

David L Robertson

List of Publications by Year in descending order

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Version: 2024-02-01

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	Differentiating between viruses and virus species by writing their names correctly. Archives of Virology, 2022, 167, 1231-1234.	2.1	33
2	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	12.4	101
3	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. Genome Biology and Evolution, 2022, 14, .	2.5	93
4	In silico prediction of HIV-1-host molecular interactions and their directionality. PLoS Computational Biology, 2022, 18, e1009720.	3.2	0
5	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. Nature Communications, 2022, 13, 1012.	12.8	10
6	Quantifying and Cataloguing Unknown Sequences within Human Microbiomes. MSystems, 2022, 7, e0146821.	3.8	2
7	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
8	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. Virus Evolution, 2022, 8, veac023.	4.9	19
9	The Evolution and Biology of SARS-CoV-2 Variants. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a041390.	6.2	110
10	Conserved recombination patterns across coronavirus subgenera. Virus Evolution, 2022, 8, .	4.9	14
11	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
12	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 2021, 184, 64-75.e11.	28.9	843
13	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. Nature Microbiology, 2021, 6, 112-122.	13.3	88
14	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
15	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	28.9	541
16	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
17	Detection of SARS-CoV-2 in respiratory samples from cats in the UK associated with human-to-cat transmission. Veterinary Record, 2021, 188, e247.	0.3	63
18	ITN-VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. Viruses, 2021, 13, 766.	3.3	5

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19	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021, 19, 409-424.	28.6	2,650
20	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
21	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). <i>Archives of Virology</i> , 2021, 166, 2633-2648.	2.1	219
22	Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses. <i>Virus Evolution</i> , 2021, 7, veab067.	4.9	2
23	The animal origin of SARS-CoV-2. <i>Science</i> , 2021, 373, 968-970.	12.6	72
24	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182
25	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	28.9	186
26	The antiviral state has shaped the CpG composition of the vertebrate interferome to avoid self-targeting. <i>PLoS Biology</i> , 2021, 19, e3001352.	5.6	18
27	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	28.9	330
28	A prenylated dsRNA sensor protects against severe COVID-19. <i>Science</i> , 2021, 374, eabj3624.	12.6	124
29	Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination. <i>PLoS Pathogens</i> , 2021, 17, e1010022.	4.7	139
30	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2020, 37, 2706-2710.	8.9	18
31	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	13.3	772
32	No evidence for distinct types in the evolution of SARS-CoV-2. <i>Virus Evolution</i> , 2020, 6, veaa034.	4.9	85
33	Predicting host taxonomic information from viral genomes: A comparison of feature representations. <i>PLoS Computational Biology</i> , 2020, 16, e1007894.	3.2	31
34	Send cat and dog samples to test for SARS-CoV-2. <i>Veterinary Record</i> , 2020, 186, 571-571.	0.3	3
35	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0
36	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0

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37	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0
38	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0
39	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		0
40	Predicting host taxonomic information from viral genomes: A comparison of feature representations. , 2020, 16, e1007894.		1
41	The Utility of Data Transformation for Alignment, De Novo Assembly and Classification of Short Read Virus Sequences. Viruses, 2019, 11, 394.	3.3	2
42	Interpreting Viral Deep Sequencing Data with GLUE. Viruses, 2019, 11, 323.	3.3	29
43	Network controllability analysis of intracellular signalling reveals viruses are actively controlling molecular systems. Scientific Reports, 2019, 9, 2066.	3.3	19
44	A signal processing method for alignment-free metagenomic binning: multi-resolution genomic binary patterns. Scientific Reports, 2019, 9, 2159.	3.3	12
45	Redefining the ancestral origins of the interleukin-1 superfamily. Nature Communications, 2018, 9, 1156.	12.8	60
46	HIV-1 group P infection. Aids, 2018, 32, 1317-1322.	2.2	1
47	Using set theory to reduce redundancy in pathway sets. BMC Bioinformatics, 2018, 19, 386.	2.6	20
48	Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. Viruses, 2018, 10, 256.	3.3	6
49	Mapping biological process relationships and disease perturbations within a pathway network. Npj Systems Biology and Applications, 2018, 4, 22.	3.0	21
50	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
51	Marginalised stack denoising autoencoders for metagenomic data binning. , 2017, , .		2
52	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
53	Kindel: indel-aware consensus for nucleotide sequence alignments. Journal of Open Source Software, 2017, 2, 282.	4.6	14
54	A Survey of Bioinformatics Database and Software Usage through Mining the Literature. PLoS ONE, 2016, 11, e0157989.	2.5	47

