

Yonatan H Grad

List of Publications by Year in descending order

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Version: 2024-02-01

124
papers

9,941
citations

66343

42
h-index

48315

88
g-index

188
all docs

188
docs citations

188
times ranked

15785
citing authors

#	ARTICLE	IF	CITATIONS
1	Epidemiology and genomics of a slow outbreak of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) in a neonatal intensive care unit: Successful chronic decolonization of MRSA-positive healthcare personnel. <i>Infection Control and Hospital Epidemiology</i> , 2023, 44, 589-596.	1.8	3
2	Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection: A Case Series From a 12-Month Longitudinal Occupational Cohort. <i>Clinical Infectious Diseases</i> , 2022, 74, 1682-1685.	5.8	9
3	Evaluating spatially adaptive guidelines for the treatment of gonorrhea to reduce the incidence of gonococcal infection and increase the effective lifespan of antibiotics. <i>PLoS Computational Biology</i> , 2022, 18, e1009842.	3.2	1
4	Trends in Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Seroprevalence in Massachusetts Estimated from Newborn Screening Specimens. <i>Clinical Infectious Diseases</i> , 2022, 75, e105-e113.	5.8	3
5	Analysis of multiple bacterial species and antibiotic classes reveals large variation in the association between seasonal antibiotic use and resistance. <i>PLoS Biology</i> , 2022, 20, e3001579.	5.6	12
6	Loci for prediction of penicillin and tetracycline susceptibility in <i>Neisseria gonorrhoeae</i> : a genome-wide association study. <i>Lancet Microbe</i> , The, 2022, 3, e376-e381.	7.3	11
7	ANTICIPATING RACIAL/ETHNIC MORTALITY DISPLACEMENT FROM COVID-19. <i>American Journal of Epidemiology</i> , 2022, 191, 1519-1520.	3.4	4
8	Sculpting the Bacterial <i>O</i> -Glycoproteome: Functional Analyses of Orthologous Oligosaccharyltransferases with Diverse Targeting Specificities. <i>MBio</i> , 2022, 13, e0379721.	4.1	2
9	Association Between COVID-19 Booster Vaccination and Omicron Infection in a Highly Vaccinated Cohort of Players and Staff in the National Basketball Association. <i>JAMA - Journal of the American Medical Association</i> , 2022, 328, 209.	7.4	21
10	Modelling methicillin-resistant <i>Staphylococcus aureus</i> decolonization: interactions between body sites and the impact of site-specific clearance. <i>Journal of the Royal Society Interface</i> , 2022, 19, .	3.4	4
11	Characterizing SARS-CoV-2 Viral Clearance Kinetics to Improve the Design of Antiviral Pharmacometric Studies. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	3.2	16
12	The Distribution and Spread of Susceptible and Resistant <i>Neisseria gonorrhoeae</i> Across Demographic Groups in a Major Metropolitan Center. <i>Clinical Infectious Diseases</i> , 2021, 73, e3146-e3155.	5.8	19
13	Distinguishing the Roles of Antibiotic Stewardship and Reductions in Outpatient Visits in Generating a 5-Year Decline in Antibiotic Prescribing. <i>Clinical Infectious Diseases</i> , 2021, 72, 1568-1576.	5.8	7
14	Implications of Test Characteristics and Population Seroprevalence on "Immune Passport" Strategies. <i>Clinical Infectious Diseases</i> , 2021, 72, e412-e414.	5.8	19
15	Potential Biases Arising From Epidemic Dynamics in Observational Seroprotection Studies. <i>American Journal of Epidemiology</i> , 2021, 190, 328-335.	3.4	11
16	Model-informed COVID-19 vaccine prioritization strategies by age and serostatus. <i>Science</i> , 2021, 371, 916-921.	12.6	588
17	Estimating SARS-CoV-2 seroprevalence and epidemiological parameters with uncertainty from serological surveys. <i>ELife</i> , 2021, 10, .	6.0	59
18	Emergence and evolution of antimicrobial resistance genes and mutations in <i>Neisseria gonorrhoeae</i> . <i>Genome Medicine</i> , 2021, 13, 51.	8.2	25

