Ben Murrell

List of Publications by Year
in descending order

78 papers	12,090 citations	117453 34 h-index	64668 79 g-index
97 all docs	97 docs citations	97 times ranked	16224 citing authors

#	Article	IF	Citations
1	SARS-CoV-2 reactive and neutralizing antibodies discovered by single-cell sequencing of plasma cells and mammalian display. Cell Reports, 2022, 38, 110242.	2.9	13
2	A bispecific monomeric nanobody induces spike trimer dimers and neutralizes SARS-CoV-2 in vivo. Nature Communications, 2022, 13, 155.	5.8	49
3	Probabilistic classification of antiâ€SARSâ€CoVâ€2 antibody responses improves seroprevalence estimates. Clinical and Translational Immunology, 2022, 11, e1379.	1.7	4
4	Multivariate mining of an alpaca immune repertoire identifies potent cross-neutralizing SARS-CoV-2 nanobodies. Science Advances, 2022, 8, eabm0220.	4.7	18
5	Neutralisation sensitivity of the SARS-CoV-2 omicron (B.1.1.529) variant: a cross-sectional study. Lancet Infectious Diseases, The, 2022, 22, 813-820.	4.6	64
6	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular Biology and Evolution, 2022, 39, .	3.5	84
7	Recombinant multimeric dog allergen prevents airway hyperresponsiveness in a model of asthma marked by vigorous <scp>T_H2</scp> and <scp>T_H17</scp> cell responses. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 2987-3001.	2.7	4
8	Conserved recombination patterns across coronavirus subgenera. Virus Evolution, 2022, 8, .	2.2	14
9	GPR43 regulates marginal zone Bâ€cell responses to foreign and endogenous antigens. Immunology and Cell Biology, 2021, 99, 234-243.	1.0	10
10	Systematic evaluation of SARSâ€CoVâ€2 antigens enables a highly specific and sensitive multiplex serological COVIDâ€19 assay. Clinical and Translational Immunology, 2021, 10, e1312.	1.7	24
11	Rhesus and cynomolgus macaque immunoglobulin heavy-chain genotyping yields comprehensive databases of germline VDJ alleles. Immunity, 2021, 54, 355-366.e4.	6.6	52
12	DNA-launched RNA replicon vaccines induce potent anti-SARS-CoV-2 immune responses in mice. Scientific Reports, 2021, 11, 3125.	1.6	17
13	SARS-CoV-2 protein subunit vaccination of mice and rhesus macaques elicits potent and durable neutralizing antibody responses. Cell Reports Medicine, 2021, 2, 100252.	3.3	33
14	Seropositivity in blood donors and pregnant women during the first year of SARSâ€CoVâ€2 transmission in Stockholm, Sweden. Journal of Internal Medicine, 2021, 290, 666-676.	2.7	34
15	Multianalyte serology in home-sampled blood enables an unbiased assessment of the immune response against SARS-CoV-2. Nature Communications, 2021, 12, 3695.	5.8	32
16	Single-cell analysis pinpoints distinct populations of cytotoxic CD4 ⁺ T cells and an IL-10 ⁺ CD109 ⁺ T _H 2 cell population in nasal polyps. Science Immunology, 2021, 6, .	5.6	30
17	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. Cell, 2021, 184, 5189-5200.e7.	13.5	186
18	Adjuvanted SARS-CoV-2 spike protein elicits neutralizing antibodies and CD4 T cell responses after a single immunization in mice. EBioMedicine, 2021, 63, 103197.	2.7	31