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55	Local binary patterns as a feature descriptor in alignment-free visualisation of metagenomic data. , 2016, , .		3
56	Challenges in the analysis of viral metagenomes. <i>Virus Evolution</i> , 2016, 2, vew022.	4.9	83
57	Binding interface change and cryptic variation in the evolution of protein-protein interactions. <i>BMC Evolutionary Biology</i> , 2016, 16, 40.	3.2	7
58	Disentangling the multigenic and pleiotropic nature of molecular function. <i>BMC Systems Biology</i> , 2015, 9, S3.	3.0	9
59	Ambiguity and variability of database and software names in bioinformatics. <i>Journal of Biomedical Semantics</i> , 2015, 6, 29.	1.6	6
60	Ebolavirus is evolving but not changing: No evidence for functional change in EBOV from 1976 to the 2014 outbreak. <i>Virology</i> , 2015, 482, 202-207.	2.4	31
61	Characterizing the Diverse Mutational Pathways Associated with R5-Tropic Maraviroc Resistance: HIV-1 That Uses the Drug-Bound CCR5 Coreceptor. <i>Journal of Virology</i> , 2015, 89, 11457-11472.	3.4	31
62	A logical model of HIV-1 interactions with the T-cell activation signalling pathway. <i>Bioinformatics</i> , 2015, 31, 1075-1083.	4.1	23
63	The Two-Phase Emergence of Non Pandemic HIV-1 Group O in Cameroon. <i>PLoS Pathogens</i> , 2015, 11, e1005029.	4.7	22
64	Factors Associated with Simian Immunodeficiency Virus Transmission in a Natural African Nonhuman Primate Host in the Wild. <i>Journal of Virology</i> , 2014, 88, 5687-5705.	3.4	77
65	Locus heterogeneity disease genes encode proteins with high interconnectivity in the human protein interaction network. <i>Frontiers in Genetics</i> , 2014, 5, 434.	2.3	8
66	The pain interactome: Connecting pain-specific protein interactions. <i>Pain</i> , 2014, 155, 2243-2252.	4.2	65
67	Extracting patterns of database and software usage from the bioinformatics literature. <i>Bioinformatics</i> , 2014, 30, i601-i608.	4.1	9
68	The utility of different bioinformatics algorithms for genotypic HIV-1 tropism testing in a large clinical cohort with multiple subtypes. <i>Aids</i> , 2014, 28, 1611-1617.	2.2	6
69	Constraints from protein structure and intra-molecular coevolution influence the fitness of HIV-1 recombinants. <i>Virology</i> , 2014, 454-455, 34-39.	2.4	12
70	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. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2167-2185.	3.2	61
71	bioNerDS: exploring bioinformatics's™ database and software use through literature mining. <i>BMC Bioinformatics</i> , 2013, 14, 194.	2.6	23
72	Alternative splicing and protein interaction data sets. <i>Nature Biotechnology</i> , 2013, 31, 292-293.	17.5	10

