

Matthew Bashton

List of Publications by Year in descending order

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33
papers

3,283
citations

394390

19
h-index

477281

29
g-index

38
all docs

38
docs citations

38
times ranked

7294
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
2	Structure, function and evolution of multidomain proteins. <i>Current Opinion in Structural Biology</i> , 2004, 14, 208-216.	5.7	379
3	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
4	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	10.0	269
5	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	7.3	232
6	The Generation of New Protein Functions by the Combination of Domains. <i>Structure</i> , 2007, 15, 85-99.	3.3	176
7	Supra-domains: Evolutionary Units Larger than Single Protein Domains. <i>Journal of Molecular Biology</i> , 2004, 336, 809-823.	4.2	157
8	The geometry of domain combination in proteins 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2002, 315, 927-939.	4.2	135
9	Small Molecule Subgraph Detector (SMSD) toolkit. <i>Journal of Cheminformatics</i> , 2009, 1, 12.	6.1	117
10	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
11	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>iScience</i> , 2021, 24, 103353.	4.1	57
12	Critical roles of arginine in growth and biofilm development by <i>Streptococcus gordonii</i> . <i>Molecular Microbiology</i> , 2015, 97, 281-300.	2.5	56
13	High prevalence of focal and multi-focal somatic genetic variants in the human brain. <i>Nature Communications</i> , 2018, 9, 4257.	12.8	54
14	PROCOGNATE: a cognate ligand domain mapping for enzymes. <i>Nucleic Acids Research</i> , 2007, 36, D618-D622.	14.5	42
15	The role of the RAS pathway in iAMP21-ALL. <i>Leukemia</i> , 2016, 30, 1824-1831.	7.2	38
16	Crowdsourcing genomic analyses of ash and ash dieback – power to the people. <i>GigaScience</i> , 2013, 2, 2.	6.4	29
17	Cognate Ligand Domain Mapping for Enzymes. <i>Journal of Molecular Biology</i> , 2006, 364, 836-852.	4.2	26
18	SH2B3 inactivation through CN-LOH 12q is uniquely associated with B-cell precursor ALL with iAMP21 or other chromosome 21 gain. <i>Leukemia</i> , 2019, 33, 1881-1894.	7.2	26

#	ARTICLE	IF	CITATIONS
19	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. <i>Lancet Microbe</i> , The, 2022, 3, e151-e158.	7.3	25
20	Persistent SARS-CoV-2 infection in patients with secondary antibody deficiency: successful clearance following combination casirivimab and imdevimab (REGN-COV2) monoclonal antibody therapy. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 85.	3.8	23
21	Minimal methylation classifier (MIMIC): A novel method for derivation and rapid diagnostic detection of disease-associated DNA methylation signatures. <i>Scientific Reports</i> , 2017, 7, 13421.	3.3	21
22	DNA methylation profiling identifies novel markers of progression in hepatitis B-related chronic liver disease. <i>Clinical Epigenetics</i> , 2016, 8, 48.	4.1	20
23	Dynamic clonal progression in xenografts of acute lymphoblastic leukemia with intrachromosomal amplification of chromosome 21. <i>Haematologica</i> , 2018, 103, 634-644.	3.5	13
24	IKZF1 Deletions with COBL Breakpoints Are Not Driven by RAG-Mediated Recombination Events in Acute Lymphoblastic Leukemia. <i>Translational Oncology</i> , 2019, 12, 726-732.	3.7	7
25	Concordance of copy number abnormality detection using SNP arrays and Multiplex Ligation-dependent Probe Amplification (MLPA) in acute lymphoblastic leukaemia. <i>Scientific Reports</i> , 2020, 10, 45.	3.3	7
26	Single-Cell Multi-Omics Reveals the Genetic, Cellular and Molecular Landscape of <i>TP53</i> Mutated Leukemic Transformation in MPN. <i>Blood</i> , 2021, 138, 3-3.	1.4	7
27	Domain-ligand mapping for enzymes. <i>Journal of Molecular Recognition</i> , 2010, 23, 194-208.	2.1	6
28	Molecular characterization and clinical outcome of B-cell precursor acute lymphoblastic leukemia with IG-MYC rearrangement. <i>Haematologica</i> , 2023, 108, 717-731.	3.5	6
29	SPEAR: Systematic ProtEin AnnotatoR. <i>Bioinformatics</i> , 2022, 38, 3827-3829.	4.1	1
30	Integrated pathway analysis of malignant rhabdoid tumour identifies key SMARCB1-pathways and therapeutic opportunities. <i>European Journal of Cancer</i> , 2016, 69, S51.	2.8	0
31	A Whole Genome In Vivo Crispr Screen in Primary ALL Predicts Leukaemic Relapse. <i>Blood</i> , 2015, 126, 2619-2619.	1.4	0
32	A Genome-Wide CRISPR Screen Implicates MYC Dysregulation in TCF3-PBX1 B-ALL. <i>Blood</i> , 2018, 132, 3915-3915.	1.4	0
33	Molecular Characterisation of Participants in the Phazar Trial Reveals Prognostic Impact of Mutations in Advanced-Phase-MPN. <i>Blood</i> , 2020, 136, 40-41.	1.4	0