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19	Reduction in Antibiotic Prescribing Attainable With a Gonococcal Vaccine. <i>Clinical Infectious Diseases</i> , 2021, 73, e1368-e1371.	5.8	0
20	SARS-CoV-2 Transmission Risk Among National Basketball Association Players, Staff, and Vendors Exposed to Individuals With Positive Test Results After COVID-19 Recovery During the 2020 Regular and Postseason. <i>JAMA Internal Medicine</i> , 2021, 181, 960-966.	5.1	32
21	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021, 13, 61.	8.2	63
22	Concerns about SARS-CoV-2 evolution should not hold back efforts to expand vaccination. <i>Nature Reviews Immunology</i> , 2021, 21, 330-335.	22.7	98
23	Childhood Respiratory Outpatient Visits Correlate With Socioeconomic Status and Drive Geographic Patterns in Antibiotic Prescribing. <i>Journal of Infectious Diseases</i> , 2021, 223, 2029-2037.	4.0	6
24	Modeling the impact of racial and ethnic disparities on COVID-19 epidemic dynamics. <i>ELife</i> , 2021, 10, .	6.0	22
25	Identification of bile acid and fatty acid species as candidate rapidly bactericidal agents for topical treatment of gonorrhoea. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2569-2577.	3.0	3
26	Viral dynamics of acute SARS-CoV-2 infection and applications to diagnostic and public health strategies. <i>PLoS Biology</i> , 2021, 19, e3001333.	5.6	133
27	Disseminated Gonococcal Infection Complicated by Prosthetic Joint Infection: Case Report and Genomic and Phylogenetic Analysis. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofaa632.	0.9	5
28	Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons. <i>New England Journal of Medicine</i> , 2021, 385, 2489-2491.	27.0	216
29	Post-discharge decolonization of patients harboring methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) USA300 strains: secondary analysis of the CLEAR Trial. <i>Infection Control and Hospital Epidemiology</i> , 2021, , 1-4.	1.8	0
30	Deciphering the Impact of Bystander Selection for Antibiotic Resistance in <i>Neisseria gonorrhoeae</i> . <i>Journal of Infectious Diseases</i> , 2020, 221, 1033-1035.	4.0	13
31	Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 417-428.	8.9	27
32	Cross-reactive memory T cells and herd immunity to SARS-CoV-2. <i>Nature Reviews Immunology</i> , 2020, 20, 709-713.	22.7	229
33	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 5374.	12.8	40
34	Reductions in commuting mobility correlate with geographic differences in SARS-CoV-2 prevalence in New York City. <i>Nature Communications</i> , 2020, 11, 4674.	12.8	105
35	Efflux Pump Antibiotic Binding Site Mutations Are Associated with Azithromycin Nonsusceptibility in Clinical <i>Neisseria gonorrhoeae</i> Isolates. <i>MBio</i> , 2020, 11, .	4.1	12
36	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 4126.	12.8	51

