David L Robertson

List of Publications by Year
in descending order

145 papers	15,646 citations	30070 54 h-index	23533 111 g-index
179 all docs	179 docs citations	179 times ranked	20548 citing authors

#	Article	IF	Citations
1	SARS-CoV-2 variants, spike mutations and immune escape. Nature Reviews Microbiology, 2021, 19, 409-424.	28.6	2,650
2	Origin of HIV-1 in the chimpanzee Pan troglodytes troglodytes. Nature, 1999, 397, 436-441.	27.8	1,405
3	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 2021, 184, 64-75.e11.	28.9	843
4	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. Nature Microbiology, 2020, 5, 1408-1417.	13.3	772
5	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	28.9	541
6	Genome-Wide Classification and Evolutionary Analysis of the bHLH Family of Transcription Factors in Arabidopsis, Poplar, Rice, Moss, and Algae Â. Plant Physiology, 2010, 153, 1398-1412.	4.8	493
7	A new human immunodeficiency virus derived from gorillas. Nature Medicine, 2009, 15, 871-872.	30.7	424
8	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	6.4	375
9	The origins of SARS-CoV-2: A critical review. Cell, 2021, 184, 4848-4856.	28.9	330
10	Choose your partners: dimerization in eukaryotic transcription factors. Trends in Biochemical Sciences, 2008, 33, 220-229.	7.5	229
11	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Archives of Virology, 2021, 166, 2633-2648.	2.1	219
12	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. Cell, 2021, 184, 5189-5200.e7.	28.9	186
13	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. Cell, 2021, 184, 5179-5188.e8.	28.9	182
14	Protein-protein interaction networks and biologyâ€"what's the connection?. Nature Biotechnology, 2008, 26, 69-72.	17.5	175
15	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. PLoS Biology, 2021, 19, e3001115.	5.6	172
16	All duplicates are not equal: the difference between small-scale and genome duplication. Genome Biology, 2007, 8, R209.	9.6	163
17	A plasmid DNA-launched SARS-CoV-2 reverse genetics system and coronavirus toolkit for COVID-19 research. PLoS Biology, 2021, 19, e3001091.	5.6	163
18	Molecular Epidemiology of Simian Immunodeficiency Virus SIVsm in U.S. Primate Centers Unravels the Origin of SIVmac and SIVstm. Journal of Virology, 2005, 79, 8991-9005.	3.4	159

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19	The history of SIVS and AIDS: epidemiology, phylogeny and biology of isolates from naturally SIV infected non-human primates (NHP) in Africa. Frontiers in Bioscience - Landmark, 2004, 9, 225.	3.0	148
20	Phylogeny and the origin of HIV-1. Nature, 2001, 410, 1047-1048.	27.8	143
21	Identification of a Highly Divergent HIV Type 2 and Proposal for a Change in HIV Type 2 Classification. AIDS Research and Human Retroviruses, 2004, 20, 666-672.	1.1	143
22	Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination. PLoS Pathogens, 2021, 17, e1010022.	4.7	139
23	Wild Mandrillus sphinx Are Carriers of Two Types of Lentivirus. Journal of Virology, 2001, 75, 7086-7096.	3.4	133
24	<i>Short Communication:</i> Cataloguing the HIV Type 1 Human Protein Interaction Network. AIDS Research and Human Retroviruses, 2008, 24, 1497-1502.	1.1	126
25	A prenylated dsRNA sensor protects against severe COVID-19. Science, 2021, 374, eabj3624.	12.6	124
26	On the origins of the extracellular matrix in vertebrates. Matrix Biology, 2007, 26, 2-11.	3.6	119
27	An Integrated View of Molecular Coevolution in Protein-Protein Interactions. Molecular Biology and Evolution, 2010, 27, 2567-2575.	8.9	119
28	Specificity in protein interactions and its relationship with sequence diversity and coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7999-8004.	7.1	114
29	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	6.5	110
30	The Evolution and Biology of SARS-CoV-2 Variants. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a041390.	6.2	110
31	The Molecular Population Genetics of HIV-1 Group O. Genetics, 2004, 167, 1059-1068.	2.9	105
32	Detection of low-frequency pretherapy chemokine (CXC motif) receptor 4 (CXCR4)-using HIV-1 with ultra-deep pyrosequencing. Aids, 2009, 23, 1209-1218.	2.2	104
33	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	12.4	101
34	Comparative Study of Adaptive Molecular Evolution in Different Human Immunodeficiency Virus Groups and Subtypes. Journal of Virology, 2004, 78, 1962-1970.	3.4	99
35	The evolution of the vertebrate metzincins; insights from Ciona intestinalis and Danio rerio. BMC Evolutionary Biology, 2007, 7, 63.	3.2	97
36	SIVagm Infection in Wild African Green Monkeys from South Africa: Epidemiology, Natural History, and Evolutionary Considerations. PLoS Pathogens, 2013, 9, e1003011.	4.7	96

