

Brett Trost

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9509703/publications.pdf>

Version: 2024-02-01

58
papers

2,251
citations

218381

26
h-index

253896

43
g-index

67
all docs

67
docs citations

67
times ranked

3681
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex Autism Spectrum Disorder with Epilepsy, Strabismus and Self-Injurious Behaviors in a Patient with a De Novo Heterozygous POLR2A Variant. <i>Genes</i> , 2022, 13, 470.	1.0	3
2	Biallelic PAN2 variants in individuals with a syndromic neurodevelopmental disorder and multiple congenital anomalies. <i>European Journal of Human Genetics</i> , 2022, 30, 611-618.	1.4	4
3	Genome-wide tandem repeat expansions contribute to schizophrenia risk. <i>Molecular Psychiatry</i> , 2022, 27, 3692-3698.	4.1	20
4	Chromosomal-level reference genome assembly of the North American wolverine (<i>Gulo gulo</i>). <i>Genome Biology</i> , 2022, 23, 1062.	0.8	2
5	Enrichment of loss-of-function and copy number variants in ventricular cardiomyopathy genes in atrial fibrillation. <i>Europace</i> , 2021, 23, 844-850.	0.7	15
6	An Epigenetically Distinct Subset of Children With Autism Spectrum Disorder Resulting From Differences in Blood Cell Composition. <i>Frontiers in Neurology</i> , 2021, 12, 612817.	1.1	5
7	Discovery of genomic variation across a generation. <i>Human Molecular Genetics</i> , 2021, 30, R174-R186.	1.4	9
8	A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. <i>Npj Genomic Medicine</i> , 2021, 6, 91.	1.7	9
9	Genome Sequencing as a Diagnostic Test in Children With Unexplained Medical Complexity. <i>JAMA Network Open</i> , 2020, 3, e2018109.	2.8	47
10	Genome-wide detection of tandem DNA repeats that are expanded in autism. <i>Nature</i> , 2020, 586, 80-86.	13.7	155
11	Clinical and associated inflammatory biomarker features predictive of short-term outcomes in non-systemic juvenile idiopathic arthritis. <i>Rheumatology</i> , 2020, 59, 2402-2411.	0.9	11
12	ExpansionHunter Denovo: a computational method for locating known and novel repeat expansions in short-read sequencing data. <i>Genome Biology</i> , 2020, 21, 102.	3.8	114
13	Associations of clinical and inflammatory biomarker clusters with juvenile idiopathic arthritis categories. <i>Rheumatology</i> , 2020, 59, 1066-1075.	0.9	9
14	A large data resource of genomic copy number variation across neurodevelopmental disorders. <i>Npj Genomic Medicine</i> , 2019, 4, 26.	1.7	118
15	Impact of DNA source on genetic variant detection from human whole-genome sequencing data. <i>Journal of Medical Genetics</i> , 2019, 56, 809-817.	1.5	32
16	Length of Uninterrupted CAG, Independent of Polyglutamine Size, Results in Increased Somatic Instability, Hastening Onset of Huntington Disease. <i>American Journal of Human Genetics</i> , 2019, 104, 1116-1126.	2.6	130
17	Glutaminase Deficiency Caused by Short Tandem Repeat Expansion in <i>GLS</i> . <i>New England Journal of Medicine</i> , 2019, 380, 1433-1441.	13.9	71
18	The Personal Genome Project Canada: findings from whole genome sequences of the inaugural 56 participants. <i>Cmaj</i> , 2018, 190, E126-E136.	0.9	57

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19	A Comprehensive Workflow for Read Depth-Based Identification of Copy-Number Variation from Whole-Genome Sequence Data. <i>American Journal of Human Genetics</i> , 2018, 102, 142-155.	2.6	156
20	Transcriptome analysis of response to <i>Plasmodiophora brassicae</i> infection in the <i>Arabidopsis</i> shoot and root. <i>BMC Genomics</i> , 2018, 19, 23.	1.2	96
21	Conservation of kinase-phosphorylation site pairings: Evidence for an evolutionarily dynamic phosphoproteome. <i>PLoS ONE</i> , 2018, 13, e0202036.	1.1	6
22	Technological advances for interrogating the human kinome. <i>Biochemical Society Transactions</i> , 2017, 45, 65-77.	1.6	26
23	<i>De Novo</i> Genome and Transcriptome Assembly of the Canadian Beaver (<i>Castor canadensis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 755-773.	0.8	18
24	Computational Analysis of the Predicted Evolutionary Conservation of Human Phosphorylation Sites. <i>PLoS ONE</i> , 2016, 11, e0152809.	1.1	9
25	DAPPLE 2: a Tool for the Homology-Based Prediction of Post-Translational Modification Sites. <i>Journal of Proteome Research</i> , 2016, 15, 2760-2767.	1.8	20
26	Investigation of the cause of geographic disparities in IDEXX ELISA sensitivity in serum samples from <i>Mycobacterium bovis</i> -infected cattle. <i>Scientific Reports</i> , 2016, 6, 22763.	1.6	20
27	Concordance between RNA-sequencing data and DNA microarray data in transcriptome analysis of proliferative and quiescent fibroblasts. <i>Royal Society Open Science</i> , 2015, 2, 150402.	1.1	20
28	Rapamycin reduces fibroblast proliferation without causing quiescence and induces STAT5A/B-mediated cytokine production. <i>Nucleus</i> , 2015, 6, 490-506.	0.6	16
29	Characterization of the Host Response to Pichinde Virus Infection in the Syrian Golden Hamster by Species-Specific Kinome Analysis. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 646-657.	2.5	16
30	Induction of tissue- and stressor-specific kinomic responses in chickens exposed to hot and cold stresses. <i>Poultry Science</i> , 2015, 94, 1333-1345.	1.5	24
31	EpiC: a rational pipeline for epitope immunogenicity characterization. <i>Bioinformatics</i> , 2015, 31, 2388-2390.	1.8	11
32	Case study: using sequence homology to identify putative phosphorylation sites in an evolutionarily distant species (honeybee). <i>Briefings in Bioinformatics</i> , 2015, 16, 820-829.	3.2	5
33	Peptide Arrays for Kinome Analysis of Livestock Species. <i>Frontiers in Veterinary Science</i> , 2014, 1, 4.	0.9	11
34	A Comparison of the Chicken and Turkey Proteomes and Phosphoproteomes in the Development of Poultry-Specific Immuno-Metabolism Kinome Peptide Arrays. <i>Frontiers in Veterinary Science</i> , 2014, 1, 22.	0.9	29
35	Identification of developmentally-specific kinotypes and mechanisms of <i>Varroa</i> mite resistance through whole-organism, kinome analysis of honeybee. <i>Frontiers in Genetics</i> , 2014, 5, 139.	1.1	40
36	Equivalent input produces different output in the UniFrac significance test. <i>BMC Bioinformatics</i> , 2014, 15, 278.	1.2	4

