

Robert Belshaw

List of Publications by Year in descending order

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39
papers

4,300
citations

172386

29
h-index

289141

40
g-index

40
all docs

40
docs citations

40
times ranked

5560
citing authors

#	ARTICLE	IF	CITATIONS
1	Human Endogenous Retrovirus Type K Promotes Proliferation and Confers Sensitivity to Antiretroviral Drugs in Merlin-Negative Schwannoma and Meningioma. <i>Cancer Research</i> , 2022, 82, 235-247.	0.4	11
2	BreakAlign: a Perl program to align chimaeric (split) genomic NGS reads and allow visual confirmation of novel retroviral integrations. <i>BMC Bioinformatics</i> , 2022, 23, 134.	1.2	2
3	Characterising a human endogenous retrovirus (HERV)-derived tumour-associated antigen: enriched RNA-Seq analysis of HERV-K(HML-2) in mantle cell lymphoma cell lines. <i>Mobile DNA</i> , 2020, 11, 9.	1.3	13
4	Variable Baseline <i>Papio cynocephalus</i> Endogenous Retrovirus (PcEV) Expression Is Upregulated in Acutely SIV-Infected Macaques and Correlated to STAT1 Expression in the Spleen. <i>Frontiers in Immunology</i> , 2019, 10, 901.	2.2	1
5	OncoSim and OncoWiki: an authentic learning approach to teaching cancer genomics. <i>BMC Medical Education</i> , 2019, 19, 407.	1.0	8
6	Overlapping genes and the proteins they encode differ significantly in their sequence composition from non-overlapping genes. <i>PLoS ONE</i> , 2018, 13, e0202513.	1.1	45
7	The decline of human endogenous retroviruses: extinction and survival. <i>Retrovirology</i> , 2015, 12, 8.	0.9	49
8	Larger Mammalian Body Size Leads to Lower Retroviral Activity. <i>PLoS Pathogens</i> , 2014, 10, e1004214.	2.1	47
9	Unfixed Endogenous Retroviral Insertions in the Human Population. <i>Journal of Virology</i> , 2014, 88, 9529-9537.	1.5	118
10	Neanderthal and Denisovan retroviruses in modern humans. <i>Current Biology</i> , 2013, 23, R994-R995.	1.8	17
11	Dating the origin and dispersal of hepatitis B virus infection in humans and primates. <i>Hepatology</i> , 2013, 57, 908-916.	3.6	131
12	Integrating Phylodynamics and Epidemiology to Estimate Transmission Diversity in Viral Epidemics. <i>PLoS Computational Biology</i> , 2013, 9, e1002876.	1.5	57
13	“There and back again”™: revisiting the pathophysiological roles of human endogenous retroviruses in the post-genomic era. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120504.	1.8	57
14	Env-less endogenous retroviruses are genomic superspreaders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7385-7390.	3.3	111
15	Detecting Remote Sequence Homology in Disordered Proteins: Discovery of Conserved Motifs in the N-Termini of Mononegavirales phosphoproteins. <i>PLoS ONE</i> , 2012, 7, e31719.	1.1	53
16	Viral mutation and substitution: units and levels. <i>Current Opinion in Virology</i> , 2011, 1, 430-435.	2.6	24
17	Why genes overlap in viruses. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 3809-3817.	1.2	132
18	Viral Mutation Rates. <i>Journal of Virology</i> , 2010, 84, 9733-9748.	1.5	1,078

