

Bent Petersen

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

6,761
citations

201674

27
h-index

149698

56
g-index

73
all docs

73
docs citations

73
times ranked

12042
citing authors

#	ARTICLE	IF	CITATIONS
1	PhageLeads: Rapid Assessment of Phage Therapeutic Suitability Using an Ensemble Machine Learning Approach. <i>Viruses</i> , 2022, 14, 342.	3.3	31
2	NetSurfP-3.0: accurate and fast prediction of protein structural features by protein language models and deep learning. <i>Nucleic Acids Research</i> , 2022, 50, W510-W515.	14.5	80
3	The genomic basis of the plant island syndrome in Darwin's giant daisies. <i>Nature Communications</i> , 2022, 13, .	12.8	6
4	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. <i>Current Biology</i> , 2021, 31, 198-206.e8.	3.9	26
5	Rapid discovery of novel prophages using biological feature engineering and machine learning. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa109.	3.2	39
6	SinEx DB 2.0 update 2020: database for eukaryotic single-exon coding sequences. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	3
7	An improved direct metatranscriptome approach increases the detection of larger-sized circular elements across kingdoms. <i>Plasmid</i> , 2021, 115, 102576.	1.4	6
8	Kouprey (<i>Bos sauveli</i>) genomes unveil polytomic origin of wild Asian Bos. <i>IScience</i> , 2021, 24, 103226.	4.1	8
9	The <i>Tetragnatha kawaiensis</i> Genome Sheds Light on the Origins of Genomic Novelty in Spiders. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	16
10	From Trees to Clouds: PhageClouds for Fast Comparison of ~640,000 Phage Genomic Sequences and Host-Centric Visualization Using Genomic Network Graphs. <i>Phage</i> , 2021, 2, 194-203.	1.7	14
11	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. <i>Current Biology</i> , 2020, 30, 108-114.e5.	3.9	24
12	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
13	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	27.8	105
14	Arctic-adapted dogs emerged at the Pleistocene-Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	12.6	60
15	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
16	Connecting moss lipid droplets to patchouli biosynthesis. <i>PLoS ONE</i> , 2020, 15, e0243620.	2.5	5
17	Connecting moss lipid droplets to patchouli biosynthesis. , 2020, 15, e0243620.		0
18	Connecting moss lipid droplets to patchouli biosynthesis. , 2020, 15, e0243620.		0

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19	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
20	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
21	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
22	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
23	Genomic analyses reveal an absence of contemporary introgressive admixture between fin whales and blue whales, despite known hybrids. PLoS ONE, 2019, 14, e0222004.	2.5	15
24	Comparative analyses identify genomic features potentially involved in the evolution of birds-of-paradise. GigaScience, 2019, 8, .	6.4	22
25	Palaeogenomic insights into the origins of French grapevine diversity. Nature Plants, 2019, 5, 595-603.	9.3	85
26	Narwhal Genome Reveals Long-Term Low Genetic Diversity despite Current Large Abundance Size. IScience, 2019, 15, 592-599.	4.1	49
27	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	12.8	612
28	The Genome and mRNA Transcriptome of the Cosmopolitan Calanoid Copepod <i>Acartia tonsa</i> Dana Improve the Understanding of Copepod Genome Size Evolution. Genome Biology and Evolution, 2019, 11, 1440-1450.	2.5	26
29	The Whole Genome Sequence and mRNA Transcriptome of the Tropical Cyclopoid Copepod <i>Apocyclops royi</i> . G3: Genes, Genomes, Genetics, 2019, 9, 1295-1302.	1.8	13
30	NetSurfPâ€2.0: Improved prediction of protein structural features by integrated deep learning. Proteins: Structure, Function and Bioinformatics, 2019, 87, 520-527.	2.6	439
31	MobiSeq: De novo SNP discovery in model and nonâ€model species through sequencing the flanking region of transposable elements. Molecular Ecology Resources, 2019, 19, 512-525.	4.8	4
32	Improved de novo genomic assembly for the domestic donkey. Science Advances, 2018, 4, eaaq0392.	10.3	46
33	Population genomics of grey wolves and wolf-like canids in North America. PLoS Genetics, 2018, 14, e1007745.	3.5	54
34	Improved ontology for eukaryotic single-exon coding sequences in biological databases. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-6.	3.0	5
35	â€œOut of the Canâ€ A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, <i>Sardina pilchardus</i> . Genes, 2018, 9, 485.	2.4	30
36	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . Current Biology, 2018, 28, 3441-3449.e5.	3.9	110

