Omega, 2020, 5, 27480-27491.	3.5	48
28	Information security at South African universitiesâ€"implications for biomedical research. International Data Privacy Law, 2020, 10, 180-186.	1.2	3
29	Accelerating genomics-based surveillance for COVID-19 response in Africa. Lancet Microbe, The, 2020, 1, e227-e228.	7.3	28
30	Cellular and Molecular Targets of Waterbuck Repellent Blend Odors in Antennae of Glossina fuscipes fuscipes Newstead, 1910. Frontiers in Cellular Neuroscience, 2020, 14, 137.	3.7	5
31	Structure based identification of novel inhibitors against ATP synthase of Mycobacterium tuberculosis: A combined in silico and in vitro study. International Journal of Biological Macromolecules, 2019, 135, 582-590.	7.5	4
32	Cheminformatics techniques in antimalarial drug discovery and development from natural products 1: basic concepts. Physical Sciences Reviews, 2019, 4, .	0.8	2
33	Designing novel possible kinase inhibitor derivatives as therapeutics against Mycobacterium tuberculosis: An in silico study. Scientific Reports, 2019, 9, 4405.	3.3	35
34	Molecular modelling and simulation studies of the Mycobacterium tuberculosis multidrug efflux pump protein Rv1258c. PLoS ONE, 2018, 13, e0207605.	2.5	23
35	Predictive classifier models built from natural products with antimalarial bioactivity using machine learning approach. PLoS ONE, 2018, 13, e0204644.	2.5	23
36	Prediction of human-*Bacillus anthracis* proteinâ€"protein interactions using multi-layer neural network. Bioinformatics, 2018, 34, 4159-4164.	4.1	25

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37	Cross-species multiple environmental stress responses: An integrated approach to identify candidate genes for multiple stress tolerance in sorghum (Sorghum bicolor (L.) Moench) and related model species. PLoS ONE, 2018, 13, e0192678.	2.5	24
38	Baobab Laboratory Information Management System: Development of an Open-Source Laboratory Information Management System for Biobanking. Biopreservation and Biobanking, 2017, 15, 116-120.	1.0	20
39	Accessing Biospecimens from the H3Africa Consortium. Biopreservation and Biobanking, 2017, 15, 95-98.	1.0	15
40	Structural and functional effects of nucleotide variation on the human TB drug metabolizing enzyme arylamine N -acetyltransferase 1. Journal of Molecular Graphics and Modelling, 2017, 75, 330-339.	2.4	13
41	Selecting a Laboratory Information Management System for Biorepositories in Low- and Middle-Income Countries: The H3Africa Experience and Lessons Learned. Biopreservation and Biobanking, 2017, 15, 111-115.	1.0	14
42	Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. Nature Communications, 2017, 8, 2062.	12.8	88
43	An integrated and comparative approach towards identification, characterization and functional annotation of candidate genes for drought tolerance in sorghum (Sorghum bicolor (L.) Moench). BMC Genetics, 2017, 18, 119.	2.7	27
44	Exploration of Scaffolds from Natural Products with Antiplasmodial Activities, Currently Registered Antimalarial Drugs and Public Malarial Screen Data. Molecules, 2016, 21, 104.	3.8	5
45	Computational characterization of Iron metabolism in the Tsetse disease vector, Glossina morsitans: IRE stem-loops. BMC Genomics, 2016, 17, 561.	2.8	2
46	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. PLoS Genetics, 2016, 12, e1005954.	3.5	105
47	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. PLoS Computational Biology, 2016, 12, e1004395.	3.2	12
48	Genome-Wide Comparative Analysis of Chemosensory Gene Families in Five Tsetse Fly Species. PLoS Neglected Tropical Diseases, 2016, 10, e0004421.	3.0	28
