

# David Åmajs

## List of Publications by Year in descending order

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114  
papers

3,464  
citations

126907

33  
h-index

175258

52  
g-index

120  
all docs

120  
docs citations

120  
times ranked

2380  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5646-5651.	7.1	251
2	<i>Treponema pallidum</i> , the syphilis spirochete: making a living as a stealth pathogen. Nature Reviews Microbiology, 2016, 14, 744-759.	28.6	184
3	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. Nature Microbiology, 2017, 2, 16245.	13.3	138
4	A Novel <i>Treponema pallidum</i> Antigen, TP0136, Is an Outer Membrane Protein That Binds Human Fibronectin. Infection and Immunity, 2008, 76, 1848-1857.	2.2	108
5	Whole Genome Sequences of Three <i>Treponema pallidum</i> ssp. <i>pertenue</i> Strains: Yaws and Syphilis Treponemes Differ in Less than 0.2% of the Genome Sequence. PLoS Neglected Tropical Diseases, 2012, 6, e1471.	3.0	106
6	Macrolide treatment failure in a case of secondary syphilis: a novel A2059G mutation in the 23S rRNA gene of <i>Treponema pallidum</i> subsp. <i>pallidum</i> . Journal of Medical Microbiology, 2009, 58, 832-836.	1.8	104
7	Characterization of Colicin S4 and Its Receptor, OmpW, a Minor Protein of the <i>Escherichia coli</i> Outer Membrane. Journal of Bacteriology, 1999, 181, 3578-3581.	2.2	98
8	Genetic diversity in <i>Treponema pallidum</i> : Implications for pathogenesis, evolution and molecular diagnostics of syphilis and yaws. Infection, Genetics and Evolution, 2012, 12, 191-202.	2.3	90
9	The Impact of DNA Extraction Methods on Stool Bacterial and Fungal Microbiota Community Recovery. Frontiers in Microbiology, 2019, 10, 821.	3.5	80
10	Whole Genome Sequence of <i>Treponema pallidum</i> ssp. <i>pallidum</i> , Strain Mexico A, Suggests Recombination between Yaws and Syphilis Strains. PLoS Neglected Tropical Diseases, 2012, 6, e1832.	3.0	73
11	Complete genome sequence of <i>Treponema pallidum</i> ssp. <i>pallidum</i> strain SS14 determined with oligonucleotide arrays. BMC Microbiology, 2008, 8, 76.	3.3	66
12	Bacteriocin synthesis in uropathogenic and commensal <i>Escherichia coli</i> : colicin E1 is a potential virulence factor. BMC Microbiology, 2010, 10, 288.	3.3	66
13	Resequencing of <i>Treponema pallidum</i> ssp. <i>pallidum</i> Strains Nichols and SS14: Correction of Sequencing Errors Resulted in Increased Separation of Syphilis Treponeme Subclusters. PLoS ONE, 2013, 8, e74319.	2.5	66
14	Complete Genome Sequence of <i>Treponema paraluis-cuniculi</i> , Strain Cuniculi A: The Loss of Infectivity to Humans Is Associated with Genome Decay. PLoS ONE, 2011, 6, e20415.	2.5	66
15	Molecular Typing of <i>Treponema pallidum</i> in the Czech Republic during 2011 to 2013: Increased Prevalence of Identified Genotypes and of Isolates with Macrolide Resistance. Journal of Clinical Microbiology, 2014, 52, 3693-3700.	3.9	62
16	Genome Analysis of <i>Treponema pallidum</i> subsp. <i>pallidum</i> and subsp. <i>pertenue</i> Strains: Most of the Genetic Differences Are Localized in Six Regions. PLoS ONE, 2010, 5, e15713.	2.5	59
17	Sequencing-based Molecular Typing of <i>Treponema pallidum</i> Strains in the Czech Republic: All Identified Genotypes are Related to the Sequence of the SS14 Strain. Acta Dermato-Venereologica, 2012, 92, 669-674.	1.3	57
18	Human extraintestinal pathogenic <i>Escherichia coli</i> strains differ in prevalence of virulence factors, phylogroups, and bacteriocin determinants. BMC Microbiology, 2016, 16, 218.	3.3	55