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73	SIVagm Infection in Wild African Green Monkeys from South Africa: Epidemiology, Natural History, and Evolutionary Considerations. <i>PLoS Pathogens</i> , 2013, 9, e1003011.	4.7	96
74	Cataloging the biomedical world of pain through semi-automated curation of molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat033.	3.0	14
75	Sensitive Cell-Based Assay for Determination of Human Immunodeficiency Virus Type 1 Coreceptor Tropism. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1517-1527.	3.9	18
76	Modular Biological Function Is Most Effectively Captured by Combining Molecular Interaction Data Types. <i>PLoS ONE</i> , 2013, 8, e62670.	2.5	16
77	The Role of Protein Interactions in Mediating Essentiality and Synthetic Lethality. <i>PLoS ONE</i> , 2013, 8, e62866.	2.5	9
78	Towards semi-automated curation: using text mining to recreate the HIV-1, human protein interaction database. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas023.	3.0	18
79	On the Origins of Mendelian Disease Genes in Man: The Impact of Gene Duplication. <i>Molecular Biology and Evolution</i> , 2012, 29, 61-69.	8.9	47
80	Evolvability of Yeast Protein-Protein Interaction Interfaces. <i>Journal of Molecular Biology</i> , 2012, 419, 387-396.	4.2	4
81	Analysis of high-depth sequence data for studying viral diversity: a comparison of next generation sequencing platforms using Segminator II. <i>BMC Bioinformatics</i> , 2012, 13, 47.	2.6	58
82	The origins of the evolutionary signal used to predict protein-protein interactions. <i>BMC Evolutionary Biology</i> , 2012, 12, 238.	3.2	8
83	Use of Four Next-Generation Sequencing Platforms to Determine HIV-1 Coreceptor Tropism. <i>PLoS ONE</i> , 2012, 7, e49602.	2.5	78
84	Using Knowledge of Protein Structural Constraints to Predict the Evolution of HIV-1. <i>Journal of Molecular Biology</i> , 2011, 410, 1023-1034.	4.2	4
85	Defining the Role of Essential Genes in Human Disease. <i>PLoS ONE</i> , 2011, 6, e27368.	2.5	89
86	An Integrated Transcriptomic and Meta-Analysis of Hepatoma Cells Reveals Factors That Influence Susceptibility to HCV Infection. <i>PLoS ONE</i> , 2011, 6, e25584.	2.5	18
87	A Twin-track Approach Has Optimized Proton and Hydride Transfer by Dynamically Coupled Tunneling during the Evolution of Protochlorophyllide Oxidoreductase. <i>Journal of Biological Chemistry</i> , 2011, 286, 11849-11854.	3.4	25
88	Characterization of Protein-Protein Interaction Interfaces from a Single Species. <i>PLoS ONE</i> , 2011, 6, e21053.	2.5	43
89	Gene Duplication and Environmental Adaptation within Yeast Populations. <i>Genome Biology and Evolution</i> , 2010, 2, 591-601.	2.5	44
90	Emergence, dominance, and possible decline of CXCR4 chemokine receptor usage during the course of HIV infection. <i>Journal of Medical Virology</i> , 2010, 82, 2004-2012.	5.0	3