49	Supporting the development of biobanks in low and medium income countries. , 2016, , .		14
50	Identification and characterization of microRNAs expressed in the African malaria vector Anopheles funestus life stages using high throughput sequencing. Malaria Journal, 2016, 15, 542.	2.3	11
51	Resistance related metabolic pathways for drug target identification in Mycobacterium tuberculosis. BMC Bioinformatics, 2016, 17, 75.	2.6	23
52	Prioritization of anti-malarial hits from nature: chemo-informatic profiling of natural products with in vitro antiplasmodial activities and currently registered anti-malarial drugs. Malaria Journal, 2016, 15, 50.	2.3	28
53	TSS seq based core promoter architecture in blood feeding Tsetse fly (Glossina morsitans morsitans) vector of Trypanosomiasis. BMC Genomics, 2015, 16, 722.	2.8	6
54	Inferring bona fide transfrags in RNA-Seq derived-transcriptome assemblies of non-model organisms. BMC Bioinformatics, 2015, 16, 58.	2.6	7

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55	Evidence for a common biological pathway linking three Parkinson's disease–causing genes: *parkin*, *PINK1* and *DJ–1*. European Journal of Neuroscience, 2015, 41, 1113-1125.	2.6	87
56	A glance at quality score: implication for de novo transcriptome reconstruction of Illumina reads. Frontiers in Genetics, 2014, 5, 17.	2.3	36
57	Gonad Differentiation in Zebrafish Is Regulated by the Canonical Wnt Signaling Pathway1. Biology of Reproduction, 2014, 90, 45.	2.7	79
58	Odorant and Gustatory Receptors in the Tsetse Fly Glossina morsitans morsitans. PLoS Neglected Tropical Diseases, 2014, 8, e2663.	3.0	51
59	International Glossina Genome Initiative 2004–2014: A Driver for Post-Genomic Era Research on the African Continent. PLoS Neglected Tropical Diseases, 2014, 8, e3024.	3.0	5
60	Human African Trypanosomiasis Research Gets a Boost: Unraveling the Tsetse Genome. PLoS Neglected Tropical Diseases, 2014, 8, e2624.	3.0	9
61	Taste and odorant receptors of the coelacanth–A gene repertoire in transition. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 403-414.	1.3	31
62	Evolution and Structural Analyses of Glossina morsitans (Diptera; Glossinidae) Tetraspanins. Insects, 2014, 5, 885-908.	2.2	4
63	Genome Sequence of the Tsetse Fly (*Glossina morsitans*): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
64	A comparative analysis of trypanosomatid SNARE proteins. Parasitology International, 2014, 63, 341-348.	1.3	17
65	Chemosensory receptors in tsetse flies provide link between chemical and behavioural ecology. Trends in Parasitology, 2014, 30, 426-428.	3.3	9
66	Enabling the genomic revolution in Africa. Science, 2014, 344, 1346-1348.	12.6	361
67	Towards inferring the global movement of beak and feather disease virus. Virology, 2014, 450-451, 24-33.	2.4	53
68	The African coelacanth genome provides insights into tetrapod evolution. Nature, 2013, 496, 311-316.	27.8	612
69	Challenges of Biobanking in South Africa to Facilitate Indigenous Research in an Environment Burdened with Human Immunodeficiency Virus, Tuberculosis, and Emerging Noncommunicable Diseases. Biopreservation and Biobanking, 2013, 11, 347-354.	1.0	44
70	DAMPD: a manually curated antimicrobial peptide database. Nucleic Acids Research, 2012, 40, D1108-D1112.	14.5	93
71	DESTAF: A database of text-mined associations for reproductive toxins potentially affecting human fertility. Reproductive Toxicology, 2012, 33, 99-105.	2.9	13
72	The genome of woodland strawberry (Fragaria vesca). Nature Genetics, 2011, 43, 109-116.	21.4	1,091

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73	HCVpro: Hepatitis C virus protein interaction database. Infection, Genetics and Evolution, 2011, 11, 1971-1977.	2.3	76