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19	Molecular characterization of <i>Treponema pallidum</i> subsp. <i>pallidum</i> in Switzerland and France with a new multilocus sequence typing scheme. <i>PLoS ONE</i> , 2018, 13, e0200773.	2.5	55
20	Whole Genome Sequence of the <i>Treponema</i> Fribourg-Blanc: Unspecified Simian Isolate Is Highly Similar to the Yaws Subspecies. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2172.	3.0	53
21	Whole Genome Sequence of the <i>Treponema pallidum</i> subsp. <i>endemicum</i> Strain Bosnia A: The Genome Is Related to Yaws <i>Treponemes</i> but Contains Few Loci Similar to Syphilis <i>Treponemes</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3261.	3.0	51
22	Bacteriocin-encoding genes and ExPEC virulence determinants are associated in human fecal <i>Escherichia coli</i> strains. <i>BMC Microbiology</i> , 2014, 14, 109.	3.3	43
23	Microcin determinants are associated with B2 phylogroup of human fecal <i>Escherichia coli</i> isolates. <i>MicrobiologyOpen</i> , 2016, 5, 490-498.	3.0	43
24	Genome Differences between <i>Treponema pallidum</i> subsp. <i>pallidum</i> Strain Nichols and <i>T. paraluisunculi</i> Strain Cuniculi A. <i>Infection and Immunity</i> , 2007, 75, 5859-5866.	2.2	42
25	Human <i>Escherichia coli</i> isolates from hemocultures: Septicemia linked to urogenital tract infections is caused by isolates harboring more virulence genes than bacteraemia linked to other conditions. <i>International Journal of Medical Microbiology</i> , 2017, 307, 182-189.	3.6	42
26	Advances in the Diagnosis of Endemic Treponematoses: Yaws, Bejel, and Pinta. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2283.	3.0	41
27	Syphilis-causing strains belong to separate SS14-like or Nichols-like groups as defined by multilocus analysis of 19 <i>Treponema pallidum</i> strains. <i>International Journal of Medical Microbiology</i> , 2014, 304, 645-653.	3.6	41
28	Nonhuman primates across sub-Saharan Africa are infected with the yaws bacterium <i>Treponema pallidum</i> subsp. <i>pertenue</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	6.5	41
29	Directly Sequenced Genomes of Contemporary Strains of Syphilis Reveal Recombination-Driven Diversity in Genes Encoding Predicted Surface-Exposed Antigens. <i>Frontiers in Microbiology</i> , 2019, 10, 1691.	3.5	39
30	Genetics of human and animal uncultivable treponemal pathogens. <i>Infection, Genetics and Evolution</i> , 2018, 61, 92-107.	2.3	38
31	Complete genome sequence of <i>Treponema pallidum</i> strain DAL-1. <i>Standards in Genomic Sciences</i> , 2012, 7, 12-21.	1.5	37
32	Macrolide Resistance in the Syphilis Spirochete, <i>Treponema pallidum</i> ssp. <i>pallidum</i> : Can We Also Expect Macrolide-Resistant Yaws Strains?. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 678-683.	1.4	37
33	Bacterial but Not Fungal Gut Microbiota Alterations Are Associated With Common Variable Immunodeficiency (CVID) Phenotype. <i>Frontiers in Immunology</i> , 2019, 10, 1914.	4.8	37
34	Human <i>Treponema pallidum</i> 11q/lj isolate belongs to subsp. <i>endemicum</i> but contains two loci with a sequence in TP0548 and TP0488 similar to subsp. <i>pertenue</i> and subsp. <i>pallidum</i> , respectively. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005434.	3.0	37
35	From microbial genome sequence to applications. <i>Research in Microbiology</i> , 2000, 151, 151-158.	2.1	35
36	Detection of <i>Treponema pallidum</i> subsp. <i>pallidum</i> from Skin Lesions, Serum, and Cerebrospinal Fluid in an Infant with Congenital Syphilis after Clindamycin Treatment of the Mother during Pregnancy. <i>Journal of Clinical Microbiology</i> , 2007, 45, 659-661.	3.9	35

