

Jon Bohlin

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

2,765
citations

304368

22
h-index

214527

47
g-index

57
all docs

57
docs citations

57
times ranked

5124
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessment of Coronavirus Disease 2019 Intervention Strategies in the Nordic Countries Using Genomic Epidemiology. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofab665.	0.4	0
2	DNA methylation in newborns conceived by assisted reproductive technology. <i>Nature Communications</i> , 2022, 13, 1896.	5.8	26
3	Evolution and dispersal of mitochondrial DNA haplogroup U5 in Northern Europe: insights from an unsupervised learning approach to phylogeography. <i>BMC Genomics</i> , 2022, 23, 354.	1.2	3
4	Age and sex effects on DNA methylation sites linked to genes implicated in severe COVID-19 and SARS-CoV-2 host cell entry. <i>PLoS ONE</i> , 2022, 17, e0269105.	1.1	2
5	Associations between epigenetic age acceleration and infertility. <i>Human Reproduction</i> , 2022, 37, 2063-2074.	0.4	8
6	An EPIC predictor of gestational age and its application to newborns conceived by assisted reproductive technologies. <i>Clinical Epigenetics</i> , 2021, 13, 82.	1.8	24
7	Macrocirculatory Parameters and Oxygen Debt Indices in Pigs During Propofol Or Alfaxalone Anesthesia When Subjected to Experimental Stepwise Hemorrhage. <i>Frontiers in Veterinary Science</i> , 2021, 8, 664112.	0.9	1
8	Retrospective meta-transcriptomic identification of severe dengue in a traveller returning from Africa to Sweden, 1990. <i>One Health</i> , 2021, 12, 100217.	1.5	1
9	Matrilineal diversity and population history of Norwegians. <i>American Journal of Physical Anthropology</i> , 2021, 176, 120-133.	2.1	3
10	Characterization of Shiga Toxin 2a Encoding Bacteriophages Isolated From High-Virulent O145:H25 Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 728116.	1.5	1
11	The impact of public health interventions in the Nordic countries during the first year of SARS-CoV-2 transmission and evolution. <i>Eurosurveillance</i> , 2021, 26, .	3.9	8
12	Blood-based epigenetic estimators of chronological age in human adults using DNA methylation data from the Illumina MethylationEPIC array. <i>BMC Genomics</i> , 2020, 21, 747.	1.2	14
13	Identification of hepatitis C virus in the common bed bug – a potential, but uncommon route for HCV infection?. <i>Emerging Microbes and Infections</i> , 2020, 9, 1429-1431.	3.0	12
14	A simple stochastic model describing genomic evolution over time of GC content in microbial symbionts. <i>Journal of Theoretical Biology</i> , 2020, 503, 110389.	0.8	5
15	Phylogeographic Dynamics of Influenza A(H9N2) Virus Crossing Egypt. <i>Frontiers in Microbiology</i> , 2020, 11, 392.	1.5	9
16	Genomic epidemiology and population structure of <i>Neisseria gonorrhoeae</i> in Norway, 2016–2017. <i>Microbial Genomics</i> , 2020, 6, .	1.0	20
17	Estimation of AT and GC content distributions of nucleotide substitution rates in bacterial core genomes. <i>Big Data Analytics</i> , 2019, 4, .	2.2	2
18	Statistical predictions with glmnet. <i>Clinical Epigenetics</i> , 2019, 11, 123.	1.8	460

