

# Tanya Golubchik

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70 papers	5,393 citations	32 h-index	73 g-index
78 ext. papers	7,172 ext. citations	14.1 avg, IF	4.71 L-index

#	Paper	IF	Citations
70	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , <b>2021</b> , 184, 64-75.e11	56.2	518
69	Diverse sources of <i>C. difficile</i> infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , <b>2013</b> , 369, 1195-205	59.2	471
68	Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 10063	17.4	348
67	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, The</i> , <b>2021</b> , 397, 1351-1362	40	316
66	Multilocus sequence typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , <b>2010</b> , 48, 770-8	9.7	310
65	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , <b>2018</b> , 379, 1403-1415	59.2	243
64	Prediction of <i>Staphylococcus aureus</i> antimicrobial resistance by whole-genome sequencing. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 1182-91	9.7	218
63	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases, The</i> , <b>2017</b> , 17, 411-421	25.5	202
62	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> , <b>2012</b> , 2,	3	197
61	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> , <b>2012</b> , 109, 4550-5	11.5	195
60	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , <b>2012</b> , 13, R118	18.3	151
59	Assessment of <i>Mycobacterium tuberculosis</i> transmission in Oxfordshire, UK, 2007-12, with whole pathogen genome sequences: an observational study. <i>Lancet Respiratory Medicine, the</i> , <b>2014</b> , 2, 285-292	35.1	149
58	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health, The</i> , <b>2021</b> , 6, e335-e345	22.4	146
57	Within-host evolution of <i>Staphylococcus aureus</i> during asymptomatic carriage. <i>PLoS ONE</i> , <b>2013</b> , 8, e61319	3.7	141
56	Clinical <i>Clostridium difficile</i> : clonality and pathogenicity locus diversity. <i>PLoS ONE</i> , <b>2011</b> , 6, e19993	3.7	131
55	Evolutionary history of the <i>Clostridium difficile</i> pathogenicity locus. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 36-52	3.9	123
54	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, The</i> , <b>2017</b> , 17, 207-214	25.5	113

53	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> , <b>2014</b> , 58, 609-18	11.6	112
52	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , <b>2021</b> , 372,	33.3	110
51	Recombination and population structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002191	6	105
50	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , <b>2014</b> , 5, 3956	17.4	90
49	Mind the gaps: evidence of bias in estimates of multiple sequence alignments. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 2433-42	8.3	90
48	Asymptomatic <i>Clostridium difficile</i> colonisation and onward transmission. <i>PLoS ONE</i> , <b>2013</b> , 8, e78445	3.7	90
47	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. <i>Nature Genetics</i> , <b>2012</b> , 44, 352-5	36.3	82
46	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> , <b>2013</b> , 207, 675-86	7.86	72
45	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 719-733	8.3	68
44	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> , <b>2015</b> , 53, 2122-31	9.7	56
43	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , <b>2017</b> , 6,	8.9	55
42	A modified RNA-Seq approach for whole genome sequencing of RNA viruses from faecal and blood samples. <i>PLoS ONE</i> , <b>2013</b> , 8, e66129	3.7	52
41	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , <b>2019</b> , 9, 7081	4.9	41
40	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> , <b>2018</b> , 56,	9.7	40
39	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , <b>2018</b> , 4, vey007	3.7	38
38	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , <b>2021</b> , 374, eabl9551	33.3	31
37	Within-host genomics of SARS-CoV-2		29
36	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , <b>2019</b> , 10, 1411	17.4	26

35	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> , <b>2014</b> , 86, 83-9	6.9	25
34	Early analysis of a potential link between viral load and the N501Y mutation in the SARS-CoV-2 spike protein		22
33	Whole-Genome Sequencing Reveals the Contribution of Long-Term Carriers in <i>Staphylococcus aureus</i> Outbreak Investigation. <i>Journal of Clinical Microbiology</i> , <b>2017</b> , 55, 2188-2197	9.7	19
32	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> , <b>2011</b> , 6, e26434	3.7	16
31	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , <b>2020</b> , 58,	9.7	15
30	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> , <b>2021</b> , 224, 595-605	7	14
29	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>iScience</i> , <b>2021</b> , 24, 103353	6.1	12
28	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , <b>2021</b> , 12, 5861	17.4	11
27	Virological and serological characterization of critically ill patients with COVID-19 in the UK: a special focus on variant detection		9
26	High prevalence of integrase mutation L74I in West African HIV-1 subtypes prior to integrase inhibitor treatment. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2020</b> , 75, 1575-1579	5.1	8
25	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> , <b>2020</b> , 12,	6.2	7
24	Rapid antibiotic resistance predictions from genome sequence data for <i>S. aureus</i> and <i>M. tuberculosis</i> .		7
23	Targeted metagenomic sequencing enhances the identification of pathogens associated with acute infection		7
22	Oxford Screening CSF and Respiratory samples (TOSCAR): 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> , <b>2018</b> , 11, 120	2.3	5
21	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , <b>2022</b> , 375, 540-545	33.3	5
20	Performance of a high-throughput next-generation sequencing method for analysis of HIV drug resistance and viral load. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2020</b> , 75, 3510-3516	5.1	5
19	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> , <b>2020</b> , 10, 9838	4.9	4
18	Easy and Accurate Reconstruction of Whole HIV Genomes from Short-Read Sequence Data		4

17	Severe infections emerge from the microbiome by adaptive evolution		4
16	Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory Syncytial Virus Infection of Infants. <i>Journal of Infectious Diseases</i> , <b>2020</b> , 222, S666-S671	7	4
15	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity		4
14	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> , <b>2020</b> , 222, 1670-1680 <sup>7</sup>		3
13	Human Herpes Virus 6 (HHV-6) - Pathogen or Passenger? A pilot study of clinical laboratory data and next generation sequencing		3
12	A comprehensive genomics solution for HIV surveillance and clinical monitoring in a global health setting		3
11	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil; an exploratory analysis of a randomised controlled trial		3
10	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , <b>2021</b> , 12, 5125	17.4	3
9	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus <i>Rosenbach</i> 1884. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2
8	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV)		2
7	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity		2
6	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> , <b>2020</b> , 36, 467-474	1.6	1
5	Lineage replacement and evolution captured by the United Kingdom Covid Infection Survey		1
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> , <b>2022</b> , 11,	8.9	1
3	Highly Sensitive Lineage Discrimination of SARS-CoV-2 Variants through Allele-Specific Probe PCR.. <i>Journal of Clinical Microbiology</i> , <b>2022</b> , e0228321	9.7	0
2	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , <b>2014</b> , 59, 752-3	11.6	
1	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load.. <i>Virus Evolution</i> , <b>2022</b> , 8, veac022	3.7	