

Bjorn Andersson

List of Publications by Year in descending order

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85
papers

9,277
citations

81900

39
h-index

54911

84
g-index

90
all docs

90
docs citations

90
times ranked

11870
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Population genomics and geographic dispersal in Chagas disease vectors: Landscape drivers and evidence of possible adaptation to the domestic setting. <i>PLoS Genetics</i> , 2022, 18, e1010019.	3.5	4
4	Microevolution of <i>Trypanosoma cruzi</i> reveals hybridization and clonal mechanisms driving rapid genome diversification. <i>ELife</i> , 2022, 11, .	6.0	9
5	Treatment outcome of imported cutaneous leishmaniasis among travelers and migrants infected with <i>Leishmania major</i> and <i>Leishmania tropica</i> : a retrospective study in European centers 2013 to 2019. <i>International Journal of Infectious Diseases</i> , 2022, 122, 375-381.	3.3	1
6	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
7	Colonization and genetic diversification processes of <i>Leishmania infantum</i> in the Americas. <i>Communications Biology</i> , 2021, 4, 139.	4.4	32
8	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
9	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
10	Skin Microbiota and Clinical Associations in Netherton Syndrome. <i>JID Innovations</i> , 2021, 1, 100008.	2.4	2
11	Differential expression and activity of arginine kinase between the American trypanosomatids <i>Trypanosoma rangeli</i> and <i>Trypanosoma cruzi</i> . <i>Experimental Parasitology</i> , 2021, 230, 108159.	1.2	0
12	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
13	Activation of a neural stem cell transcriptional program in parenchymal astrocytes. <i>ELife</i> , 2020, 9, .	6.0	51
14	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. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1131, 271-279.	1.6	6
15	Microbe-host interplay in atopic dermatitis and psoriasis. <i>Nature Communications</i> , 2019, 10, 4703.	12.8	217
16	Meiotic sex in Chagas disease parasite <i>Trypanosoma cruzi</i> . <i>Nature Communications</i> , 2019, 10, 3972.	12.8	58
17	The ketogenic diet influences taxonomic and functional composition of the gut microbiota in children with severe epilepsy. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 5.	6.4	179
18	Characterization of Evolutionarily Conserved <i>Trypanosoma cruzi</i> NatC and NatA-N-Terminal Acetyltransferase Complexes. <i>Journal of Parasitology Research</i> , 2019, 2019, 1-11.	1.2	3

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19	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
20	Discovering viral genomes in human metagenomic data by predicting unknown protein families. <i>Scientific Reports</i> , 2018, 8, 28.	3.3	14
21	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
22	Performing Skin Microbiome Research: A Method to the Madness. <i>Journal of Investigative Dermatology</i> , 2017, 137, 561-568.	0.7	164
23	Reading and editing the <i>Pleurodeles waltl</i> genome reveals novel features of tetrapod regeneration. <i>Nature Communications</i> , 2017, 8, 2286.	12.8	123
24	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
25	Parasite genomicsâ€”Time to think bigger. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005463.	3.0	6
26	Comparative genomic analyses of freshly isolated <i>Giardia intestinalis</i> assemblage A isolates. <i>BMC Genomics</i> , 2015, 16, 697.	2.8	55
27	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
28	<i>Trypanosoma cruzi</i> Clone Dm28c Draft Genome Sequence. <i>Genome Announcements</i> , 2014, 2, .	0.8	39
29	Genome of the Avirulent Human-Infective <i>Trypanosoma rangeli</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3176.	3.0	72
30	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
31	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
32	Transcriptome Profiling of <i>Giardia intestinalis</i> Using Strand-specific RNA-Seq. <i>PLoS Computational Biology</i> , 2013, 9, e1003000.	3.2	56
33	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
34	Multiple Mitochondrial Introgression Events and Heteroplasmy in <i>Trypanosoma cruzi</i> Revealed by Maxicircle MLST and Next Generation Sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1584.	3.0	104
35	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
36	Characterization of the Viral Microbiome in Patients with Severe Lower Respiratory Tract Infections, Using Metagenomic Sequencing. <i>PLoS ONE</i> , 2012, 7, e30875.	2.5	154