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37	Ebola Virus Modulates Transforming Growth Factor β 2 Signaling and Cellular Markers of Mesenchyme-Like Transition in Hepatocytes. <i>Journal of Virology</i> , 2014, 88, 9877-9892.	1.5	49
38	A better sequence-read simulator program for metagenomics. <i>BMC Bioinformatics</i> , 2014, 15, S14.	1.2	43
39	Divergent Immune Responses to Mycobacterium avium subsp. paratuberculosis Infection Correlate with Kinome Responses at the Site of Intestinal Infection. <i>Infection and Immunity</i> , 2013, 81, 2861-2872.	1.0	33
40	Kinotypes: stable species- and individual-specific profiles of cellular kinase activity. <i>BMC Genomics</i> , 2013, 14, 854.	1.2	17
41	Computational phosphorylation site prediction in plants using random forests and organism-specific instance weights. <i>Bioinformatics</i> , 2013, 29, 686-694.	1.8	46
42	DAPPLE: a pipeline for the homology-based prediction of phosphorylation sites. <i>Bioinformatics</i> , 2013, 29, 1693-1695.	1.8	37
43	PIIKA 2: An Expanded, Web-Based Platform for Analysis of Kinome Microarray Data. <i>PLoS ONE</i> , 2013, 8, e80837.	1.1	60
44	Systems Kinomics Demonstrates Congo Basin Monkeypox Virus Infection Selectively Modulates Host Cell Signaling Responses as Compared to West African Monkeypox Virus. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015701.	2.5	59
45	A Systematic Approach for Analysis of Peptide Array Kinome Data. <i>Science Signaling</i> , 2012, 5, pl2.	1.6	53
46	Complete Genome Sequence of the Beer Spoilage Organism <i>Pediococcus clausenii</i> ATCC BAA-344T. <i>Journal of Bacteriology</i> , 2012, 194, 1271-1272.	1.0	40
47	Comparing the Similarity of Different Groups of Bacteria to the Human Proteome. <i>PLoS ONE</i> , 2012, 7, e34007.	1.1	6
48	Pentamers Not Found in the Universal Proteome Can Enhance Antigen Specific Immune Responses and Adjuvant Vaccines. <i>PLoS ONE</i> , 2012, 7, e43802.	1.1	28
49	Computational prediction of eukaryotic phosphorylation sites. <i>Bioinformatics</i> , 2011, 27, 2927-2935.	1.8	145
50	The oligodeoxynucleotide sequences corresponding to never-expressed peptide motifs are mainly located in the non-coding strand. <i>BMC Bioinformatics</i> , 2010, 11, 383.	1.2	12
51	Analysis and comparison of the pan-genomic properties of sixteen well-characterized bacterial genera. <i>BMC Microbiology</i> , 2010, 10, 258.	1.3	9
52	Bacterial peptides are intensively present throughout the human proteome. <i>Self/nonself</i> , 2010, 1, 71-74.	2.0	26
53	No human protein is exempt from bacterial motifs, not even one. <i>Self/nonself</i> , 2010, 1, 328-334.	2.0	69
54	Statistical characterization of the GxxxG glycine repeats in the flagellar biosynthesis protein FliH and its Type III secretion homologue YscL. <i>BMC Microbiology</i> , 2009, 9, 72.	1.3	4

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55	Codon number shapes peptide redundancy in the universal proteome composition. <i>Peptides</i> , 2009, 30, 1940-1944.	1.2	16
56	Rare peptide segments are found significantly more often in proto-oncoproteins than control proteins: implications for immunology and oncology. <i>Journal of the Royal Society Interface</i> , 2009, 6, 123-127.	1.5	7
57	Strength in numbers: achieving greater accuracy in MHC-I binding prediction by combining the results from multiple prediction tools. <i>Immunome Research</i> , 2007, 3, 5.	0.1	56
58	Peptidology: short amino acid modules in cell biology and immunology. <i>Amino Acids</i> , 2007, 33, 703-707.	1.2	89