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37	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. Genome Biology and Evolution, 2022, 14, .	2.5	93
38	Defining the Role of Essential Genes in Human Disease. PLoS ONE, 2011, 6, e27368.	2.5	89
39	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. Nature Microbiology, 2021, 6, 112-122.	13.3	88
40	HIVâ€"host interactions: a map of viral perturbation of the host system. Aids, 2009, 23, 549-554.	2.2	87
41	No evidence for distinct types in the evolution of SARS-CoV-2. Virus Evolution, 2020, 6, veaa034.	4.9	85
42	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular Biology and Evolution, 2022, 39, .	8.9	84
43	Convergent evolution of gene networks by singleâ€gene duplications in higher eukaryotes. EMBO Reports, 2004, 5, 274-279.	4.5	83
44	Challenges in the analysis of viral metagenomes. Virus Evolution, 2016, 2, vew022.	4.9	83
45	Use of Four Next-Generation Sequencing Platforms to Determine HIV-1 Coreceptor Tropism. PLoS ONE, 2012, 7, e49602.	2.5	78
46	Factors Associated with Siman Immunodeficiency Virus Transmission in a Natural African Nonhuman Primate Host in the Wild. Journal of Virology, 2014, 88, 5687-5705.	3.4	77
47	The Evolutionary Analysis of Emerging Low Frequency HIV-1 CXCR4 Using Variants through Timeâ€"An Ultra-Deep Approach. PLoS Computational Biology, 2010, 6, e1001022.	3.2	72
48	The animal origin of SARS-CoV-2. Science, 2021, 373, 968-970.	12.6	72
49	Molecular Mechanisms of Recombination Restriction in the Envelope Gene of the Human Immunodeficiency Virus. PLoS Pathogens, 2009, 5, e1000418.	4.7	70
50	The pain interactome: Connecting pain-specific protein interactions. Pain, 2014, 155, 2243-2252.	4.2	65
51	Detection of SARSâ€CoVâ€2 in respiratory samples from cats in the UK associated with humanâ€toâ€cat transmission. Veterinary Record, 2021, 188, e247.	0.3	63
52	Sensitive Deep-Sequencing-Based HIV-1 Genotyping Assay To Simultaneously Determine Susceptibility to Protease, Reverse Transcriptase, Integrase, and Maturation Inhibitors, as Well as HIV-1 Coreceptor Tropism. Antimicrobial Agents and Chemotherapy, 2014, 58, 2167-2185.	3.2	61
53	Redefining the ancestral origins of the interleukin-1 superfamily. Nature Communications, 2018, 9, 1156.	12.8	60
54	Identifying the Important HIV-1 Recombination Breakpoints. PLoS Computational Biology, 2008, 4, e1000178.	3.2	58