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37	The role of <i>Coespillover</i> in antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29063-29068.	7.1	27
38	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
39	Aggregated mobility data could help fight COVID-19. Science, 2020, 368, 145-146.	12.6	303
40	Identification of Hidden Population Structure in Time-Scaled Phylogenies. Systematic Biology, 2020, 69, 884-896.	5.6	26
41	The frontiers of addressing antibiotic resistance in <i>Neisseria gonorrhoeae</i> . Translational Research, 2020, 220, 122-137.	5.0	20
42	Combining genomics and epidemiology to track mumps virus transmission in the United States. PLoS Biology, 2020, 18, e3000611.	5.6	37
43	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. Nature Microbiology, 2020, 5, 455-464.	13.3	74
44	Adaptive guidelines for the treatment of gonorrhea to increase the effective life span of antibiotics among men who have sex with men in the United States: A mathematical modeling study. PLoS Medicine, 2020, 17, e1003077.	8.4	6
45	Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. Science, 2020, 368, 860-868.	12.6	2,103
46	Individual quarantine versus active monitoring of contacts for the mitigation of COVID-19: a modelling study. Lancet Infectious Diseases, The, 2020, 20, 1025-1033.	9.1	168
47	RNA polymerase mutations cause cephalosporin resistance in clinical <i>Neisseria gonorrhoeae</i> isolates. ELife, 2020, 9, .	6.0	31
48	Potential impact of outpatient stewardship interventions on antibiotic exposures of common bacterial pathogens. ELife, 2020, 9, .	6.0	10
49	Targeted surveillance strategies for efficient detection of novel antibiotic resistance variants. ELife, 2020, 9, .	6.0	6
50	Using rapid point-of-care tests to inform antibiotic choice to mitigate drug resistance in gonorrhoea. Eurosurveillance, 2020, 25, .	7.0	8
51	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
52	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
53	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
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55	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
56	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
57	Title is missing!. , 2020, 17, e1003077.		0
58	Title is missing!. , 2020, 17, e1003077.		0
59	Title is missing!. , 2020, 17, e1003077.		0
60	Title is missing!. , 2020, 17, e1003077.		0
61	Applications of genomics to slow the spread of multidrug-resistant <i>Neisseria gonorrhoeae</i> . Annals of the New York Academy of Sciences, 2019, 1435, 93-109.	3.8	31
62	The impact of antimicrobials on gonococcal evolution. Nature Microbiology, 2019, 4, 1941-1950.	13.3	91
63	Surveillance to maintain the sensitivity of genotype-based antibiotic resistance diagnostics. PLoS Biology, 2019, 17, e3000547.	5.6	15
64	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data. PLoS Computational Biology, 2019, 15, e1007349.	3.2	64
65	Bridging of <i>Neisseria gonorrhoeae</i> lineages across sexual networks in the HIV pre-exposure prophylaxis era. Nature Communications, 2019, 10, 3988.	12.8	69
66	Impact of Species Diversity on the Design of RNA-Based Diagnostics for Antibiotic Resistance in <i>Neisseria gonorrhoeae</i> . Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	22
67	Outpatient Antibiotic Prescribing in Massachusetts, 2011–2015. Open Forum Infectious Diseases, 2019, 6, ofz169.	0.9	17
68	Cumulative Probability of Receiving an Antibiotic Prescription over Time. New England Journal of Medicine, 2019, 380, 1872-1873.	27.0	5
69	A Bayesian model of acquisition and clearance of bacterial colonization incorporating within-host variation. PLoS Computational Biology, 2019, 15, e1006534.	3.2	7
70	Antimicrobial Resistance in <i>Neisseria gonorrhoeae</i> : Proceedings of the STAR Sexually Transmitted Infection—Clinical Trial Group Programmatic Meeting. Sexually Transmitted Diseases, 2019, 46, e18-e25.	1.7	15
71	Case-based surveillance of antimicrobial resistance with full susceptibility profiles. JAC-Antimicrobial Resistance, 2019, 1, dlz070.	2.1	19
72	Multi-strain Tn-Seq reveals common daptomycin resistance determinants in <i>Staphylococcus aureus</i> . PLoS Pathogens, 2019, 15, e1007862.	4.7	68