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19	The RNA Virus Database. <i>Nucleic Acids Research</i> , 2009, 37, D431-D435.	6.5	14
20	Pacing a small cage: mutation and RNA viruses. <i>Trends in Ecology and Evolution</i> , 2008, 23, 188-193.	4.2	136
21	Conserved Footprints of APOBEC3G on Hypermutated Human Immunodeficiency Virus Type 1 and Human Endogenous Retrovirus HERV-K(HML2) Sequences. <i>Journal of Virology</i> , 2008, 82, 8743-8761.	1.5	75
22	Phylogenetic Evidence for Deleterious Mutation Load in RNA Viruses and Its Contribution to Viral Evolution. <i>Molecular Biology and Evolution</i> , 2007, 24, 845-852.	3.5	133
23	Rate of Recombinational Deletion among Human Endogenous Retroviruses. <i>Journal of Virology</i> , 2007, 81, 9437-9442.	1.5	110
24	The evolution of genome compression and genomic novelty in RNA viruses. <i>Genome Research</i> , 2007, 17, 1496-1504.	2.4	139
25	High Copy Number in Human Endogenous Retrovirus Families is Associated with Copying Mechanisms in Addition to Reinfection. <i>Molecular Biology and Evolution</i> , 2005, 22, 814-817.	3.5	132
26	Genomewide Screening Reveals High Levels of Insertional Polymorphism in the Human Endogenous Retrovirus Family HERV-K(HML2): Implications for Present-Day Activity. <i>Journal of Virology</i> , 2005, 79, 12507-12514.	1.5	198
27	Long-term reinfection of the human genome by endogenous retroviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4894-4899.	3.3	350
28	Inferring life history from ovipositor morphology in parasitoid wasps using phylogenetic regression and discriminant analysis. <i>Zoological Journal of the Linnean Society</i> , 2003, 139, 213-228.	1.0	46
29	The value of the ITS2 region for the identification of species boundaries between <i>Alloxysta</i> hyperparasitoids (Hymenoptera: Charipidae) of aphids. <i>European Journal of Entomology</i> , 2003, 100, 449-453.	1.2	16
30	Robustness of Ancestral State Estimates: Evolution of Life History Strategy in Ichneumonoid Parasitoids. <i>Systematic Biology</i> , 2002, 51, 450-477.	2.7	120
31	Simultaneous Molecular and Morphological Analysis of Braconid Relationships (Insecta: Hymenoptera: Braconidae). <i>Journal of Molecular Evolution</i> , 2002, 54, 210-226.	0.8	78
32	The Phylogenetic Analysis of Variable-Length Sequence Data: Elongation Factor ϵ Introns in European Populations of the Parasitoid Wasp Genus <i>Pauesia</i> (Hymenoptera: Braconidae: Aphidiinae). <i>Molecular Biology and Evolution</i> , 2001, 18, 1117-1131.	3.5	39
33	Paraphyletic taxa and taxonomic chaining: evaluating the classification of braconine wasps (Hymenoptera: Braconidae) using 28S D2-3 rDNA sequences and morphological characters. <i>Biological Journal of the Linnean Society</i> , 2001, 73, 411-424.	0.7	52
34	Noise and Incongruence: Interpreting Results of the Incongruence Length Difference Test. <i>Molecular Phylogenetics and Evolution</i> , 2000, 17, 401-406.	1.2	241
35	Incongruence Between Morphological Data Sets: An Example from the Evolution of Endoparasitism Among Parasitic Wasps (Hymenoptera: Braconidae). <i>Systematic Biology</i> , 1999, 48, 436-454.	2.7	55
36	A phylogenetic reconstruction of the Ichneumonoidea (Hymenoptera) based on the D2 variable region of 28S ribosomal RNA. <i>Systematic Entomology</i> , 1998, 23, 109-123.	1.7	124

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37	A Molecular Phylogeny of the Aphidiinae (Hymenoptera: Braconidae). <i>Molecular Phylogenetics and Evolution</i> , 1997, 7, 281-293.	1.2	218
38	Comparisons of dipteran, hymenopteran and coleopteran parasitoids: provisional phylogenetic explanations. <i>Biological Journal of the Linnean Society</i> , 1993, 48, 213-226.	0.7	49
39	Taxonomy and biology of the supposedly lepto-biotic ant genus <i>Paedalgus</i> (Hym.: Formicidae). <i>Systematic Entomology</i> , 1993, 18, 181-189.	1.7	13