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19	RDP5: a computer program for analyzing recombination in, and removing signals of recombination from, nucleotide sequence datasets. Virus Evolution, 2021, 7, veaa087.	2.2	257
20	Beta RBD boost broadens antibody-mediated protection against SARS-CoV-2 variants in animal models. Cell Reports Medicine, 2021, 2, 100450.	3.3	17
21	HyPhy 2.5â€"A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. Molecular Biology and Evolution, 2020, 37, 295-299.	3.5	342
22	Evolutionary Analyses of Base-Pairing Interactions in DNA and RNA Secondary Structures. Molecular Biology and Evolution, 2020, 37, 576-592.	3.5	6
23	SARS-CoV-2 exposure, symptoms and seroprevalence in healthcare workers in Sweden. Nature Communications, 2020, 11, 5064.	5.8	243
24	Vaccine elicitation of HIV broadly neutralizing antibodies from engineered B cells. Nature Communications, 2020, 11, 5850.	5.8	38
25	An alpaca nanobody neutralizes SARS-CoV-2 by blocking receptor interaction. Nature Communications, 2020, 11, 4420.	5.8	261
26	Picomolar SARS-CoV-2 Neutralization Using Multi-Arm PEG Nanobody Constructs. Biomolecules, 2020, 10, 1661.	1.8	27
27	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. Nature Communications, 2020, 11, 5588.	5.8	132
28	Long-read amplicon denoising. Nucleic Acids Research, 2019, 47, e104-e104.	6.5	31
29	Rapid and Focused Maturation of a VRC01-Class HIV Broadly Neutralizing Antibody Lineage Involves Both Binding and Accommodation of the N276-Glycan. Immunity, 2019, 51, 141-154.e6.	6.6	71
30	Rapid Germinal Center and Antibody Responses in Non-human Primates after a Single Nanoparticle Vaccine Immunization. Cell Reports, 2019, 29, 1756-1766.e8.	2.9	47
31	Hepatitis C virus genotype 1 and 2 recombinant genomes and the phylogeographic history of the 2k/1b lineage. Virus Evolution, 2019, 5, vez041.	2.2	5
32	Slow Delivery Immunization Enhances HIV Neutralizing Antibody and Germinal Center Responses via Modulation of Immunodominance. Cell, 2019, 177, 1153-1171.e28.	13.5	293
33	Combined HIV-1 sequence and integration site analysis informs viral dynamics and allows reconstruction of replicating viral ancestors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25891-25899.	3.3	78
34	An MPER antibody neutralizes HIV-1 using germline features shared among donors. Nature Communications, 2019, 10, 5389.	5.8	44
35	Vaccine-Induced Protection from Homologous Tier 2 SHIV Challenge in Nonhuman Primates Depends on Serum-Neutralizing Antibody Titers. Immunity, 2019, 50, 241-252.e6.	6.6	153
36	Reprogramming the antigen specificity of B cells using genome-editing technologies. ELife, 2019, 8, .	2.8	69

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37	Intrapatient viral diversity and treatment outcome in patients with genotype 3a hepatitis C virus infection on sofosbuvirâ€containing regimens. Journal of Viral Hepatitis, 2018, 25, 344-353.	1.0	3
38	Maintenance and reappearance of extremely divergent intra-host HIV-1 variants. Virus Evolution, 2018, 4, vey030.	2.2	5
39	Full-Length Envelope Analyzer (FLEA): A tool for longitudinal analysis of viral amplicons. PLoS Computational Biology, 2018, 14, e1006498.	1.5	5
40	HIV Superinfection Drives De Novo Antibody Responses and Not Neutralization Breadth. Cell Host and Microbe, 2018, 24, 593-599.e3.	5.1	24
41	RIFRAF: a frame-resolving consensus algorithm. Bioinformatics, 2018, 34, 3817-3824.	1.8	4
42	Glycoengineering HIV-1 Env creates â€˜superchargedâ€™ and â€˜hybridâ€™ glycans to increase neutralizing antibody potency, breadth and saturation. PLoS Pathogens, 2018, 14, e1007024.	2.1	22
43	Growth of HIV-1 Molecular Transmission Clusters in New York City. Journal of Infectious Diseases, 2018, 218, 1943-1953.	1.9	75
44	Antibody 10-1074 suppresses viremia in HIV-1-infected individuals. Nature Medicine, 2017, 23, 185-191.	15.2	399
45	Detecting and Analyzing Genetic Recombination Using RDP4. Methods in Molecular Biology, 2017, 1525, 433-460.	0.4	113
46	HIV Envelope Glycoform Heterogeneity and Localized Diversity Govern the Initiation and Maturation of a V2 Apex Broadly Neutralizing Antibody Lineage. Immunity, 2017, 47, 990-1003.e9.	6.6	90
47	Extra-epitopic hepatitis C virus polymorphisms confer resistance to broadly neutralizing antibodies by modulating binding to scavenger receptor B1. PLoS Pathogens, 2017, 13, e1006235.	2.1	47
48	Social and Genetic Networks of HIV-1 Transmission in New York City. PLoS Pathogens, 2017, 13, e1006000.	2.1	157
49	The Evolutionary Histories of Antiretroviral Proteins SERINC3 and SERINC5 Do Not Support an Evolutionary Arms Race in Primates. Journal of Virology, 2016, 90, 8085-8089.	1.5	40
50	Early Antibody Lineage Diversification and Independent Limb Maturation Lead to Broad HIV-1 Neutralization Targeting the Env High-Mannose Patch. Immunity, 2016, 44, 1215-1226.	6.6	138
51	Using HIV Sequence and Epidemiologic Data to Assess the Effect of Self-referral Testing for Acute HIV Infection on Incident Diagnoses in San Diego, California. Clinical Infectious Diseases, 2016, 63, 101-107.	2.9	20
52	Cell-free mitochondrial DNA in CSF is associated with early viral rebound, inflammation, and severity of neurocognitive deficits in HIV infection. Journal of NeuroVirology, 2016, 22, 191-200.	1.0	31
53	Rapid Sequencing of Complete<i>env</i>Genes from Primary HIV-1 Samples. Virus Evolution, 2016, 2, vew018.	2.2	30
54	Discovering General Multidimensional Associations. PLoS ONE, 2016, 11, e0151551.	1.1	7

