

Bent Petersen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3579627/publications.pdf>

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	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
2	Recalibrating <i>Equus</i> evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	27.8	717
3	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	12.8	612
4	A generic method for assignment of reliability scores applied to solvent accessibility predictions. <i>BMC Structural Biology</i> , 2009, 9, 51.	2.3	555
5	NetSurfPâ€2.0: Improved prediction of protein structural features by integrated deep learning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 520-527.	2.6	439
6	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
7	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
8	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
9	Evolutionary Genomics and Conservation of the Endangered Przewalskiâ€™s Horse. <i>Current Biology</i> , 2015, 25, 2577-2583.	3.9	161
10	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
11	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
12	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017, 6, 1-13.	6.4	137
13	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	27.8	130
14	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018, 28, 3441-3449.e5.	3.9	110
15	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	27.8	105
16	Palaeogenomic insights into the origins of French grapevine diversity. <i>Nature Plants</i> , 2019, 5, 595-603.	9.3	85
17	NetTurnP â€“ 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
18	<i>Plasmodium falciparum</i> var genes expressed in children with severe malaria encode CIDR domains. <i>EMBO Molecular Medicine</i> , 2016, 8, 839-850.	6.9	81

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19	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
20	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
21	Within-host microevolution of <i>Pseudomonas aeruginosa</i> in Italian cystic fibrosis patients. <i>BMC Microbiology</i> , 2015, 15, 218.	3.3	62
22	Arctic-adapted dogs emerged at the Pleistocene–Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	12.6	60
23	Population genomics of grey wolves and wolf-like canids in North America. <i>PLoS Genetics</i> , 2018, 14, e1007745.	3.5	54
24	Narwhal Genome Reveals Long-Term Low Genetic Diversity despite Current Large Abundance Size. <i>IScience</i> , 2019, 15, 592-599.	4.1	49
25	Improved de novo genomic assembly for the domestic donkey. <i>Science Advances</i> , 2018, 4, eaaq0392.	10.3	46
26	Rapid discovery of novel prophages using biological feature engineering and machine learning. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa109.	3.2	39
27	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
28	Determinants of personal ultraviolet-radiation exposure doses on a sun holiday. <i>British Journal of Dermatology</i> , 2013, 168, 1073-1079.	1.5	34
29	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
30	PhageLeads: Rapid Assessment of Phage Therapeutic Suitability Using an Ensemble Machine Learning Approach. <i>Viruses</i> , 2022, 14, 342.	3.3	31
31	“Out of the Can” A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, <i>Sardina pilchardus</i> . <i>Genes</i> , 2018, 9, 485.	2.4	30
32	The Genome and mRNA Transcriptome of the Cosmopolitan Calanoid Copepod <i>Acartia tonsa</i> Dana Improve the Understanding of Copepod Genome Size Evolution. <i>Genome Biology and Evolution</i> , 2019, 11, 1440-1450.	2.5	26
33	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. <i>Current Biology</i> , 2021, 31, 198-206.e8.	3.9	26
34	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
35	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
36	Antibodies to Intercellular Adhesion Molecule 1-Binding <i>Plasmodium falciparum</i> Erythrocyte Membrane Protein 1-DBL α 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

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37	Comparative analyses identify genomic features potentially involved in the evolution of birds-of-paradise. <i>GigaScience</i> , 2019, 8, .	6.4	22
38	The Mechanism of Gastrin Release in Cysteamine-Induced Duodenal Ulcer. <i>Scandinavian Journal of Gastroenterology</i> , 1982, 17, 609-612.	1.5	20
39	Gene expression plasticity across hosts of an invasive scale insect species. <i>PLoS ONE</i> , 2017, 12, e0176956.	2.5	20
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 <i>Tetragnatha kauaiensis</i> Genome Sheds Light on the Origins of Genomic Novelty in Spiders. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	16
42	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
43	Genomic analyses reveal an absence of contemporary introgressive admixture between fin whales and blue whales, despite known hybrids. <i>PLoS ONE</i> , 2019, 14, e0222004.	2.5	15
44	From Trees to Clouds: PhageClouds for Fast Comparison of ~4640,000 Phage Genomic Sequences and Host-Centric Visualization Using Genomic Network Graphs. <i>Phage</i> , 2021, 2, 194-203.	1.7	14
45	Using expected sequence features to improve basecalling accuracy of amplicon pyrosequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 176.	2.6	13
46	The Whole Genome Sequence and mRNA Transcriptome of the Tropical Cyclopoid Copepod <i>Apocyclops royi</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1295-1302.	1.8	13
47	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
48	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
49	Kouprey (<i>Bos sauveli</i>) genomes unveil polytomic origin of wild Asian Bos. <i>IScience</i> , 2021, 24, 103226.	4.1	8
50	Genome Sequence of <i>Talaromyces atrovirens</i> , Which Produces Red Colorants for the Food Industry. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
51	An improved direct metagenome approach increases the detection of larger-sized circular elements across kingdoms. <i>Plasmid</i> , 2021, 115, 102576.	1.4	6
52	The genomic basis of the plant island syndrome in Darwin's giant daisies. <i>Nature Communications</i> , 2022, 13, .	12.8	6
53	Improved ontology for eukaryotic single-exon coding sequences in biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-6.	3.0	5
54	Connecting moss lipid droplets to patchouli biosynthesis. <i>PLoS ONE</i> , 2020, 15, e0243620.	2.5	5

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55	MobiSeq: De novo SNP discovery in model and non-model species through sequencing the flanking region of transposable elements. <i>Molecular Ecology Resources</i> , 2019, 19, 512-525.	4.8	4
56	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
57	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
58	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
59	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
60	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
61	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0
62	Connecting moss lipid droplets to patchoulol biosynthesis. , 2020, 15, e0243620.		0