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37	Comparison of CDC and sequence-based molecular typing of syphilis treponemes: tpr and arp loci are variable in multiple samples from the same patient. BMC Microbiology, 2013, 13, 178.	3.3	35
38	Molecular typing of Treponema pallidum isolates from Buenos Aires, Argentina: Frequent Nichols-like isolates and low levels of macrolide resistance. PLoS ONE, 2017, 12, e0172905.	2.5	33
39	Structure of rrn operons in pathogenic non-cultivable treponemes: sequence but not genomic position of intergenic spacers correlates with classification of Treponema pallidum and Treponema paraluisanculi strains. Journal of Medical Microbiology, 2013, 62, 196-207.	1.8	32
40	Sequence Variation of Rare Outer Membrane Protein $\beta$ -Barrel Domains in Clinical Strains Provides Insights into the Evolution of <i>Treponema pallidum</i> subsp. <i>pallidum</i> , the Syphilis Spirochete. MBio, 2018, 9, .	4.1	29
41	Fibroblast growth factor receptor influences primary cilium length through an interaction with intestinal cell kinase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4316-4325.	7.1	29
42	Multi-locus sequence typing of Treponema pallidum subsp. pallidum present in clinical samples from France: Infecting treponemes are genetically diverse and belong to 18 allelic profiles. PLoS ONE, 2018, 13, e0201068.	2.5	28
43	Colicin Z, a structurally and functionally novel colicin type that selectively kills enteroinvasive Escherichia coli and Shigella strains. Scientific Reports, 2019, 9, 11127.	3.3	28
44	Characterizing the Syphilis-Causing Treponema pallidum ssp. pallidum Proteome Using Complementary Mass Spectrometry. PLoS Neglected Tropical Diseases, 2016, 10, e0004988.	3.0	28
45	Isolation of Treponema DNA from Necrophagous Flies in a Natural Ecosystem. EBioMedicine, 2016, 11, 85-90.	6.1	27
46	Complete genome sequences of two strains of Treponema pallidum subsp. pertenue from Ghana, Africa: Identical genome sequences in samples isolated more than 7 years apart. PLoS Neglected Tropical Diseases, 2017, 11, e0005894.	3.0	27
47	BAC Library of T. pallidum DNA in E. coli. Genome Research, 2002, 12, 515-522.	5.5	26
48	Complete sequence of low-copy-number plasmid MccC7-H22 of probiotic Escherichia coli H22 and the prevalence of mcc genes among human E. coli. Plasmid, 2008, 59, 1-10.	1.4	26
49	Identification of AHK2- and AHK3-like cytokinin receptors in Brassica napus reveals two subfamilies of AHK2 orthologues. Journal of Experimental Botany, 2015, 66, 339-353.	4.8	26
50	Molecular Typing of Syphilis-Causing Strains Among Human Immunodeficiency Virus-Positive Patients in Antwerp, Belgium. Sexually Transmitted Diseases, 2017, 44, 376-379.	1.7	25
51	Characterization of four <i>Escherichia albertii</i> isolates collected from animals living in Antarctica and Patagonia. Journal of Veterinary Medical Science, 2018, 80, 138-146.	0.9	25
52	A public database for the new MLST scheme for <i>Treponema pallidum</i> subsp. <i>pallidum</i> : surveillance and epidemiology of the causative agent of syphilis. PeerJ, 2019, 6, e6182.	2.0	23
53	Treponema pallidum 11qj Subtype May Correspond to a Treponema pallidum Subsp. Endemicum Strain. Sexually Transmitted Diseases, 2016, 43, 517-518.	1.7	22
54	Complete genome sequences of two strains of Treponema pallidum subsp. pertenue from Indonesia: Modular structure of several treponemal genes. PLoS Neglected Tropical Diseases, 2018, 12, e0006867.	3.0	21