74	Dragon exploratory system on Hepatitis C Virus (DESHCV). Infection, Genetics and Evolution, 2011, 11, 734-739.	2.3	13
75	Evolutionary genomics of Glossina morsitans immune-related CLIP domain serine proteases and serine protease inhibitors. Infection, Genetics and Evolution, 2011, 11, 740-745.	2.3	7
76	DDPC: Dragon Database of Genes associated with Prostate Cancer. Nucleic Acids Research, 2011, 39, D980-D985.	14.5	38
77	Genome-wide SNP identification by high-throughput sequencing and selective mapping allows sequence assembly positioning using a framework genetic linkage map. BMC Biology, 2010, 8, 155.	3.8	19
78	Database for exploration of functional context of genes implicated in ovarian cancer. Nucleic Acids Research, 2009, 37, D820-D823.	14.5	37
79	Expansion Mechanisms and Functional Annotations of Hypothetical Genes in the Rice Genome. Plant Physiology, 2009, 150, 1997-2008.	4.8	19
80	DDEC: Dragon database of genes implicated in esophageal cancer. BMC Cancer, 2009, 9, 219.	2.6	24
81	DDESC: Dragon database for exploration of sodium channels in human. BMC Genomics, 2008, 9, 622.	2.8	17
82	Transcriptomic Analyses Reveal Novel Genes with Sexually Dimorphic Expression in the Zebrafish Gonad and Brain. PLoS ONE, 2008, 3, e1791.	2.5	107
83	Global Expression Profiling in Zebrafish Reveals Genes with Potential Roles in Sexual Differentiation. Biology of Reproduction, 2008, 78, 116-116.	2.7	1
84	Tetraodon genome analysis provides further evidence for whole-genome duplication in the ray-finned fish lineage. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2006, 1, 13-19.	1.0	9
85	Comparative genomics in cyprinids: common carp ESTs help the annotation of the zebrafish genome. BMC Bioinformatics, 2006, 7, S2.	2.6	40
86	Mice and Men: Their Promoter Properties. PLoS Genetics, 2006, 2, e54.	3.5	95
87	Using UniGene, STACK, and TIGR indices. , 2005, , .		1
88	COMPARISON OF CORE PROMOTERS IN FUGU RUBRIPES AND HUMAN. , 2005, , .		0
89	MOLECULAR PHYLOGENETIC ANALYSIS: UNDERSTANDING GENOME EVOLUTION. Series on Advances in Bioinformatics and Computational Biology, 2005, , 645-651.	0.2	0
90	Extensive Expansion of the Claudin Gene Family in the Teleost Fish, *Fugu rubripes*. Genome Research, 2004, 14, 1248-1257.	5.5	156

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91	Comparative Analysis of the Testis and Ovary Transcriptomes in Zebrafish by Combining Experimental and Computational Tools. Comparative and Functional Genomics, 2004, 5, 403-418.	2.0	48
92	Fugu Genome Analysis Provides Evidence for a Whole-Genome Duplication Early During the Evolution of Ray-Finned Fishes. Molecular Biology and Evolution, 2004, 21, 1146-1151.	8.9	490
93	Hox gene clusters in the Indonesian coelacanth, Latimeria menadoensis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1084-1088.	7.1	54
94	eVOC: A Controlled Vocabulary for Unifying Gene Expression Data. Genome Research, 2003, 13, 1222-1230.	5.5	144
95	Whole-Genome Shotgun Assembly and Analysis of the Genome of <i>Fugu rubripes</i>. Science, 2002, 297, 1301-1310.	12.6	1,432
96	Assessment of the parallelization approach ofd2_cluster for high-performance sequence clustering. Journal of Computational Chemistry, 2002, 23, 755-757.	3.3	15
97	STACK: Sequence Tag Alignment and Consensus Knowledgebase. Nucleic Acids Research, 2001, 29, 234-238.	14.5	112
98	A Comprehensive Approach to Clustering of Expressed Human Gene Sequence: The Sequence Tag Alignment and Consensus Knowledge Base. Genome Research, 1999, 9, 1143-1155.	5.5	175
99	Dealing with Duplicated Genomes of Teleosts. , 0, , 511-524.		0