

Gary Van Domselaar

List of Publications by Year in descending order

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papers

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citations

117625

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102487

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all docs

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docs citations

96
times ranked

7462
citing authors

#	ARTICLE	IF	CITATIONS
1	Colorectal Cancer Screening in Inflammatory Bowel Diseases—Can Characterization of GI Microbiome Signatures Enhance Neoplasia Detection?. <i>Gastroenterology</i> , 2022, 162, 1409-1423.e1.	1.3	10
2	Metagenomic Analysis of the Pediatric-Onset Multiple Sclerosis Gut Microbiome. <i>Neurology</i> , 2022, 98, .	1.1	15
3	Correlation between Phenotypic and In Silico Detection of Antimicrobial Resistance in <i>Salmonella enterica</i> in Canada Using Staramr. <i>Microorganisms</i> , 2022, 10, 292.	3.6	60
4	Stability of the gut microbiota in persons with paediatric-onset multiple sclerosis and related demyelinating diseases. <i>Multiple Sclerosis Journal</i> , 2022, 28, 1819-1824.	3.0	2
5	The need for linked genomic surveillance of SARS-CoV-2. <i>Canada Communicable Disease Report</i> , 2022, 48, 131-139.	1.3	13
6	The metabolic potential of the paediatric-onset multiple sclerosis gut microbiome. <i>Multiple Sclerosis and Related Disorders</i> , 2022, 63, 103829.	2.0	8
7	Universal antibody targeting the highly conserved fusion peptide provides cross-protection in mice. <i>Human Vaccines and Immunotherapeutics</i> , 2022, 18, .	3.3	1
8	Economic evaluation of whole genome sequencing for pathogen identification and surveillance – results of case studies in Europe and the Americas 2016 to 2019. <i>Eurosurveillance</i> , 2021, 26, .	7.0	25
9	The origins and potential future of SARS-CoV-2 variants of concern in the evolving COVID-19 pandemic. <i>Current Biology</i> , 2021, 31, R918-R929.	3.9	246
10	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel. <i>Microbial Genomics</i> , 2021, 7, .	2.0	4
11	Single Immunization of a Vaccine Vected by a Novel Recombinant Vaccinia Virus Affords Effective Protection Against Respiratory Syncytial Virus Infection in Cotton Rats. <i>Frontiers in Immunology</i> , 2021, 12, 747866.	4.8	7
12	Synthetic vaccine affords full protection to mice against lethal challenge of influenza B virus of both genetic lineages. <i>IScience</i> , 2021, 24, 103328.	4.1	4
13	Microbiome-Mediated Immune Signaling in Inflammatory Bowel Disease and Colorectal Cancer: Support From Meta-omics Data. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 716604.	3.7	9
14	The gut microbiota in pediatric multiple sclerosis and demyelinating syndromes. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 2252-2269.	3.7	34
15	The multiple sclerosis gut microbiota: A systematic review. <i>Multiple Sclerosis and Related Disorders</i> , 2020, 37, 101427.	2.0	102
16	Detection of Antimicrobial Resistance Using Proteomics and the Comprehensive Antibiotic Resistance Database: A Case Study. <i>Proteomics - Clinical Applications</i> , 2020, 14, e1800182.	1.6	30
17	Whole genome sequencing to study the phylogenetic structure of serotype a <i>Haemophilus influenzae</i> recovered from patients in Canada. <i>Canadian Journal of Microbiology</i> , 2020, 66, 99-110.	1.7	7
18	Assessment of Inter-Laboratory Variation in the Characterization and Analysis of the Mucosal Microbiota in Crohn's Disease and Ulcerative Colitis. <i>Frontiers in Microbiology</i> , 2020, 11, 2028.	3.5	8