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55	Colicin FY inhibits pathogenic <i>Yersinia enterocolitica</i> in mice. <i>Scientific Reports</i> , 2018, 8, 12242.	3.3	21
56	Bacteriocin production by mucosal bacteria in current and previous colorectal neoplasia. <i>BMC Cancer</i> , 2020, 20, 39.	2.6	20
57	Is there a difference between hare syphilis and rabbit syphilis? Cross infection experiments between rabbits and hares. <i>Veterinary Microbiology</i> , 2013, 164, 190-194.	1.9	19
58	A Retrospective Study on Genetic Heterogeneity within <i>Treponema</i> Strains: Subpopulations Are Genetically Distinct in a Limited Number of Positions. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004110.	3.0	19
59	Multilocus Sequence Typing of <i>Treponema pallidum</i> subsp. <i>pallidum</i> in Cuba From 2012 to 2017. <i>Journal of Infectious Diseases</i> , 2019, 219, 1138-1145.	4.0	18
60	Experimental Administration of the Probiotic <i>Escherichia coli</i> Strain Nissle 1917 Results in Decreased Diversity of <i>E. coli</i> Strains in Pigs. <i>Current Microbiology</i> , 2012, 64, 205-210.	2.2	17
61	<i>Escherichia coli</i> isolates from patients with inflammatory bowel disease: ExPEC virulence- and colicin-determinants are more frequent compared to healthy controls. <i>International Journal of Medical Microbiology</i> , 2018, 308, 498-504.	3.6	17
62	Porcine pathogenic <i>Escherichia coli</i> strains differ from human fecal strains in occurrence of bacteriocin types. <i>Veterinary Microbiology</i> , 2019, 232, 121-127.	1.9	17
63	MLST typing of <i>Treponema pallidum</i> subsp. <i>pallidum</i> in the Czech Republic during 2004-2017: Clinical isolates belonged to 25 allelic profiles and harbored 8 novel allelic variants. <i>PLoS ONE</i> , 2019, 14, e0217611.	2.5	16
64	Evolutionary Processes in the Emergence and Recent Spread of the Syphilis Agent, <i>Treponema pallidum</i> . <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	16
65	Analysis of <i>Treponema pallidum</i> Strains From China Using Improved Methods for Whole-Genome Sequencing From Primary Syphilis Chancres. <i>Journal of Infectious Diseases</i> , 2021, 223, 848-853.	4.0	15
66	Non-antibiotic antibacterial peptides and proteins of <i>Escherichia coli</i> : efficacy and potency of bacteriocins. <i>Expert Review of Anti-Infective Therapy</i> , 2021, 19, 309-322.	4.4	15
67	Colicins U and Y inhibit growth of <i>Escherichia coli</i> strains via recognition of conserved OmpA extracellular loop 1. <i>International Journal of Medical Microbiology</i> , 2016, 306, 486-494.	3.6	14
68	Sequencing of <i>Treponema pallidum</i> subsp. <i>pallidum</i> from isolate UZ1974 using Anti-Treponemal Antibodies Enrichment: First complete whole genome sequence obtained directly from human clinical material. <i>PLoS ONE</i> , 2018, 13, e0202619.	2.5	14
69	Strain diversity of <i>Treponema pallidum</i> subsp. <i>pertenue</i> suggests rare interspecies transmission in African nonhuman primates. <i>Scientific Reports</i> , 2019, 9, 14243.	3.3	14
70	The Molecular Typing Data of Recently Identified Subtype 11q/j of <i>Treponema pallidum</i> subsp. <i>pallidum</i> Suggest Imported Case of Yaws. <i>Sexually Transmitted Diseases</i> , 2014, 41, 552-553.	1.7	13
71	Patients With Common Variable Immunodeficiency (CVID) Show Higher Gut Bacterial Diversity and Levels of Low-Abundance Genes Than the Healthy Housemates. <i>Frontiers in Immunology</i> , 2021, 12, 671239.	4.8	13
72	<i>Escherichia coli</i> Strains Producing Selected Bacteriocins Inhibit Porcine Enterotoxigenic <i>Escherichia coli</i> (ETEC) under both <i>In Vitro</i> and <i>In Vivo</i> Conditions. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0312120.	3.1	13