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55	Analysis of high-depth sequence data for studying viral diversity: a comparison of next generation sequencing platforms using Segminator II. BMC Bioinformatics, 2012, 13, 47.	2.6	58
56	Patterns of HIV-1 Protein Interaction Identify Perturbed Host-Cellular Subsystems. PLoS Computational Biology, 2010, 6, e1000863.	3.2	57
57	The characterisation of six ADAMTS proteases in the basal chordate Ciona intestinalis provides new insights into the vertebrate ADAMTS family. International Journal of Biochemistry and Cell Biology, 2005, 37, 1838-1845.	2.8	55
58	Phylogenetic characteristics of three new HIV-1 N strains and implications for the origin of group N. Aids, 2004, 18, 1371-1381.	2.2	54
59	Sequence determinants of breakpoint location during HIV-1 intersubtype recombination. Nucleic Acids Research, 2006, 34, 5203-5216.	14.5	53
60	Detection and Partial Characterization of Simian Immunodeficiency Virus SIVsm Strains from Bush Meat Samples from Rural Sierra Leone. Journal of Virology, 2005, 79, 2631-2636.	3.4	48
61	Kuru experiments triggered the emergence of pathogenic SIVmac. Aids, 2006, 20, 317-321.	2.2	48
62	The integrins of the urochordate Ciona intestinalis provide novel insights into the molecular evolution of the vertebrate integrin family. BMC Evolutionary Biology, 2005, 5, 31.	3.2	47
63	On the Origins of Mendelian Disease Genes in Man: The Impact of Gene Duplication. Molecular Biology and Evolution, 2012, 29, 61-69.	8.9	47
64	A Survey of Bioinformatics Database and Software Usage through Mining the Literature. PLoS ONE, 2016, 11, e0157989.	2.5	47
65	The Collagens of Hydra Provide Insight into the Evolution of Metazoan Extracellular Matrices. Journal of Biological Chemistry, 2007, 282, 6792-6802.	3.4	44
66	Gene Duplication and Environmental Adaptation within Yeast Populations. Genome Biology and Evolution, 2010, 2, 591-601.	2.5	44
67	Reconstruction of ancestral protein interaction networks for the bZIP transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20449-20453.	7.1	43
68	Characterization of Protein-Protein Interaction Interfaces from a Single Species. PLoS ONE, 2011, 6, e21053.	2.5	43
69	Evidence of Recombination between Divergent Hepatitis E Viruses. Journal of Virology, 2005, 79, 9306-9314.	3.4	41
70	The distribution of HIV-1 recombination breakpoints. Infection, Genetics and Evolution, 2007, 7, 717-723.	2.3	38
71	A protein interaction atlas for the nuclear receptors: properties and quality of a hub-based dimerisation network. BMC Systems Biology, 2007, 1, 34.	3.0	38
72	Differentiating between viruses and virus species by writing their names correctly. Archives of Virology, 2022, 167, 1231-1234.	2.1	33

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73	Understanding the diversification of HIV-1 groups M and O. Aids, 2007, 21, 1693-1700.	2.2	32
74	Ebolavirus is evolving but not changing: No evidence for functional change in EBOV from 1976 to the 2014 outbreak. Virology, 2015, 482, 202-207.	2.4	31
75	Characterizing the Diverse Mutational Pathways Associated with R5-Tropic Maraviroc Resistance: HIV-1 That Uses the Drug-Bound CCR5 Coreceptor. Journal of Virology, 2015, 89, 11457-11472.	3.4	31
76	Predicting host taxonomic information from viral genomes: A comparison of feature representations. PLoS Computational Biology, 2020, 16, e1007894.	3.2	31
77	Interpreting Viral Deep Sequencing Data with GLUE. Viruses, 2019, 11, 323.	3.3	29
78	The biological context of HIV-1 host interactions reveals subtle insights into a system hijack. BMC Systems Biology, 2010, 4, 80.	3.0	28
79	HIV Type 1 Genetic Diversity and Genotypic Drug Susceptibility in the Republic of Moldova. AIDS Research and Human Retroviruses, 2001, 17, 1297-1304.	1.1	27
80	Reduction/oxidation-phosphorylation control of DNA binding in the bZIP dimerization network. BMC Genomics, 2006, 7, 107.	2.8	27
81	Constraints on HIV-1 Diversity from Protein Structure. Journal of Virology, 2010, 84, 12995-13003.	3.4	25
82	A Twin-track Approach Has Optimized Proton and Hydride Transfer by Dynamically Coupled Tunneling during the Evolution of Protochlorophyllide Oxidoreductase. Journal of Biological Chemistry, 2011, 286, 11849-11854.	3.4	25
83	The Evolution of Protein Interaction Networks in Regulatory Proteins. Comparative and Functional Genomics, 2004, 5, 79-84.	2.0	24
84	Back to basics â€" how the evolution of the extracellular matrix underpinned vertebrate evolution. International Journal of Experimental Pathology, 2009, 90, 95-100.	1.3	24
85	bioNerDS: exploring bioinformaticsâ€™ database and software use through literature mining. BMC Bioinformatics, 2013, 14, 194.	2.6	23
86	A logical model of HIV-1 interactions with the T-cell activation signalling pathway. Bioinformatics, 2015, 31, 1075-1083.	4.1	23
87	The Two-Phase Emergence of Non Pandemic HIV-1 Group O in Cameroon. PLoS Pathogens, 2015, 11, e1005029.	4.7	22
88	<i>CTree</i>: comparison of clusters between phylogenetic trees made easy. Bioinformatics, 2007, 23, 2952-2953.	4.1	21
89	Mapping biological process relationships and disease perturbations within a pathway network. Npj Systems Biology and Applications, 2018, 4, 22.	3.0	21
90	Using set theory to reduce redundancy in pathway sets. BMC Bioinformatics, 2018, 19, 386.	2.6	20

