

Bjorn Andersson

List of Publications by Year in descending order

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85
papers

9,277
citations

81889

39
h-index

54911

84
g-index

90
all docs

90
docs citations

90
times ranked

11870
citing authors

#	ARTICLE	IF	CITATIONS
1	Cloning of a human parvovirus by molecular screening of respiratory tract samples. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12891-12896.	7.1	1,398
2	The Norway spruce genome sequence and conifer genome evolution. Nature, 2013, 497, 579-584.	27.8	1,303
3	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. Science, 2005, 309, 409-415.	12.6	1,273
4	Comparative Genomics of Trypanosomatid Parasitic Protozoa. Science, 2005, 309, 404-409.	12.6	713
5	Identification of a Third Human Polyomavirus. Journal of Virology, 2007, 81, 4130-4136.	3.4	574
6	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	27.8	391
7	Draft Genome Sequencing of Giardia intestinalis Assemblage B Isolate GS: Is Human Giardiasis Caused by Two Different Species?. PLoS Pathogens, 2009, 5, e1000560.	4.7	236
8	Microbe-host interplay in atopic dermatitis and psoriasis. Nature Communications, 2019, 10, 4703.	12.8	217
9	The ketogenic diet influences taxonomic and functional composition of the gut microbiota in children with severe epilepsy. Npj Biofilms and Microbiomes, 2019, 5, 5.	6.4	179
10	Performing Skin Microbiome Research: A Method to the Madness. Journal of Investigative Dermatology, 2017, 137, 561-568.	0.7	164
11	Characterization of the Viral Microbiome in Patients with Severe Lower Respiratory Tract Infections, Using Metagenomic Sequencing. PLoS ONE, 2012, 7, e30875.	2.5	154
12	Shotgun Sequencing Analysis of Trypanosoma cruzi I Sylvio X10/1 and Comparison with T. cruzi VI CL Brener. PLoS Neglected Tropical Diseases, 2011, 5, e984.	3.0	129
13	Genome analysis and comparative genomics of a Giardia intestinalis assemblage E isolate. BMC Genomics, 2010, 11, 543.	2.8	125
14	Reading and editing the Pleurodeles waltl genome reveals novel features of tetrapod regeneration. Nature Communications, 2017, 8, 2286.	12.8	123
15	Dynamics of HIV-1 Quasispecies during Antiviral Treatment Dissected Using Ultra-Deep Pyrosequencing. PLoS ONE, 2010, 5, e11345.	2.5	112
16	Multiple Mitochondrial Introgression Events and Heteroplasmy in Trypanosoma cruzi Revealed by Maxicircle MLST and Next Generation Sequencing. PLoS Neglected Tropical Diseases, 2012, 6, e1584.	3.0	104
17	Gene synteny and evolution of genome architecture in trypanosomatids. Molecular and Biochemical Parasitology, 2004, 134, 183-191.	1.1	92
18	Toll-Like Receptor 4 Promoter Polymorphisms: Common TLR4 Variants May Protect against Severe Urinary Tract Infection. PLoS ONE, 2010, 5, e10734.	2.5	90

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19	Inherited Susceptibility to Acute Pyelonephritis: A Family Study of Urinary Tract Infection. <i>Journal of Infectious Diseases</i> , 2007, 195, 1227-1234.	4.0	86
20	A Genetic Basis of Susceptibility to Acute Pyelonephritis. <i>PLoS ONE</i> , 2007, 2, e825.	2.5	85
21	PCR-Induced Transitions Are the Major Source of Error in Cleaned Ultra-Deep Pyrosequencing Data. <i>PLoS ONE</i> , 2013, 8, e70388.	2.5	78
22	Messenger RNA processing sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 125-134.	1.1	73
23	Genome of the Avirulent Human-Infective Trypanosome "Trypanosoma rangeli". <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3176.	3.0	72
24	Chromosomal copy number variation reveals differential levels of genomic plasticity in distinct <i>Trypanosoma cruzi</i> strains. <i>BMC Genomics</i> , 2015, 16, 499.	2.8	68
25	Repetitive DNA is associated with centromeric domains in <i>Trypanosoma brucei</i> but not <i>Trypanosoma cruzi</i> . <i>Genome Biology</i> , 2007, 8, R37.	9.6	67
26	Intraclonal Variations Among <i>Streptococcus pneumoniae</i> Isolates Influence the Likelihood of Invasive Disease in Children. <i>Journal of Infectious Diseases</i> , 2014, 209, 377-388.	4.0	61
27	Proteomics in <i>Trypanosoma cruzi</i> – localization of novel proteins to various organelles. <i>Proteomics</i> , 2008, 8, 2735-2749.	2.2	60
28	Meiotic sex in Chagas disease parasite <i>Trypanosoma cruzi</i> . <i>Nature Communications</i> , 2019, 10, 3972.	12.8	58
29	Classification of DNA sequences using Bloom filters. <i>Bioinformatics</i> , 2010, 26, 1595-1600.	4.1	57
30	Comparative genomic analysis of human infective <i>Trypanosoma cruzi</i> lineages with the bat-restricted subspecies <i>T. cruzi marinkellei</i> . <i>BMC Genomics</i> , 2012, 13, 531.	2.8	57
31	Transcriptome Profiling of <i>Giardia intestinalis</i> Using Strand-specific RNA-Seq. <i>PLoS Computational Biology</i> , 2013, 9, e1003000.	3.2	56
32	Comparative genomic analyses of freshly isolated <i>Giardia intestinalis</i> assemblage A isolates. <i>BMC Genomics</i> , 2015, 16, 697.	2.8	55
33	Diversity of the sarco/endoplasmic reticulum Ca ²⁺ -ATPase orthologue of <i>Plasmodium falciparum</i> (PfATP6). <i>Infection, Genetics and Evolution</i> , 2008, 8, 340-345.	2.3	52
34	Activation of a neural stem cell transcriptional program in parenchymal astrocytes. <i>ELife</i> , 2020, 9, .	6.0	51
35	Telomere and subtelomere of <i>Trypanosoma cruzi</i> chromosomes are enriched in (pseudo)genes of retrotransposon hot spot and trans-sialidase-like gene families: the origins of <i>T. cruzi</i> telomeres. <i>Gene</i> , 2005, 346, 153-161.	2.2	47
36	Database of <i>Trypanosoma cruzi</i> repeated genes: 20 000 additional gene variants. <i>BMC Genomics</i> , 2007, 8, 391.	2.8	47