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73	Novel Temperate Phages of <i>Salmonella enterica</i> subsp. <i>salamae</i> and subsp. <i>diarizonae</i> and Their Activity against Pathogenic <i>S. enterica</i> subsp. <i>enterica</i> Isolates. <i>PLoS ONE</i> , 2017, 12, e0170734.	2.5	12
74	Identification of positively selected genes in human pathogenic treponemes: Syphilis-, yaws-, and bejel-causing strains differ in sets of genes showing adaptive evolution. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007463.	3.0	12
75	Human <i>Escherichia coli</i> strains of different geographical and time source: bacteriocin types and their gene sequences are population-specific. <i>Environmental Microbiology Reports</i> , 2012, 4, 459-466.	2.4	11
76	Isolated populations of <i>Ixodes lividus</i> ticks in the Czech Republic and Belgium host genetically homogeneous <i>Rickettsia vini</i> . <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 479-484.	2.7	11
77	A retrospective study on nested PCR detection of syphilis treponemes in clinical samples: PCR detection contributes to the diagnosis of syphilis in patients with seronegative and serodiscrepant results. <i>PLoS ONE</i> , 2020, 15, e0237949.	2.5	11
78	Determinants encoding fimbriae type 1 in fecal <i>Escherichia coli</i> are associated with increased frequency of bacteriocinogeny. <i>BMC Microbiology</i> , 2015, 15, 201.	3.3	9
79	Gene target selection for loop-mediated isothermal amplification for rapid discrimination of <i>Treponema pallidum</i> subspecies. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006396.	3.0	9
80	Trial of Three Rounds of Mass Azithromycin Administration for Yaws Eradication. <i>New England Journal of Medicine</i> , 2022, 386, 47-56.	27.0	9
81	Unique Activity Spectrum of Colicin FY: All 110 Characterized <i>Yersinia enterocolitica</i> Isolates Were Colicin FY Susceptible. <i>PLoS ONE</i> , 2013, 8, e81829.	2.5	8
82	Recognition of pore-forming colicin Y by its cognate immunity protein. <i>FEMS Microbiology Letters</i> , 2006, 258, 108-113.	1.8	7
83	First report of hare treponematoses seroprevalence of European brown hares ( <i>Lepus europaeus</i> ) in the Czech Republic: seroprevalence negatively correlates with altitude of sampling areas. <i>BMC Veterinary Research</i> , 2019, 15, 350.	1.9	7
84	Whole genome sequence of the <i>Treponema pallidum</i> subsp. <i>endemicum</i> strain Iraq B: A subpopulation of bejel treponemes contains full-length <i>tprF</i> and <i>tprG</i> genes similar to those present in <i>T. p. pertenuis</i> strains. <i>PLoS ONE</i> , 2020, 15, e0230926.	2.5	7
85	Genetic recombination in <i>Treponema pallidum</i> . <i>Sexually Transmitted Diseases</i> , 2021, Publish Ahead of Print, e7-e10.	1.7	7
86	Macrolide resistance in yaws. <i>Lancet</i> , The, 2018, 391, 1555-1556.	13.7	6
87	Reanalysis of Chinese <i>Treponema pallidum</i> samples: all Chinese samples cluster with SS14-like group of syphilis-causing treponemes. <i>BMC Research Notes</i> , 2018, 11, 16.	1.4	6
88	Colicin U from <i>Shigella boydii</i> Forms Voltage-Dependent Pores. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	6
89	Administration of the Probiotic <i>Escherichia coli</i> Strain AO 34/86 Resulted in a Stable Colonization of the Human Intestine During the First Year of Life. <i>Probiotics and Antimicrobial Proteins</i> , 2020, 12, 343-350.	3.9	6
90	High syphilis seropositivity in European brown hares ( <i>Lepus europaeus</i> ), Lower Saxony, Germany. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2240-2244.	3.0	6