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37	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
38	FAAST: Flow-space Assisted Alignment Search Tool. <i>BMC Bioinformatics</i> , 2011, 12, 293.	2.6	8
39	An unbiased metagenomic search for infectious agents using monozygotic twins discordant for chronic fatigue. <i>BMC Microbiology</i> , 2011, 11, 2.	3.3	21
40	Shotgun Sequencing Analysis of <i>Trypanosoma cruzi</i> I Sylvio X10/1 and Comparison with <i>T. cruzi</i> VI CL Brenner. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e984.	3.0	129
41	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
42	Genome analysis and comparative genomics of a <i>Giardia intestinalis</i> assemblage E isolate. <i>BMC Genomics</i> , 2010, 11, 543.	2.8	125
43	Toll-Like Receptor 4 Promoter Polymorphisms: Common TLR4 Variants May Protect against Severe Urinary Tract Infection. <i>PLoS ONE</i> , 2010, 5, e10734.	2.5	90
44	Classification of DNA sequences using Bloom filters. <i>Bioinformatics</i> , 2010, 26, 1595-1600.	4.1	57
45	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
46	Dynamics of HIV-1 Quasispecies during Antiviral Treatment Dissected Using Ultra-Deep Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e11345.	2.5	112
47	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
48	Draft Genome Sequencing of <i>Giardia intestinalis</i> Assemblage B Isolate GS: Is Human Giardiasis Caused by Two Different Species?. <i>PLoS Pathogens</i> , 2009, 5, e1000560.	4.7	236
49	Proteomics in <i>Trypanosoma cruzi</i> – localization of novel proteins to various organelles. <i>Proteomics</i> , 2008, 8, 2735-2749.	2.2	60
50	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
51	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
52	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
53	Identification of a Third Human Polyomavirus. <i>Journal of Virology</i> , 2007, 81, 4130-4136.	3.4	574
54	A Genetic Basis of Susceptibility to Acute Pyelonephritis. <i>PLoS ONE</i> , 2007, 2, e825.	2.5	85

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55	Database of <i>Trypanosoma cruzi</i> repeated genes: 20 000 additional gene variants. <i>BMC Genomics</i> , 2007, 8, 391.	2.8	47
56	GRATâ€™ genome-scale rapid alignment tool. <i>Computer Methods and Programs in Biomedicine</i> , 2007, 86, 87-92.	4.7	3
57	Characterization of a <i>Trypanosoma cruzi</i> acetyltransferase: cellular location, activity and structureâ†. <i>Molecular and Biochemical Parasitology</i> , 2007, 152, 123-131.	1.1	5
58	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
59	DNPtrapper: an assembly editing tool for finishing and analysis of complex repeat regions. <i>BMC Bioinformatics</i> , 2006, 7, 155.	2.6	13
60	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
61	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
62	Strand asymmetry patterns in trypanosomatid parasites. <i>Experimental Parasitology</i> , 2005, 109, 143-149.	1.2	8
63	Messenger RNA processing sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 125-134.	1.1	73
64	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
65	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
66	MAOA haplotypes associated with thrombocyte-MAO activity. <i>BMC Genetics</i> , 2005, 6, 46.	2.7	37
67	Cloning of a human parvovirus by molecular screening of respiratory tract samples. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12891-12896.	7.1	1,398
68	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415.	12.6	1,273
69	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	12.6	713
70	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
71	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
72	ReDiT: Repeat Discrepancy Tagger--a shotgun assembly finishing aid. <i>Bioinformatics</i> , 2004, 20, 803-804.	4.1	4

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73	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	27.8	391
74	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	1.1	92
75	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
76	A graphical tool for parasite genome annotation. <i>Computer Methods and Programs in Biomedicine</i> , 2004, 73, 55-60.	4.7	2
77	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
78	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
79	Separation of nearly identical repeats in shotgun assemblies using defined nucleotide positions, DNPs. <i>Bioinformatics</i> , 2002, 18, 379-388.	4.1	24
80	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
81	<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
82	Gene Survey of the Pathogenic Protozoan <i>Trypanosoma cruzi</i> . <i>Genome Research</i> , 2000, 10, 1103-1107.	5.5	41
83	A chromosome-specific dispersed gene family in <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 1999, 100, 229-234.	1.1	0
84	Simultaneous Shotgun Sequencing of Multiple cDN A Clones. <i>DNA Sequence</i> , 1997, 7, 63-70.	0.7	15
85	Complete sequence of a 38.4-kb human cosmid insert containing the polymorphic marker DXS455 from Xq28. <i>DNA Sequence</i> , 1995, 5, 219-223.	0.7	5