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73	Genetic determinants of genus-level glycan diversity in a bacterial protein glycosylation system. <i>PLoS Genetics</i> , 2019, 15, e1008532.	3.5	16
74	Azithromycin Susceptibility Among <i>Neisseria gonorrhoeae</i> Isolates and Seasonal Macrolide Use. <i>Journal of Infectious Diseases</i> , 2019, 219, 619-623.	4.0	41
75	Interaction Patterns of Men Who Have Sex With Men on a Geosocial Networking Mobile App in Seven United States Metropolitan Areas: Observational Study. <i>Journal of Medical Internet Research</i> , 2019, 21, e13766.	4.3	5
76	Response to comment on 'The distribution of antibiotic use and its association with antibiotic resistance'. <i>ELife</i> , 2019, 8, .	6.0	1
77	Poor Immunogenicity, Not Vaccine Strain Egg Adaptation, May Explain the Low H3N2 Influenza Vaccine Effectiveness in 2012–2013. <i>Clinical Infectious Diseases</i> , 2018, 67, 327-333.	5.8	53
78	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	2.9	51
79	Vaccine waning and mumps re-emergence in the United States. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	101
80	Trends in Antibiotic Susceptibility in <i>Staphylococcus aureus</i> in Boston, Massachusetts, from 2000 to 2014. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	37
81	Racial/Ethnic Disparities in Antimicrobial Drug Use, United States, 2014–2015. <i>Emerging Infectious Diseases</i> , 2018, 24, 2126-2128.	4.3	26
82	Estimating the proportion of bystander selection for antibiotic resistance among potentially pathogenic bacterial flora. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11988-E11995.	7.1	141
83	Response to Skowronski and De Serres. <i>Clinical Infectious Diseases</i> , 2018, 67, 1476-1476.	5.8	0
84	Multidrug-resistant <i>Neisseria gonorrhoeae</i> : implications for future treatment strategies. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 599.	9.1	9
85	Testing for gonorrhoea should routinely include the pharynx. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 716-717.	9.1	13
86	Clinically prevalent mutations in <i>Mycobacterium tuberculosis</i> alter propionate metabolism and mediate multidrug tolerance. <i>Nature Microbiology</i> , 2018, 3, 1032-1042.	13.3	132
87	Trends in outpatient antibiotic use and prescribing practice among US older adults, 2011-15: observational study. <i>BMJ: British Medical Journal</i> , 2018, 362, k3155.	2.3	58
88	Azithromycin Resistance through Interspecific Acquisition of an Epistasis-Dependent Efflux Pump Component and Transcriptional Regulator in <i>Neisseria gonorrhoeae</i> . <i>MBio</i> , 2018, 9, .	4.1	133
89	The distribution of antibiotic use and its association with antibiotic resistance. <i>ELife</i> , 2018, 7, .	6.0	132
90	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1135-1140.	7.1	158

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91	WGS to predict antibiotic MICs for <i>Neisseria gonorrhoeae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1937-1947.	3.0	169
92	Comparing nonpharmaceutical interventions for containing emerging epidemics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4023-4028.	7.1	219
93	Use of whole-genome sequencing data to analyze 23S rRNA-mediated azithromycin resistance. <i>International Journal of Antimicrobial Agents</i> , 2017, 49, 252-254.	2.5	23
94	Genomic Characterization of Urethritis-Associated <i>Neisseria meningitidis</i> Shows that a Wide Range of <i>N. meningitidis</i> Strains Can Cause Urethritis. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3374-3383.	3.9	24
95	Deep sequencing of RSV from an adult challenge study and from naturally infected infants reveals heterogeneous diversification dynamics. <i>Virology</i> , 2017, 510, 289-296.	2.4	10
96	Impact of Rapid Susceptibility Testing and Antibiotic Selection Strategy on the Emergence and Spread of Antibiotic Resistance in Gonorrhea. <i>Journal of Infectious Diseases</i> , 2017, 216, 1141-1149.	4.0	62
97	Vaccine waning and mumps re-emergence in the USA. <i>Open Forum Infectious Diseases</i> , 2017, 4, S25-S25.	0.9	0
98	Systematic analysis of protein identity between Zika virus and other arthropod-borne viruses. <i>Bulletin of the World Health Organization</i> , 2017, 95, 517-525.	3.3	52
99	Metagenomic Sequencing of an Echovirus 30 Genome From Cerebrospinal Fluid of a Patient With Aseptic Meningitis and Orchitis. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx138.	0.9	13
100	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1295-1303.	9.1	149
101	Genomic analyses of <i>Neisseria gonorrhoeae</i> reveal an association of the gonococcal genetic island with antimicrobial resistance. <i>Journal of Infection</i> , 2016, 73, 578-587.	3.3	54
102	Genomic Epidemiology of Gonococcal Resistance to Extended-Spectrum Cephalosporins, Macrolides, and Fluoroquinolones in the United States, 2000–2013. <i>Journal of Infectious Diseases</i> , 2016, 214, 1579-1587.	4.0	186
103	The novel 2016 WHO <i>Neisseria gonorrhoeae</i> reference strains for global quality assurance of laboratory investigations: phenotypic, genetic and reference genome characterization. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3096-3108.	3.0	246
104	Biodiversity and hypervirulence of <i>Listeria monocytogenes</i> . <i>Nature Genetics</i> , 2016, 48, 229-230.	21.4	8
105	Improving Control of Antibiotic-Resistant Gonorrhea by Integrating Research Agendas Across Disciplines: Key Questions Arising From Mathematical Modeling. <i>Journal of Infectious Diseases</i> , 2016, 213, 883-890.	4.0	38
106	Origin and Proliferation of Multiple-Drug Resistance in Bacterial Pathogens. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 101-116.	6.6	183
107	K-Pax2: Bayesian identification of cluster-defining amino acid positions in large sequence datasets. <i>Microbial Genomics</i> , 2015, 1, e000025.	2.0	12
108	Genomic epidemiology of <i>Neisseria gonorrhoeae</i> with reduced susceptibility to cefixime in the USA: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2014, 14, 220-226.	9.1	193