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19	Surveillance of <i>Enterococcus</i> spp. reveals distinct species and antimicrobial resistance diversity across a One-Health continuum. <i>Scientific Reports</i> , 2020, 10, 3937.	3.3	109
20	Performance comparison of next generation sequencing analysis pipelines for HIV-1 drug resistance testing. <i>Scientific Reports</i> , 2020, 10, 1634.	3.3	45
21	PD-1 of <i>Sigmodon hispidus</i> : Gene identification, characterization and preliminary evaluation of expression in inactivated RSV vaccine-induced enhanced respiratory disease. <i>Scientific Reports</i> , 2019, 9, 11638.	3.3	1
22	The evolving nature of <i>Bordetella pertussis</i> in Ontario, Canada, 2009–2017: strains with shifting genotypes and pertactin deficiency. <i>Canadian Journal of Microbiology</i> , 2019, 65, 823-830.	1.7	5
23	Comparative diversity of microbiomes and Resistomes in beef feedlots, downstream environments and urban sewage influent. <i>BMC Microbiology</i> , 2019, 19, 197.	3.3	34
24	The Gut Microbiome as a Target for IBD Treatment: Are We There Yet?. <i>Current Treatment Options in Gastroenterology</i> , 2019, 17, 115-126.	0.8	90
25	A MiSeq-HyDRA platform for enhanced HIV drug resistance genotyping and surveillance. <i>Scientific Reports</i> , 2019, 9, 8970.	3.3	36
26	Unveiling Integrated Functional Pathways Leading to Enhanced Respiratory Disease Associated With Inactivated Respiratory Syncytial Viral Vaccine. <i>Frontiers in Immunology</i> , 2019, 10, 597.	4.8	9
27	The Gut Microbiome in Inflammatory Bowel Disease: Lessons Learned From Other Immune-Mediated Inflammatory Diseases. <i>American Journal of Gastroenterology</i> , 2019, 114, 1051-1070.	0.4	53
28	Visualizing and comparing circular genomes using the CGView family of tools. <i>Briefings in Bioinformatics</i> , 2019, 20, 1576-1582.	6.5	177
29	Shared genome analyses of notable listeriosis outbreaks, highlighting the critical importance of epidemiological evidence, input datasets and interpretation criteria. <i>Microbial Genomics</i> , 2019, 5, .	2.0	11
30	Eleven High-Quality Reference Genome Sequences and 360 Draft Assemblies of Shiga Toxin-Producing <i>Escherichia coli</i> Isolates from Human, Food, Animal, and Environmental Sources in Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
31	Whole genome typing of the recently emerged Canadian serogroup W <i>Neisseria meningitidis</i> sequence type 11 clonal complex isolates associated with invasive meningococcal disease. <i>International Journal of Infectious Diseases</i> , 2018, 69, 55-62.	3.3	16
32	Impact of sequencing depth on the characterization of the microbiome and resistome. <i>Scientific Reports</i> , 2018, 8, 5890.	3.3	174
33	Universal type/subtype-specific antibodies for quantitative analyses of neuraminidase in trivalent influenza vaccines. <i>Scientific Reports</i> , 2018, 8, 1067.	3.3	6
34	A randomized trial to determine the impact of a digestion resistant starch composition on the gut microbiome in older and mid-age adults. <i>Clinical Nutrition</i> , 2018, 37, 797-807.	5.0	110
35	A comparative study of the gut microbiota in immune-mediated inflammatory diseases—does a common dysbiosis exist?. <i>Microbiome</i> , 2018, 6, 221.	11.1	303
36	Bioinformatic data processing pipelines in support of next-generation sequencing-based HIV-1 drug resistance testing: the Winnipeg Consensus. <i>Journal of the International AIDS Society</i> , 2018, 21, e25193.	3.0	34