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55	Broadly Neutralizing Antibody Responses in a Large Longitudinal Sub-Saharan HIV Primary Infection Cohort. PLoS Pathogens, 2016, 12, e1005369.	2.1	241
56	Assigning and visualizing germline genes in antibody repertoires. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140240.	1.8	20
57	HIV Transmission Networks in the San Diegoâ€"Tijuana Border Region. EBioMedicine, 2015, 2, 1456-1463.	2.7	51
58	Recreational Fish-Findersâ€"An Inexpensive Alternative to Scientific Echo-Sounders for Unravelling the Links between Marine Top Predators and Their Prey. PLoS ONE, 2015, 10, e0140936.	1.1	9
59	The genomes of many yam species contain transcriptionally active endogenous geminiviral sequences that may be functionally expressed. Virus Evolution, 2015, 1, vev002.	2.2	30
60	RDP4: Detection and analysis of recombination patterns in virus genomes. Virus Evolution, 2015, 1, vev003.	2.2	2,621
61	RELAX: Detecting Relaxed Selection in a Phylogenetic Framework. Molecular Biology and Evolution, 2015, 32, 820-832.	3.5	535
62	Less Is More: An Adaptive Branch-Site Random Effects Model for Efficient Detection of Episodic Diversifying Selection. Molecular Biology and Evolution, 2015, 32, 1342-1353.	3.5	631
63	Gene-Wide Identification of Episodic Selection. Molecular Biology and Evolution, 2015, 32, 1365-1371.	3.5	493
64	Next generation sequencing improves detection of drug resistance mutations in infants after PMTCT failure. Journal of Clinical Virology, 2015, 62, 48-53.	1.6	36
65	On the Validity of Evolutionary Models with Site-Specific Parameters. PLoS ONE, 2014, 9, e94534.	1.1	12
66	R2-equitability is satisfiable. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2160-E2160.	3.3	13
67	IDEPI: Rapid Prediction of HIV-1 Antibody Epitopes and Other Phenotypic Features from Sequence Data Using a Flexible Machine Learning Platform. PLoS Computational Biology, 2014, 10, e1003842.	1.5	24
68	Evidence of Pervasive Biologically Functional Secondary Structures within the Genomes of Eukaryotic Single-Stranded DNA Viruses. Journal of Virology, 2014, 88, 1972-1989.	1.5	31
69	Identification of broadly neutralizing antibody epitopes in the HIV-1 envelope glycoprotein using evolutionary models. Virology Journal, 2013, 10, 347.	1.4	14
70	FUBAR: A Fast, Unconstrained Bayesian AppRoximation for Inferring Selection. Molecular Biology and Evolution, 2013, 30, 1196-1205.	3.5	1,056
71	Detecting Individual Sites Subject to Episodic Diversifying Selection. PLoS Genetics, 2012, 8, e1002764.	1.5	1,455
72	Degenerate Primer IDs and the Birthday Problem. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1330-E1330.	3.3	21

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73	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. Methods in Molecular Biology, 2012, 856, 239-272.	0.4	31
74	Deep Sequencing Reveals Minor Protease Resistance Mutations in Patients Failing a Protease Inhibitor Regimen. Journal of Virology, 2012, 86, 6231-6237.	1.5	63
75	Modeling HIV-1 Drug Resistance as Episodic Directional Selection. PLoS Computational Biology, 2012, 8, e1002507.	1.5	36
76	A Random Effects Branch-Site Model for Detecting Episodic Diversifying Selection. Molecular Biology and Evolution, 2011, 28, 3033-3043.	3.5	383
77	Non-Negative Matrix Factorization for Learning Alignment-Specific Models of Protein Evolution. PLoS ONE, 2011, 6, e28898.	1.1	11
78	HIV Coinfection Provides Insights for the Design of Vaccine Cocktails to Elicit Broadly Neutralizing Antibodies. Journal of Virology, 0, , .	1.5	0