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91	Effect of dataset selection on the topological interpretation of protein interaction networks. BMC Genomics, 2005, 6, 131.	2.8	19
92	Network controllability analysis of intracellular signalling reveals viruses are actively controlling molecular systems. Scientific Reports, 2019, 9, 2066.	3.3	19
93	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. Virus Evolution, 2022, 8, veac023.	4.9	19
94	An Integrated Transcriptomic and Meta-Analysis of Hepatoma Cells Reveals Factors That Influence Susceptibility to HCV Infection. PLoS ONE, 2011, 6, e25584.	2.5	18
95	Towards semi-automated curation: using text mining to recreate the HIV-1, human protein interaction database. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas023.	3.0	18
96	Sensitive Cell-Based Assay for Determination of Human Immunodeficiency Virus Type 1 Coreceptor Tropism. Journal of Clinical Microbiology, 2013, 51, 1517-1527.	3.9	18
97	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. Molecular Biology and Evolution, 2020, 37, 2706-2710.	8.9	18
98	The antiviral state has shaped the CpG composition of the vertebrate interferome to avoid self-targeting. PLoS Biology, 2021, 19, e3001352.	5.6	18
99	Protein Interactions from Complexes: A Structural Perspective. Comparative and Functional Genomics, 2007, 2007, 1-5.	2.0	16
100	Modular Biological Function Is Most Effectively Captured by Combining Molecular Interaction Data Types. PLoS ONE, 2013, 8, e62670.	2.5	16
101	Molecular Epidemiology of Simian T-Cell Lymphotropic Virus Type 1 in Wild and Captive Sooty Mangabeys. Journal of Virology, 2005, 79, 2541-2548.	3.4	15
102	Methodology capture: discriminating between the "best" and the rest of community practice. BMC Bioinformatics, 2008, 9, 359.	2.6	15
103	Cataloging the biomedical world of pain through semi-automated curation of molecular interactions. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat033.	3.0	14
104	Kindel: indel-aware consensus for nucleotide sequence alignments. Journal of Open Source Software, 2017, 2, 282.	4.6	14
105	Conserved recombination patterns across coronavirus subgenera. Virus Evolution, 2022, 8, .	4.9	14
106	HIV Type 1 Diversity in Northeastern Romania in 2000-2001 Based on Phylogenetic Analysis ofpolSequences from Patients Failing Antiretroviral Therapy. AIDS Research and Human Retroviruses, 2003, 19, 1155-1161.	1.1	12
107	Constraints from protein structure and intra-molecular coevolution influence the fitness of HIV-1 recombinants. Virology, 2014, 454-455, 34-39.	2.4	12
108	A signal processing method for alignment-free metagenomic binning: multi-resolution genomic binary patterns. Scientific Reports, 2019, 9, 2159.	3.3	12