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37	Gene Survey of the Pathogenic Protozoan <i>Trypanosoma cruzi</i> . <i>Genome Research</i> , 2000, 10, 1103-1107.	5.5	41
38	Identification of non-autonomous non-LTR retrotransposons in the genome of <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 124, 73-78.	1.1	41
39	Molecular Characterization of Serine-, Alanine-, and Proline-Rich Proteins of <i>Trypanosoma cruzi</i> and Their Possible Role in Host Cell Infection. <i>Infection and Immunity</i> , 2006, 74, 1537-1546.	2.2	41
40	Preclinical Assessment of the Treatment of Second-Stage African Trypanosomiasis with Cordycepin and Deoxycoformycin. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e495.	3.0	39
41	<i>Trypanosoma cruzi</i> Clone Dm28c Draft Genome Sequence. <i>Genome Announcements</i> , 2014, 2, .	0.8	39
42	MAOA haplotypes associated with thrombocyte-MAO activity. <i>BMC Genetics</i> , 2005, 6, 46.	2.7	37
43	A Solanesyl-diphosphate Synthase Localizes in Glycosomes of <i>Trypanosoma cruzi</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 39339-39348.	3.4	35
44	The Short Non-Coding Transcriptome of the Protozoan Parasite <i>Trypanosoma cruzi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1283.	3.0	35
45	Serotonin receptor 2C (HTR2C) and schizophrenia: Examination of possible medication and genetic influences on expression levels. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2005, 134B, 84-89.	1.7	32
46	Colonization and genetic diversification processes of <i>Leishmania infantum</i> in the Americas. <i>Communications Biology</i> , 2021, 4, 139.	4.4	32
47	Repeat-Driven Generation of Antigenic Diversity in a Major Human Pathogen, <i>Trypanosoma cruzi</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 614665.	3.9	25
48	Separation of nearly identical repeats in shotgun assemblies using defined nucleotide positions, DNPs. <i>Bioinformatics</i> , 2002, 18, 379-388.	4.1	24
49	Comparative karyotyping as a tool for genome structure analysis of <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2006, 147, 30-38.	1.1	22
50	Mutation screening of a haplotype block around the insulin degrading enzyme gene and association with Alzheimer's disease. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2005, 136B, 69-71.	1.7	21
51	The <i>Trypanosoma cruzi</i> genome; conserved core genes and extremely variable surface molecule families. <i>Research in Microbiology</i> , 2011, 162, 619-625.	2.1	21
52	An unbiased metagenomic search for infectious agents using monozygotic twins discordant for chronic fatigue. <i>BMC Microbiology</i> , 2011, 11, 2.	3.3	21
53	Refining wet lab experiments with in silico searches: A rational quest for diagnostic peptides in visceral leishmaniasis. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007353.	3.0	16
54	Microbial and transcriptional differences elucidate atopic dermatitis heterogeneity across skin sites. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1173-1187.	5.7	16