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19	Evolution of Genomic Base Composition: From Single Cell Microbes to Multicellular Animals. Computational and Structural Biotechnology Journal, 2019, 17, 362-370.	1.9	24
20	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging, 2019, 11, 4238-4253.	1.4	79
21	Transfer of a bla CTX-M-1-carrying plasmid between different Escherichia coli strains within the human gut explored by whole genome sequencing analyses. Scientific Reports, 2018, 8, 280.	1.6	28
22	Global expansion of <i>Mycobacterium tuberculosis</i> lineage 4 shaped by colonial migration and local adaptation. Science Advances, 2018, 4, eaat5869.	4.7	130
23	Draft Genome Sequence of a Potentially Novel Streptococcus Species Belonging to the Streptococcus mitis Group. Genome Announcements, 2018, 6, .	0.8	3
24	Re-visiting the evolution, dispersal and epidemiology of Zika virus in Asia. Emerging Microbes and Infections, 2018, 7, 1-8.	3.0	39
25	Acquisition of virulence genes by a carrier strain gave rise to the ongoing epidemics of meningococcal disease in West Africa. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5510-5515.	3.3	45
26	Modeling of the GC content of the substituted bases in bacterial core genomes. BMC Genomics, 2018, 19, 589.	1.2	16
27	Whole-genome sequencing and antimicrobial resistance in Brucella melitensis from a Norwegian perspective. Scientific Reports, 2018, 8, 8538.	1.6	37
28	A genomic view of experimental intraspecies and interspecies transformation of a rifampicin-resistance allele into Neisseria meningitidis. Microbial Genomics, 2018, 4, .	1.0	10
29	The nucleotide composition of microbial genomes indicates differential patterns of selection on core and accessory genomes. BMC Genomics, 2017, 18, 151.	1.2	55
30	Hot chicks, cold feet. Physiology and Behavior, 2017, 179, 42-48.	1.0	27
31	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. Human Molecular Genetics, 2017, 26, 4067-4085.	1.4	211
32	Characterizing the virome of Ixodes ricinus ticks from northern Europe. Scientific Reports, 2017, 7, 10870.	1.6	92
33	Impact of extensive antibiotic treatment on faecal carriage of antibiotic-resistant enterobacteria in children in a low resistance prevalence setting. PLoS ONE, 2017, 12, e0187618.	1.1	14
34	Rapid scoring of genes in microbial pan-genome-wide association studies with Scoary. Genome Biology, 2016, 17, 238.	3.8	472
35	Prediction of gestational age based on genome-wide differentially methylated regions. Genome Biology, 2016, 17, 207.	3.8	132
36	Prevalence and epidemiology of meningococcal carriage in Southern Ethiopia prior to implementation of MenAfriVac, a conjugate vaccine. BMC Infectious Diseases, 2016, 16, 639.	1.3	20

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37	Armed conflict and population displacement as drivers of the evolution and dispersal of <i>Mycobacterium tuberculosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13881-13886.	3.3	76
38	Maternal plasma folate impacts differential DNA methylation in an epigenome-wide meta-analysis of newborns. Nature Communications, 2016, 7, 10577.	5.8	219
39	Genome expansion in bacteria: the curious case of <i>Chlamydia trachomatis</i> . BMC Research Notes, 2015, 8, 512.	0.6	3
40	Effect of maternal gestational weight gain on offspring DNA methylation: a follow-up to the ALSPAC cohort study. BMC Research Notes, 2015, 8, 321.	0.6	12
41	An evolutionary analysis of genome expansion and pathogenicity in <i>Escherichia coli</i> . BMC Genomics, 2014, 15, 882.	1.2	25
42	Microevolution of <i>Renibacterium salmoninarum</i> : evidence for intercontinental dissemination associated with fish movements. ISME Journal, 2014, 8, 746-756.	4.4	32
43	Positive correlations between genomic %AT and genome size within strains of bacterial species. Environmental Microbiology Reports, 2014, 6, 278-286.	1.0	18
44	Veillonella, Firmicutes: Microbes disguised as Gram negatives. Standards in Genomic Sciences, 2013, 9, 431-448.	1.5	47
45	Amino Acid Usage Is Asymmetrically Biased in AT- and GC-Rich Microbial Genomes. PLoS ONE, 2013, 8, e69878.	1.1	36
46	Relative entropy differences in bacterial chromosomes, plasmids, phages and genomic islands. BMC Genomics, 2012, 13, 66.	1.2	17
47	Growth comparison of several <i>Escherichia coli</i> strains exposed to various concentrations of lactoferrin using linear spline regression. Microbial Informatics and Experimentation, 2012, 2, 5.	7.6	19
48	Genomic Signatures in Microbes—Properties and Applications. Scientific World Journal, The, 2011, 11, 715-725.	0.8	20
49	Genomic comparisons of <i>Brucella</i> spp. and closely related bacteria using base compositional and proteome based methods. BMC Evolutionary Biology, 2010, 10, 249.	3.2	24
50	Analysis of intra-genomic GC content homogeneity within prokaryotes. BMC Genomics, 2010, 11, 464.	1.2	39
51	Stretches of alternating pyrimidine/purines and purines are respectively linked with pathogenicity and growth temperature in prokaryotes. BMC Genomics, 2009, 10, 346.	1.2	6
52	Examination of Genome Homogeneity in Prokaryotes Using Genomic Signatures. PLoS ONE, 2009, 4, e8113.	1.1	21
53	Reliability and applications of statistical methods based on oligonucleotide frequencies in bacterial and archaeal genomes. BMC Genomics, 2008, 9, 104.	1.2	35
54	Investigations of Oligonucleotide Usage Variance Within and Between Prokaryotes. PLoS Computational Biology, 2008, 4, e1000057.	1.5	53