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37	Identification of immunodominant CD8 epitope in the stalk domain of influenza B viral hemagglutinin. <i>Biochemical and Biophysical Research Communications</i> , 2018, 502, 226-231.	2.1	6
38	Whole genome sequencing and phylogenetic analysis of strains of the agent of Lyme disease <i>Borrelia burgdorferi</i> from Canadian emergence zones. <i>Scientific Reports</i> , 2018, 8, 10552.	3.3	34
39	A Fungal World: Could the Gut Mycobiome Be Involved in Neurological Disease?. <i>Frontiers in Microbiology</i> , 2018, 9, 3249.	3.5	80
40	First Complete Genome Sequence of <i>Haemophilus influenzae</i> Serotype a. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
41	Baseline Practices for the Application of Genomic Data Supporting Regulatory Food Safety. <i>Journal of AOAC INTERNATIONAL</i> , 2017, 100, 721-731.	1.5	25
42	Neptune: a bioinformatics tool for rapid discovery of genomic variation in bacterial populations. <i>Nucleic Acids Research</i> , 2017, 45, e159-e159.	14.5	16
43	A Comparative Analysis of the Lyve-SET Phylogenomics Pipeline for Genomic Epidemiology of Foodborne Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 375.	3.5	137
44	Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. <i>Frontiers in Microbiology</i> , 2017, 8, 909.	3.5	87
45	Context Is Everything: Harmonization of Critical Food Microbiology Descriptors and Metadata for Improved Food Safety and Surveillance. <i>Frontiers in Microbiology</i> , 2017, 8, 1068.	3.5	39
46	A Robust PCR Protocol for HIV Drug Resistance Testing on Low-Level Viremia Samples. <i>BioMed Research International</i> , 2017, 2017, 1-6.	1.9	10
47	Phylogenetic analysis of emergent <i>Streptococcus pneumoniae</i> serotype 22F causing invasive pneumococcal disease using whole genome sequencing. <i>PLoS ONE</i> , 2017, 12, e0178040.	2.5	21
48	Application of whole genome sequence analysis to the study of <i>Mycobacterium tuberculosis</i> in Nunavut, Canada. <i>PLoS ONE</i> , 2017, 12, e0185656.	2.5	17
49	SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. <i>Microbial Genomics</i> , 2017, 3, e000116.	2.0	119
50	A Study of the Infant Nasal Microbiome Development over the First Year of Life and in Relation to Their Primary Adult Caregivers Using cpn60 Universal Target (UT) as a Phylogenetic Marker. <i>PLoS ONE</i> , 2016, 11, e0152493.	2.5	33
51	The Gut Microbiota in Immune-Mediated Inflammatory Diseases. <i>Frontiers in Microbiology</i> , 2016, 7, 1081.	3.5	315
52	Microbiome profiling of drinking water in relation to incidence of inflammatory bowel disease. <i>Canadian Journal of Microbiology</i> , 2016, 62, 781-793.	1.7	12
53	Genomic Epidemiology and Molecular Resistance Mechanisms of Azithromycin-Resistant <i>Neisseria gonorrhoeae</i> in Canada from 1997 to 2014. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1304-1313.	3.9	124
54	A Primer on Infectious Disease Bacterial Genomics. <i>Clinical Microbiology Reviews</i> , 2016, 29, 881-913.	13.6	42

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55	Draft Genome Sequences of <i>Burkholderia contaminans</i> FFI-28, a Strain Isolated from a Contaminated Pharmaceutical Solution. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
56	Microbiome Survey of the Inflamed and Noninflamed Gut at Different Compartments Within the Gastrointestinal Tract of Inflammatory Bowel Disease Patients. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 817-825.	1.9	114
57	Sequence database versioning for command line and Galaxy bioinformatics servers. <i>Bioinformatics</i> , 2016, 32, 1275-1277.	4.1	5
58	Comparison of Sample Preparation Methods Used for the Next-Generation Sequencing of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2016, 11, e0148676.	2.5	54
59	Development and applications of universal H7 subtype-specific antibodies for the analysis of influenza H7N9 vaccines. <i>Vaccine</i> , 2015, 33, 1129-1134.	3.8	10
60	Next generation sequencing of the hepatitis C virus NS5B gene reveals potential novel S282 drug resistance mutations. <i>Virology</i> , 2015, 477, 1-9.	2.4	36
61	Whole-Genome Phylogenomic Heterogeneity of <i>Neisseria gonorrhoeae</i> Isolates with Decreased Cephalosporin Susceptibility Collected in Canada between 1989 and 2013. <i>Journal of Clinical Microbiology</i> , 2015, 53, 191-200.	3.9	103
62	<i>Tatumella saanichensis</i> sp. nov., isolated from a cystic fibrosis patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1959-1966.	1.7	23
63	A universal monoclonal antibody protects against all influenza A and B viruses by targeting a highly conserved epitope in the viral neuraminidase. <i>BMC Genomics</i> , 2014, 15, P8.	2.8	1
64	Universal anti-neuraminidase antibody inhibiting all influenza A subtypes. <i>Antiviral Research</i> , 2013, 100, 567-574.	4.1	95
65	A monoclonal antibody targeting a highly conserved epitope in influenza B neuraminidase provides protection against drug resistant strains. <i>Biochemical and Biophysical Research Communications</i> , 2013, 441, 226-229.	2.1	45
66	Low abundance drug resistance variants in transmitted HIV drug resistance surveillance specimens identified using tagged pooled pyrosequencing. <i>Journal of Virological Methods</i> , 2013, 187, 314-320.	2.1	12
67	Evolutionary Dynamics of <i>Vibrio cholerae</i> O1 following a Single-Source Introduction to Haiti. <i>MBio</i> , 2013, 4, .	4.1	118
68	The Universal Epitope of Influenza A Viral Neuraminidase Fundamentally Contributes to Enzyme Activity and Viral Replication. <i>Journal of Biological Chemistry</i> , 2013, 288, 18283-18289.	3.4	25
69	Comparative Genomics Reveal That Host-Innate Immune Responses Influence the Clinical Prevalence of <i>Legionella pneumophila</i> Serogroups. <i>PLoS ONE</i> , 2013, 8, e67298.	2.5	33
70	Pyrosequencing Dried Blood Spots Reveals Differences in HIV Drug Resistance between Treatment Naïve and Experienced Patients. <i>PLoS ONE</i> , 2013, 8, e56170.	2.5	12
71	BacMap: an up-to-date electronic atlas of annotated bacterial genomes. <i>Nucleic Acids Research</i> , 2012, 40, D599-D604.	14.5	19
72	Whole-Genome Sequence of Livestock-Associated ST398 Methicillin-Resistant <i>Staphylococcus aureus</i> Isolated from Humans in Canada. <i>Journal of Bacteriology</i> , 2012, 194, 6627-6628.	2.2	35

