

Tanya Golubchik

List of Publications by Year in Descending Order

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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	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
69	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load.. <i>Virus Evolution</i> , 2022 , 8, veac022	3.7	
68	Highly Sensitive Lineage Discrimination of SARS-CoV-2 Variants through Allele-Specific Probe PCR.. <i>Journal of Clinical Microbiology</i> , 2022 , e0228321	9.7	0
67	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,	8.9	1
66	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021 , 374, eabl9551	33.3	31
65	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , 2021 , 12, 5861	17.4	11
64	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>IScience</i> , 2021 , 24, 103353	6.1	12
63	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021 , 372,	33.3	110
62	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> , 2021 , 397, 1351-1362	40	316
61	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	7	14
60	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> , 2021 , 6, e335-e345	22.4	146
59	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021 , 184, 64-75.e11	56.2	518
58	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021 , 12, 5125	17.4	3
57	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	7	3
56	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	4.9	4
55	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,	6.2	7
54	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	5.1	8

53	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	1.6	1
52	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	15
51	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	7	4
50	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	5.1	5
49	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019 , 9, 7081	4.9	41
48	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> , 2019 , 8,	1.3	2
47	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019 , 10, 1411	17.4	26
46	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> , 2018 , 11, 120	2.3	5
45	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,	9.7	40
44	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018 , 4, vey007	3.7	38
43	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018 , 379, 1403-1415	59.2	243
42	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018 , 35, 719-733	8.3	68
41	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , 2017 , 17, 411-421	25.5	202
40	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	9.7	19
39	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> , 2017 , 17, 207-214	25.5	113
38	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017 , 6,	8.9	55
37	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, 2122-31	9.7	56
36	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	17.4	348

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> , 2014 , 86, 83-9	6.9	25
34	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014 , 59, 752-3	11.6	
33	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014 , 5, 3956	17.4	90
32	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, 609-18	11.6	112
31	Prediction of <i>Staphylococcus aureus</i> antimicrobial resistance by whole-genome sequencing. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 1182-91	9.7	218
30	Evolutionary history of the <i>Clostridium difficile</i> pathogenicity locus. <i>Genome Biology and Evolution</i> , 2014 , 6, 36-52	3.9	123
29	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	35.1	149
28	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, 675-86	7.86	72
27	Diverse sources of <i>C. difficile</i> infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , 2013 , 369, 1195-205	59.2	471
26	Within-host evolution of <i>Staphylococcus aureus</i> during asymptomatic carriage. <i>PLoS ONE</i> , 2013 , 8, e61319	3.7	141
25	A modified RNA-Seq approach for whole genome sequencing of RNA viruses from faecal and blood samples. <i>PLoS ONE</i> , 2013 , 8, e66129	3.7	52
24	Asymptomatic <i>Clostridium difficile</i> colonisation and onward transmission. <i>PLoS ONE</i> , 2013 , 8, e78445	3.7	90
23	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. <i>Nature Genetics</i> , 2012 , 44, 352-5	36.3	82
22	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,	3	197
21	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012 , 13, R118	18.3	151
20	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, 4550-5	11.5	195
19	Clinical <i>Clostridium difficile</i> : clonality and pathogenicity locus diversity. <i>PLoS ONE</i> , 2011 , 6, e19993	3.7	131
18	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	3.7	16

17	Recombination and population structure in Salmonella enterica. <i>PLoS Genetics</i> , 2011 , 7, e1002191	6	105
16	Multilocus sequence typing of Clostridium difficile. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 770-8	9.7	310
15	Mind the gaps: evidence of bias in estimates of multiple sequence alignments. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2433-42	8.3	90
14	Lineage replacement and evolution captured by the United Kingdom Covid Infection Survey		1
13	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV)		2
12	Rapid antibiotic resistance predictions from genome sequence data for S. aureus and M. tuberculosis.		7
11	Easy and Accurate Reconstruction of Whole HIV Genomes from Short-Read Sequence Data		4
10	Severe infections emerge from the microbiome by adaptive evolution		4
9	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity		2
8	Within-host genomics of SARS-CoV-2		29
7	Human Herpes Virus 6 (HHV-6) - Pathogen or Passenger? A pilot study of clinical laboratory data and next generation sequencing		3
6	A comprehensive genomics solution for HIV surveillance and clinical monitoring in a global health setting		3
5	Targeted metagenomic sequencing enhances the identification of pathogens associated with acute infection		7
4	Virological and serological characterization of critically ill patients with COVID-19 in the UK: a special focus on variant detection		9
3	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity		4
2	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil; an exploratory analysis of a randomised controlled trial		3
1	Early analysis of a potential link between viral load and the N501Y mutation in the SARS-COV-2 spike protein		22