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91	The biological context of HIV-1 host interactions reveals subtle insights into a system hijack. BMC Systems Biology, 2010, 4, 80.	3.0	28
92	Constraints on HIV-1 Diversity from Protein Structure. Journal of Virology, 2010, 84, 12995-13003.	3.4	25
93	The Evolutionary Analysis of Emerging Low Frequency HIV-1 CXCR4 Using Variants through Time—An Ultra-Deep Approach. PLoS Computational Biology, 2010, 6, e1001022.	3.2	72
94	Patterns of HIV-1 Protein Interaction Identify Perturbed Host-Cellular Subsystems. PLoS Computational Biology, 2010, 6, e1000863.	3.2	57
95	An Integrated View of Molecular Coevolution in Protein-Protein Interactions. Molecular Biology and Evolution, 2010, 27, 2567-2575.	8.9	119
96	Genome-Wide Classification and Evolutionary Analysis of the bHLH Family of Transcription Factors in Arabidopsis, Poplar, Rice, Moss, and Algae. Plant Physiology, 2010, 153, 1398-1412.	4.8	493
97	Molecular Mechanisms of Recombination Restriction in the Envelope Gene of the Human Immunodeficiency Virus. PLoS Pathogens, 2009, 5, e1000418.	4.7	70
98	HIV—host interactions: a map of viral perturbation of the host system. Aids, 2009, 23, 549-554.	2.2	87
99	JNets: Exploring networks by integrating annotation. BMC Bioinformatics, 2009, 10, 95.	2.6	10
100	Back to basics — how the evolution of the extracellular matrix underpinned vertebrate evolution. International Journal of Experimental Pathology, 2009, 90, 95-100.	1.3	24
101	A new human immunodeficiency virus derived from gorillas. Nature Medicine, 2009, 15, 871-872.	30.7	424
102	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
103	Evolution in protein interaction networks: co-evolution, rewiring and the role of duplication. Biochemical Society Transactions, 2009, 37, 768-771.	3.4	9
104	Protein-protein interaction networks and biology—what's the connection?. Nature Biotechnology, 2008, 26, 69-72.	17.5	175
105	Methodology capture: discriminating between the "best" and the rest of community practice. BMC Bioinformatics, 2008, 9, 359.	2.6	15
106	Choose your partners: dimerization in eukaryotic transcription factors. Trends in Biochemical Sciences, 2008, 33, 220-229.	7.5	229
107	Short Communication: Cataloguing the HIV Type 1 Human Protein Interaction Network. AIDS Research and Human Retroviruses, 2008, 24, 1497-1502.	1.1	126
108	Identifying the Important HIV-1 Recombination Breakpoints. PLoS Computational Biology, 2008, 4, e1000178.	3.2	58

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109	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
110	<i>CTree</i>: comparison of clusters between phylogenetic trees made easy. Bioinformatics, 2007, 23, 2952-2953.	4.1	21
111	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
112	The Collagens of Hydra Provide Insight into the Evolution of Metazoan Extracellular Matrices. Journal of Biological Chemistry, 2007, 282, 6792-6802.	3.4	44
113	Protein Interactions from Complexes: A Structural Perspective. Comparative and Functional Genomics, 2007, 2007, 1-5.	2.0	16
114	Understanding the diversification of HIV-1 groups M and O. Aids, 2007, 21, 1693-1700.	2.2	32
115	On the origins of the extracellular matrix in vertebrates. Matrix Biology, 2007, 26, 2-11.	3.6	119
116	All duplicates are not equal: the difference between small-scale and genome duplication. Genome Biology, 2007, 8, R209.	9.6	163
117	The distribution of HIV-1 recombination breakpoints. Infection, Genetics and Evolution, 2007, 7, 717-723.	2.3	38
118	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
119	SHARKview: a tool for the visualization of systems biology data. BMC Systems Biology, 2007, 1, .	3.0	0
120	An exploration of alternative visualisations of the basic helix-loop-helix protein interaction network. BMC Bioinformatics, 2007, 8, 289.	2.6	7
121	The evolution of the vertebrate metzincins; insights from <i>Ciona intestinalis</i> and <i>Danio rerio</i> . BMC Evolutionary Biology, 2007, 7, 63.	3.2	97
122	Kuru experiments triggered the emergence of pathogenic SIVmac. Aids, 2006, 20, 317-321.	2.2	48
123	Reduction/oxidation-phosphorylation control of DNA binding in the bZIP dimerization network. BMC Genomics, 2006, 7, 107.	2.8	27
124	Sequence determinants of breakpoint location during HIV-1 intersubtype recombination. Nucleic Acids Research, 2006, 34, 5203-5216.	14.5	53
125	Phylogenetic relationships of methionine aminopeptidase 2 among Encephalitozoon species and genotypes of microsporidia. Molecular and Biochemical Parasitology, 2005, 140, 141-152.	1.1	4
126	The integrins of the urochordate <i>Ciona intestinalis</i> provide novel insights into the molecular evolution of the vertebrate integrin family. BMC Evolutionary Biology, 2005, 5, 31.	3.2	47