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37	Antibodies to Intercellular Adhesion Molecule 1-Binding Plasmodium falciparum Erythrocyte Membrane Protein 1-DBL β Are Biomarkers of Protective Immunity to Malaria in a Cohort of Young Children from Papua New Guinea. <i>Infection and Immunity</i> , 2018, 86, .	2.2	23
38	Genome Sequence of <i>Talaromyces atrovirens</i> , Which Produces Red Colorants for the Food Industry. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
39	Complete mitochondrial genome of the Oriental Hornet, <i>Vespa orientalis</i> F. (Hymenoptera: Vespidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 139-140.	0.4	10
40	The first draft reference genome of the American mink (<i>Neovison vison</i>). <i>Scientific Reports</i> , 2017, 7, 14564.	3.3	16
41	The wolf reference genome sequence (<i>Canis lupus lupus</i>) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , 2017, 18, 495.	2.8	73
42	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017, 6, 1-13.	6.4	137
43	Diversity, Prevalence, and Longitudinal Occurrence of Type II Toxin-Antitoxin Systems of <i>Pseudomonas aeruginosa</i> Infecting Cystic Fibrosis Lungs. <i>Frontiers in Microbiology</i> , 2017, 8, 1180.	3.5	23
44	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	27.8	130
45	Gene expression plasticity across hosts of an invasive scale insect species. <i>PLoS ONE</i> , 2017, 12, e0176956.	2.5	20
46	<i>Plasmodium falciparum</i> var genes expressed in children with severe malaria encode CIDR β 1 domains. <i>EMBO Molecular Medicine</i> , 2016, 8, 839-850.	6.9	81
47	Using expected sequence features to improve basecalling accuracy of amplicon pyrosequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 176.	2.6	13
48	Within-host microevolution of <i>Pseudomonas aeruginosa</i> in Italian cystic fibrosis patients. <i>BMC Microbiology</i> , 2015, 15, 218.	3.3	62
49	Structural Conservation Despite Huge Sequence Diversity Allows EPCR Binding by the PfEMP1 Family Implicated in Severe Childhood Malaria. <i>Cell Host and Microbe</i> , 2015, 17, 118-129.	11.0	141
50	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. <i>Current Biology</i> , 2015, 25, 2577-2583.	3.9	161
51	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6889-97.	7.1	139
52	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	7.1	260
53	Light protection of the skin after photodynamic therapy reduces inflammation: an unblinded randomized controlled study. <i>British Journal of Dermatology</i> , 2014, 171, 175-178.	1.5	33
54	Speciation with gene flow in equids despite extensive chromosomal plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18655-18660.	7.1	183

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55	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
56	Determinants of personal ultraviolet-radiation exposure doses on a sun holiday. <i>British Journal of Dermatology</i> , 2013, 168, 1073-1079.	1.5	34
57	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	27.8	717
58	NetTurnP – Neural Network Prediction of Beta-turns by Use of Evolutionary Information and Predicted Protein Sequence Features. <i>PLoS ONE</i> , 2010, 5, e15079.	2.5	83
59	A generic method for assignment of reliability scores applied to solvent accessibility predictions. <i>BMC Structural Biology</i> , 2009, 9, 51.	2.3	555
60	Effect of Intravenous and Intrajejunal Fat Infusion on Gastric Acid Secretion and Plasma Neurotensin-like Immunoreactivity in Man. <i>Scandinavian Journal of Gastroenterology</i> , 1984, 19, 48-51.	1.5	15
61	The Mechanism of Gastrin Release in Cysteamine-Induced Duodenal Ulcer. <i>Scandinavian Journal of Gastroenterology</i> , 1982, 17, 609-612.	1.5	20
62	Acid Secretory Potency and Elimination of the 15-Leucine Gastrin-17 Analogue in Man. <i>Scandinavian Journal of Gastroenterology</i> , 1981, 16, 437-440.	1.5	11