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109	JNets: Exploring networks by integrating annotation. BMC Bioinformatics, 2009, 10, 95.	2.6	10
110	Alternative splicing and protein interaction data sets. Nature Biotechnology, 2013, 31, 292-293.	17.5	10
111	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. Nature Communications, 2022, 13, 1012.	12.8	10
112	Evolution in protein interaction networks: co-evolution, rewiring and the role of duplication. Biochemical Society Transactions, 2009, 37, 768-771.	3.4	9
113	Extracting patterns of database and software usage from the bioinformatics literature. Bioinformatics, 2014, 30, i601-i608.	4.1	9
114	Disentangling the multigenic and pleiotropic nature of molecular function. BMC Systems Biology, 2015, 9, S3.	3.0	9
115	T-RECs: rapid and large-scale detection of recombination events among different evolutionary lineages of viral genomes. BMC Bioinformatics, 2017, 18, 13.	2.6	9
116	The Role of Protein Interactions in Mediating Essentiality and Synthetic Lethality. PLoS ONE, 2013, 8, e62866.	2.5	9
117	A Link between SIVsm in Sooty Mangabeys (SM) in Wild-Living Monkeys in Sierra Leone and SIVsm in an American-Based SM Colony. AIDS Research and Human Retroviruses, 2004, 20, 1348-1351.	1.1	8
118	The origins of the evolutionary signal used to predict protein-protein interactions. BMC Evolutionary Biology, 2012, 12, 238.	3.2	8
119	Locus heterogeneity disease genes encode proteins with high interconnectivity in the human protein interaction network. Frontiers in Genetics, 2014, 5, 434.	2.3	8
120	An exploration of alternative visualisations of the basic helix-loop-helix protein interaction network. BMC Bioinformatics, 2007, 8, 289.	2.6	7
121	Binding interface change and cryptic variation in the evolution of protein-protein interactions. BMC Evolutionary Biology, 2016, 16, 40.	3.2	7
122	Protein structural disorder of the envelope V3 loop contributes to the switch in human immunodeficiency virus type 1 cell tropism. PLoS ONE, 2017, 12, e0185790.	2.5	7
123	The utility of different bioinformatics algorithms for genotypic HIV-1 tropism testing in a large clinical cohort with multiple subtypes. Aids, 2014, 28, 1611-1617.	2.2	6
124	Ambiguity and variability of database and software names in bioinformatics. Journal of Biomedical Semantics, 2015, 6, 29.	1.6	6
125	Bioinformatics Meets Virology: The European Virus Bioinformatics Centerâ€™s Second Annual Meeting. Viruses, 2018, 10, 256.	3.3	6
126	ITNâ€”VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. Viruses, 2021, 13, 766.	3.3	5

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127	Phylogenetic relationships of methionine aminopeptidase 2 among Encephalitozoon species and genotypes of microsporidia. Molecular and Biochemical Parasitology, 2005, 140, 141-152.	1.1	4
128	Using Knowledge of Protein Structural Constraints to Predict the Evolution of HIV-1. Journal of Molecular Biology, 2011, 410, 1023-1034.	4.2	4
129	Evolvability of Yeast Proteinâ€"Protein Interaction Interfaces. Journal of Molecular Biology, 2012, 419, 387-396.	4.2	4
130	Emergence, dominance, and possible decline of CXCR4 chemokine receptor usage during the course of HIV infection. Journal of Medical Virology, 2010, 82, 2004-2012.	5.0	3
131	Local binary patterns as a feature descriptor in alignment-free visualisation of metagenomic data. , 2016, , .		3
132	Send cat and dog samples to test for SARSâ€CoVâ€2. Veterinary Record, 2020, 186, 571-571.	0.3	3
133	Marginalised stack denoising autoencoders for metagenomic data binning. , 2017, , .		2
134	The Utility of Data Transformation for Alignment, De Novo Assembly and Classification of Short Read Virus Sequences. Viruses, 2019, 11, 394.	3.3	2
135	Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses. Virus Evolution, 2021, 7, veab067.	4.9	2
136	Quantifying and Cataloguing Unknown Sequences within Human Microbiomes. MSystems, 2022, 7, e0146821.	3.8	2
137	HIV-1 group P infection. Aids, 2018, 32, 1317-1322.	2.2	1
138	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		1
139	SHARKview: a tool for the visualization of systems biology data. BMC Systems Biology, 2007, 1, .	3.0	0
140	In silico prediction of HIV-1-host molecular interactions and their directionality. PLoS Computational Biology, 2022, 18, e1009720.	3.2	0
141	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0
142	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0
143	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0
144	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0

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145	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0