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127	Effect of dataset selection on the topological interpretation of protein interaction networks. <i>BMC Genomics</i> , 2005, 6, 131.	2.8	19
128	Evidence of Recombination between Divergent Hepatitis E Viruses. <i>Journal of Virology</i> , 2005, 79, 9306-9314.	3.4	41
129	Detection and Partial Characterization of Simian Immunodeficiency Virus SIVsm Strains from Bush Meat Samples from Rural Sierra Leone. <i>Journal of Virology</i> , 2005, 79, 2631-2636.	3.4	48
130	Molecular Epidemiology of Simian Immunodeficiency Virus SIVsm in U.S. Primate Centers Unravels the Origin of SIVmac and SIVstm. <i>Journal of Virology</i> , 2005, 79, 8991-9005.	3.4	159
131	Molecular Epidemiology of Simian T-Cell Lymphotropic Virus Type 1 in Wild and Captive Sooty Mangabeys. <i>Journal of Virology</i> , 2005, 79, 2541-2548.	3.4	15
132	The characterisation of six ADAMTS proteases in the basal chordate <i>Ciona intestinalis</i> provides new insights into the vertebrate ADAMTS family. <i>International Journal of Biochemistry and Cell Biology</i> , 2005, 37, 1838-1845.	2.8	55
133	The history of SIVS and AIDS: epidemiology, phylogeny and biology of isolates from naturally SIV infected non-human primates (NHP) in Africa. <i>Frontiers in Bioscience - Landmark</i> , 2004, 9, 225.	3.0	148
134	Identification of a Highly Divergent HIV Type 2 and Proposal for a Change in HIV Type 2 Classification. <i>AIDS Research and Human Retroviruses</i> , 2004, 20, 666-672.	1.1	143
135	Comparative Study of Adaptive Molecular Evolution in Different Human Immunodeficiency Virus Groups and Subtypes. <i>Journal of Virology</i> , 2004, 78, 1962-1970.	3.4	99
136	The Molecular Population Genetics of HIV-1 Group O. <i>Genetics</i> , 2004, 167, 1059-1068.	2.9	105
137	Phylogenetic characteristics of three new HIV-1 N strains and implications for the origin of group N. <i>Aids</i> , 2004, 18, 1371-1381.	2.2	54
138	Convergent evolution of gene networks by single gene duplications in higher eukaryotes. <i>EMBO Reports</i> , 2004, 5, 274-279.	4.5	83
139	The Evolution of Protein Interaction Networks in Regulatory Proteins. <i>Comparative and Functional Genomics</i> , 2004, 5, 79-84.	2.0	24
140	A Link between SIVsm in Sooty Mangabeys (SM) in Wild-Living Monkeys in Sierra Leone and SIVsm in an American-Based SM Colony. <i>AIDS Research and Human Retroviruses</i> , 2004, 20, 1348-1351.	1.1	8
141	HIV Type 1 Diversity in Northeastern Romania in 2000-2001 Based on Phylogenetic Analysis of pol Sequences from Patients Failing Antiretroviral Therapy. <i>AIDS Research and Human Retroviruses</i> , 2003, 19, 1155-1161.	1.1	12
142	Phylogeny and the origin of HIV-1. <i>Nature</i> , 2001, 410, 1047-1048.	27.8	143
143	Wild <i>Mandrillus sphinx</i> Are Carriers of Two Types of Lentivirus. <i>Journal of Virology</i> , 2001, 75, 7086-7096.	3.4	133
144	HIV Type 1 Genetic Diversity and Genotypic Drug Susceptibility in the Republic of Moldova. <i>AIDS Research and Human Retroviruses</i> , 2001, 17, 1297-1304.	1.1	27

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145	Origin of HIV-1 in the chimpanzee <i>Pan troglodytes troglodytes</i> . <i>Nature</i> , 1999, 397, 436-441.	27.8	1,405