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55	Simultaneous Shotgun Sequencing of Multiple cDN A Clones. <i>DNA Sequence</i> , 1997, 7, 63-70.	0.7	15
56	Discovering viral genomes in human metagenomic data by predicting unknown protein families. <i>Scientific Reports</i> , 2018, 8, 28.	3.3	14
57	<i>Trypanosoma cruzi</i> : A Putative Vacuolar ATP Synthase Subunit and a CAAX Prenyl Protease-Encoding Gene, as Examples of Gene Identification in Genome Projects. <i>Experimental Parasitology</i> , 2000, 95, 176-186.	1.2	13
58	DNPtrapper: an assembly editing tool for finishing and analysis of complex repeat regions. <i>BMC Bioinformatics</i> , 2006, 7, 155.	2.6	13
59	2b-RAD genotyping for population genomic studies of Chagas disease vectors: <i>Rhodnius ecuadoriensis</i> in Ecuador. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005710.	3.0	13
60	Identification and characterization of serine proteinase inhibitors from <i>Neospora caninum</i> . <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 101-107.	1.1	12
61	Analyses of an Expressed Sequence Tag Library from <i>Taenia solium</i> , <i>Cysticercus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e919.	3.0	12
62	trap: Tandem Repeat Assembly Program produces improved shotgun assemblies of repetitive sequences. <i>Computer Methods and Programs in Biomedicine</i> , 2003, 70, 47-59.	4.7	11
63	Virome definition in cerebrospinal fluid of patients with neurological complications after hematopoietic stem cell transplantation. <i>Journal of Clinical Virology</i> , 2018, 108, 112-120.	3.1	10
64	Better detection of Torque teno virus in children with leukemia by metagenomic sequencing than by quantitative PCR. <i>Journal of Medical Virology</i> , 2022, 94, 634-641.	5.0	10
65	ANALYSIS OF 5-HYDROXYTRYPTAMINE 2C RECEPTOR GENE PROMOTER VARIANTS AS ALCOHOL-DEPENDENCE RISK FACTORS. <i>Alcohol and Alcoholism</i> , 2004, 39, 380-385.	1.6	9
66	Divergent clonal differentiation trajectories establish CD8+ memory T cell heterogeneity during acute viral infections in humans. <i>Cell Reports</i> , 2021, 35, 109174.	6.4	9
67	Microevolution of <i>Trypanosoma cruzi</i> reveals hybridization and clonal mechanisms driving rapid genome diversification. <i>ELife</i> , 2022, 11, .	6.0	9
68	Strand asymmetry patterns in trypanosomatid parasites. <i>Experimental Parasitology</i> , 2005, 109, 143-149.	1.2	8
69	FAAST: Flow-space Assisted Alignment Search Tool. <i>BMC Bioinformatics</i> , 2011, 12, 293.	2.6	8
70	Transcriptome-based identification of novel endotypes in adult atopic dermatitis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 1486-1498.	5.7	8
71	High genome plasticity and frequent genetic exchange in <i>Leishmania tropica</i> isolates from Afghanistan, Iran and Syria. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0010110.	3.0	8
72	Trypanothione synthetase locus in <i>Trypanosoma cruzi</i> CL Brener strain shows an extensive allelic divergence. <i>Acta Tropica</i> , 2003, 87, 269-278.	2.0	7

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73	Parasite genomicsâ€”Time to think bigger. PLoS Neglected Tropical Diseases, 2017, 11, e0005463.	3.0	6
74	Expression of the Inositol 1,4,5-Trisphosphate Receptor and the Ryanodine Receptor Ca ²⁺ -Release Channels in the Beta-Cells and Alpha-Cells of the Human Islets of Langerhans. Advances in Experimental Medicine and Biology, 2020, 1131, 271-279.	1.6	6
75	Complete sequence of a 38.4-kb human cosmid insert containing the polymorphic marker DXS455 from Xq28. DNA Sequence, 1995, 5, 219-223.	0.7	5
76	Characterization of a Trypanosoma cruzi acetyltransferase: cellular location, activity and structureâ€†. Molecular and Biochemical Parasitology, 2007, 152, 123-131.	1.1	5
77	ReDiT: Repeat Discrepancy Tagger—a shotgun assembly finishing aid. Bioinformatics, 2004, 20, 803-804.	4.1	4
78	Population genomics and geographic dispersal in Chagas disease vectors: Landscape drivers and evidence of possible adaptation to the domestic setting. PLoS Genetics, 2022, 18, e1010019.	3.5	4
79	GRATâ€”genome-scale rapid alignment tool. Computer Methods and Programs in Biomedicine, 2007, 86, 87-92.	4.7	3
80	Characterization of Evolutionarily Conserved<i> Trypanosoma cruzi</i> NatC and NatA-N-Terminal Acetyltransferase Complexes. Journal of Parasitology Research, 2019, 2019, 1-11.	1.2	3
81	A graphical tool for parasite genome annotation. Computer Methods and Programs in Biomedicine, 2004, 73, 55-60.	4.7	2
82	Skin Microbiota and Clinical Associations in Netherton Syndrome. JID Innovations, 2021, 1, 100008.	2.4	2
83	Treatment outcome of imported cutaneous leishmaniasis among travelers and migrants infected with Leishmania major and Leishmania tropica: a retrospective study in European centers 2013 to 2019. International Journal of Infectious Diseases, 2022, 122, 375-381.	3.3	1
84	A chromosome-specific dispersed gene family in Trypanosoma cruzi. Molecular and Biochemical Parasitology, 1999, 100, 229-234.	1.1	0
85	Differential expression and activity of arginine kinase between the American trypanosomatids Trypanosoma rangeli and Trypanosoma cruzi. Experimental Parasitology, 2021, 230, 108159.	1.2	0