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91	Systematic Feature Filtering in Exploratory Metabolomics: Application toward Biomarker Discovery. <i>Analytical Chemistry</i> , 2021, 93, 9103-9110.	6.5	6
92	Inactivation of colicinâ€Ÿ by intramembrane helixâ€“helix interaction with its immunity protein. <i>FEBS Journal</i> , 2008, 275, 5325-5331.	4.7	5
93	Genome sequences of two Antarctic strains of <i>Pseudomonas prosekii</i> : insights into adaptation to extreme conditions. <i>Archives of Microbiology</i> , 2020, 202, 447-454.	2.2	5
94	No bejel among Surinamese, Antillean and Dutch syphilis diagnosed patients in Amsterdam between 2006â€“2018 evidenced by multi-locus sequence typing of <i>Treponema pallidum</i> isolates. <i>PLoS ONE</i> , 2020, 15, e0230288.	2.5	5
95	Why Are There Two Genetically Distinct Syphilis-Causing Strains?. <i>Forum on Immunopathological Diseases and Therapeutics</i> , 2016, 7, 181-190.	0.1	5
96	Genetic diversity of <i>Leptospira</i> isolates in Lao PDR and genome analysis of an outbreak strain. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0010076.	3.0	5
97	Complete Genome Sequence of <i>Pragia fontium</i> 24613, an Environmental Bacterium from the Family <i>Enterobacteriaceae</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
98	Genotyping of <i>Treponema pallidum</i> in Cuba (2018â€“2019): Increased Circulation of Recombinant Genotype and No New <i>Treponema pallidum</i> Subspecies endemicum Infection Among Syphilis Patients. <i>Sexually Transmitted Diseases</i> , 2020, 47, e39-e41.	1.7	3
99	Whole genome sequences of <i>Treponema pallidum</i> subsp. <i>endemicum</i> isolated from Cuban patients: The non-clonal character of isolates suggests a persistent human infection rather than a single outbreak. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0009900.	3.0	3
100	Free-Living Enterobacterium <i>Pragia fontium</i> 24613: Complete Genome Sequence and Metabolic Profiling. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431770086.	1.2	2
101	The distribution of lagomorph syphilis caused by <i>Treponema paraluisleporidarum</i> in Europe. <i>European Journal of Wildlife Research</i> , 2021, 67, 1.	1.4	2
102	First evidence of high-molecular-weight bacteriocin (tailocin) produced by Antarctic <i>Pseudomonas</i> spp.. <i>Czech Polar Reports</i> , 2018, 8, 178-185.	0.6	2
103	Low-dose versus standard-dose azithromycin for treatment of yaws. <i>The Lancet Global Health</i> , 2018, 6, e357-e358.	6.3	1
104	The Arg753Gln Polymorphism of Toll-Like Receptor 2 Has a Lower Occurrence in Patients with Syphilis, Suggesting Its Protective Effect in Czech and Slovak Individuals. <i>Infection and Immunity</i> , 2020, 89, .	2.2	1
105	Complete Chromosomal Sequences of Two <i>Borrelia miyamotoi</i> Samples Obtained from <i>Ixodes ricinus</i> Eggs in Czechia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
106	Penicillin Treatment Failure in Rabbit Syphilis Due to the Persistence of Treponemes ( <i>Treponema</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1 2021, 8, 675631.	2.2	1
107	Pyocinâ€“mediated antagonistic interactions in <i>Pseudomonas</i> spp. isolated in James Ross Island, Antarctica. <i>Environmental Microbiology</i> , 2022, 24, 1294-1307.	3.8	1
108	Complete Genome Sequence of Bacteriophage SEN8, a Temperate Phage Isolated from <i>Salmonella enterica</i> subsp. <i>salamae</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	0

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109	Genetic Stability of the Typing Loci Used in the Multilocus Sequence Typing and Enhanced CDC Typing of Syphilis Treponemes. <i>Sexually Transmitted Diseases</i> , 2019, 46, e70-e70.	1.7	0
110	Comparative Pathogenomics of Spirochetes. , 0, , 141-159.		0
111	Title is missing!. , 2020, 15, e0230288.		0
112	Title is missing!. , 2020, 15, e0230288.		0
113	Title is missing!. , 2020, 15, e0230288.		0
114	Title is missing!. , 2020, 15, e0230288.		0