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109	Within-Host Whole-Genome Deep Sequencing and Diversity Analysis of Human Respiratory Syncytial Virus Infection Reveals Dynamics of Genomic Diversity in the Absence and Presence of Immune Pressure. <i>Journal of Virology</i> , 2014, 88, 7286-7293.	3.4	53
110	<i>In Vitro</i> Selection of <i>Neisseria gonorrhoeae</i> Mutants with Elevated MIC Values and Increased Resistance to Cephalosporins. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 6986-6989.	3.2	20
111	Contrasting within- and between-host immune selection shapes <i>Neisseria</i> Opa repertoires. <i>Scientific Reports</i> , 2014, 4, 6554.	3.3	7
112	Comparative Genomics of Recent Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: Short-Term Evolution of an Emerging Pathogen. <i>MBio</i> , 2013, 4, e00452-12.	4.1	68
113	Deciphering the Origins and Tracking the Evolution of Cholera Epidemics with Whole-Genome-Based Molecular Epidemiology. <i>MBio</i> , 2013, 4, e00670-13.	4.1	12
114	A Patient with Fevers and Fatigue. <i>New England Journal of Medicine</i> , 2013, 368, e9.	27.0	1
115	Cholera Modeling. <i>Epidemiology</i> , 2012, 23, 523-530.	2.7	61
116	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	7.1	262
117	Reply to Guy et al.: Support for a bottleneck in the 2011 <i>Escherichia coli</i> O104:H4 outbreak in Germany. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3629-E3630.	7.1	2
118	Secular Trends in <i>Helicobacter pylori</i> Seroprevalence in Adults in the United States: Evidence for Sustained Race/Ethnic Disparities. <i>American Journal of Epidemiology</i> , 2012, 175, 54-59.	3.4	128
119	Bitter Pills. <i>New England Journal of Medicine</i> , 2010, 363, 1847-1851.	27.0	0
120	Bitter Pills. <i>New England Journal of Medicine</i> , 2010, 363, e26.	27.0	1
121	Prediction of similarly acting cis-regulatory modules by subsequence profiling and comparative genomics in <i>Drosophila melanogaster</i> and <i>D.pseudoobscura</i> . <i>Bioinformatics</i> , 2004, 20, 2738-2750.	4.1	59
122	Identification of many microRNAs that copurify with polyribosomes in mammalian neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 360-365.	7.1	528
123	Computational and Experimental Identification of <i>C. elegans</i> microRNAs. <i>Molecular Cell</i> , 2003, 11, 1253-1263.	9.7	289
124	Bridging of <i>Neisseria Gonorrhoeae</i> Across Diverse Sexual Networks in the HIV Pre-Exposure Prophylaxis (PrEP) Era: A Clinical and Molecular Epidemiological Study. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1