

# Tanya Golubchik

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

8,095  
citations

109321

35  
h-index

155660

55  
g-index

78  
all docs

78  
docs citations

78  
times ranked

12572  
citing authors

#	ARTICLE	IF	CITATIONS
1	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	12.6	39
2	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	4.9	1
3	Highly Sensitive Lineage Discrimination of SARS-CoV-2 Variants through Allele-Specific Probe PCR. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0228321.	3.9	5
4	Deep-sequence phylogenetics to quantify patterns of HIV transmission in the context of a universal testing and treatment trial “BCPP/Ya Tsie trial. <i>ELife</i> , 2022, 11, .	6.0	12
5	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
6	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
7	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 variant of concern 202012/01 (B.1.1.7): an exploratory analysis of a randomised controlled trial. <i>Lancet</i> , The, 2021, 397, 1351-1362.	13.7	540
8	Virological Characterization of Critically Ill Patients With COVID-19 in the United Kingdom: Interactions of Viral Load, Antibody Status, and B.1.1.7 Infection. <i>Journal of Infectious Diseases</i> , 2021, 224, 595-605.	4.0	20
9	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	10.0	269
10	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021, 12, 5125.	12.8	16
11	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , 2021, 12, 5861.	12.8	38
12	The impact of viral mutations on recognition by SARS-CoV-2 specific T <sub>H</sub> cells. <i>iScience</i> , 2021, 24, 103353.	4.1	57
13	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
14	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	39
15	Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory Syncytial Virus Infection of Infants. <i>Journal of Infectious Diseases</i> , 2020, 222, S666-S671.	4.0	11
16	Performance of a high-throughput next-generation sequencing method for analysis of HIV drug resistance and viral load. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3510-3516.	3.0	13
17	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. <i>Journal of Infectious Diseases</i> , 2020, 222, 1670-1680.	4.0	12
18	Epstein-Barr virus reactivation in sepsis due to community-acquired pneumonia is associated with increased morbidity and an immunosuppressed host transcriptomic endotype. <i>Scientific Reports</i> , 2020, 10, 9838.	3.3	13

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19	Phylogenetic and Demographic Characterization of Directed HIV-1 Transmission Using Deep Sequences from High-Risk and General Population Cohorts/Groups in Uganda. <i>Viruses</i> , 2020, 12, 331.	3.3	17
20	High prevalence of integrase mutation L74I in West African HIV-1 subtypes prior to integrase inhibitor treatment. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1575-1579.	3.0	12
21	Recombination Analysis of Near Full-Length HIV-1 Sequences and the Identification of a Potential New Circulating Recombinant Form from Rakai, Uganda. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 467-474.	1.1	4
22	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019, 9, 7081.	3.3	75
23	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus <i>Staphylococcus</i> Rosenbach 1884. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
24	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019, 10, 1411.	12.8	50
25	Oxford Screening CSF and Respiratory samples (â€”OSCARâ€™): results of a pilot study to screen clinical samples from a diagnostic microbiology laboratory for viruses using Illumina next generation sequencing. <i>BMC Research Notes</i> , 2018, 11, 120.	1.4	6
26	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	4.9	64
27	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
28	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	8.9	122
29	Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from <i>Staphylococcus aureus</i> Whole-Genome Sequences. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	61
30	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 411-421.	9.1	269
31	Whole-Genome Sequencing Reveals the Contribution of Long-Term Carriers in <i>Staphylococcus aureus</i> Outbreak Investigation. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2188-2197.	3.9	26
32	Transmission of <i>Staphylococcus aureus</i> between health-care workers, the environment, and patients in an intensive care unit: a longitudinal cohort study based on whole-genome sequencing. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 207-214.	9.1	155
33	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	6.0	93
34	Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 10063.	12.8	479
35	Extensive Within-Host Diversity in Fecally Carried Extended-Spectrum-Beta-Lactamase-Producing <i>Escherichia coli</i> Isolates: Implications for Transmission Analyses. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2122-2131.	3.9	84
36	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014, 59, 752-753.	5.8	0

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37	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	12.8	128
38	Whole-Genome Sequencing Shows That Patient-to-Patient Transmission Rarely Accounts for Acquisition of <i>Staphylococcus aureus</i> in an Intensive Care Unit. <i>Clinical Infectious Diseases</i> , 2014, 58, 609-618.	5.8	142
39	Prediction of <i>Staphylococcus aureus</i> Antimicrobial Resistance by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1182-1191.	3.9	303
40	Evolutionary History of the <i>Clostridium difficile</i> Pathogenicity Locus. <i>Genome Biology and Evolution</i> , 2014, 6, 36-52.	2.5	190
41	Assessment of <i>Mycobacterium tuberculosis</i> transmission in Oxfordshire, UK, 2007-12, with whole pathogen genome sequences: an observational study. <i>Lancet Respiratory Medicine</i> , 2014, 2, 285-292.	10.7	199
42	Healthcare-associated outbreak of methicillin-resistant <i>Staphylococcus aureus</i> bacteraemia: role of a cryptic variant of an epidemic clone. <i>Journal of Hospital Infection</i> , 2014, 86, 83-89.	2.9	31
43	Recombinational Switching of the <i>Clostridium difficile</i> S-Layer and a Novel Glycosylation Gene Cluster Revealed by Large-Scale Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2013, 207, 675-686.	4.0	93
44	Diverse Sources of <i>C. difficile</i> Infection Identified on Whole-Genome Sequencing. <i>New England Journal of Medicine</i> , 2013, 369, 1195-1205.	27.0	595
45	Genotypic prediction of anti-microbial susceptibilities in <i>Staphylococcus aureus</i> . <i>Journal of Infection</i> , 2013, 67, 345-346.	3.3	0
46	Within-Host Evolution of <i>Staphylococcus aureus</i> during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	2.5	194
47	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. <i>PLoS ONE</i> , 2013, 8, e66129.	2.5	62
48	Asymptomatic <i>Clostridium difficile</i> Colonisation and Onward Transmission. <i>PLoS ONE</i> , 2013, 8, e78445.	2.5	113
49	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555.	7.1	244
50	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. <i>Nature Genetics</i> , 2012, 44, 352-355.	21.4	144
51	A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. <i>BMJ Open</i> , 2012, 2, e001124.	1.9	228
52	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	9.6	199
53	Clinical <i>Clostridium difficile</i> : Clonality and Pathogenicity Locus Diversity. <i>PLoS ONE</i> , 2011, 6, e19993.	2.5	150
54	Identification of Antigens Specific to Non-Tuberculous Mycobacteria: The Mce Family of Proteins as a Target of T Cell Immune Responses. <i>PLoS ONE</i> , 2011, 6, e26434.	2.5	20

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55	Recombination and Population Structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2011, 7, e1002191.	3.5	135
56	Multilocus Sequence Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 770-778.	3.9	399
57	Mind the Gaps: Evidence of Bias in Estimates of Multiple Sequence Alignments. <i>Molecular Biology and Evolution</i> , 2007, 24, 2433-2442.	8.9	108