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73	Comparative Genomics of <i>Vibrio cholerae</i> from Haiti, Asia, and Africa. <i>Emerging Infectious Diseases</i> , 2011, 17, 2113-21.	4.3	136
74	Quantitative Analyses of all Influenza Type A Viral Hemagglutinins and Neuraminidases using Universal Antibodies in Simple Slot Blot Assays. <i>Journal of Visualized Experiments</i> , 2011, , .	0.3	12
75	Recent Developments in Bioinformatics Analyses of Influenza A Virus Surface Glycoproteins and their Biological Relevance. <i>Current Bioinformatics</i> , 2011, 6, 415-426.	1.5	11
76	A Comparison of Parallel Pyrosequencing and Sanger Clone-Based Sequencing and Its Impact on the Characterization of the Genetic Diversity of HIV-1. <i>PLoS ONE</i> , 2011, 6, e26745.	2.5	35
77	High-throughput genome sequencing of two <i>Listeria monocytogenes</i> clinical isolates during a large foodborne outbreak. <i>BMC Genomics</i> , 2010, 11, 120.	2.8	306
78	A simple slot blot for the detection of virtually all subtypes of the influenza A viral hemagglutinins using universal antibodies targeting the fusion peptide. <i>Nature Protocols</i> , 2010, 5, 14-19.	12.0	37
79	Interactive microbial genome visualization with GView. <i>Bioinformatics</i> , 2010, 26, 3125-3126.	4.1	347
80	Livestock-associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 in Humans, Canada. <i>Emerging Infectious Diseases</i> , 2010, 16, 587-594.	4.3	105
81	Universal antibodies against the highly conserved influenza fusion peptide cross-neutralize several subtypes of influenza A virus. <i>Biochemical and Biophysical Research Communications</i> , 2010, 403, 247-251.	2.1	48
82	Aurintricarboxylic Acid Is a Potent Inhibitor of Influenza A and B Virus Neuraminidases. <i>PLoS ONE</i> , 2009, 4, e8350.	2.5	48
83	Universal antibodies and their applications to the quantitative determination of virtually all subtypes of the influenza A viral hemagglutinins. <i>Vaccine</i> , 2008, 26, 6068-6076.	3.8	64
84	Systematic Analysis of Host Immunological Pressure on the Envelope Gene of Human Immunodeficiency Virus Type 1 by an Immunobioinformatics Approach. <i>Current HIV Research</i> , 2008, 6, 370-379.	0.5	6
85	Molecular typing of a <i>Legionella pneumophila</i> outbreak in Ontario, Canada. <i>Journal of Medical Microbiology</i> , 2007, 56, 336-341.	1.8	45
86	BacMap: an interactive picture atlas of annotated bacterial genomes. <i>Nucleic Acids Research</i> , 2004, 33, D317-D320.	14.5	48
87	Genomic Characterization of <i>Enterococcus hirae</i> From Beef Cattle Feedlots and Associated Environmental Continuum. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5