

# 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  | 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       |
| 2  | Genome-wide detection of tandem DNA repeats that are expanded in autism. <i>Nature</i> , 2020, 586, 80-86.   | 13.7 | 155       |
| 3  | Computational prediction of eukaryotic phosphorylation sites. <i>Bioinformatics</i> , 2011, 27, 2927-2935.   | 1.8  | 145       |
| 4  | 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       |
| 5  | A large data resource of genomic copy number variation across neurodevelopmental disorders. <i>Npj Genomic Medicine</i> , 2019, 4, 26.   | 1.7  | 118       |
| 6  | 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       |
| 7  | 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        |
| 8  | Peptidology: short amino acid modules in cell biology and immunology. <i>Amino Acids</i> , 2007, 33, 703-707.  | 1.2  | 89        |
| 9  | Glutaminase Deficiency Caused by Short Tandem Repeat Expansion in <i>&lt;i&gt;GLS&lt;/i&gt;</i> . <i>New England Journal of Medicine</i> , 2019, 380, 1433-1441.   | 13.9 | 71        |
| 10 | No human protein is exempt from bacterial motifs, not even one. <i>Self/nonself</i> , 2010, 1, 328-334.  | 2.0  | 69        |
| 11 | PIIKA 2: An Expanded, Web-Based Platform for Analysis of Kinome Microarray Data. <i>PLoS ONE</i> , 2013, 8, e80837.  | 1.1  | 60        |
| 12 | 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        |
| 13 | 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        |
| 14 | 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        |
| 15 | A Systematic Approach for Analysis of Peptide Array Kinome Data. <i>Science Signaling</i> , 2012, 5, pl2.  | 1.6  | 53        |
| 16 | Ebola Virus Modulates Transforming Growth Factor $\beta^2$ Signaling and Cellular Markers of Mesenchyme-Like Transition in Hepatocytes. <i>Journal of Virology</i> , 2014, 88, 9877-9892.  | 1.5  | 49        |
| 17 | Genome Sequencing as a Diagnostic Test in Children With Unexplained Medical Complexity. <i>JAMA Network Open</i> , 2020, 3, e2018109.  | 2.8  | 47        |
| 18 | Computational phosphorylation site prediction in plants using random forests and organism-specific instance weights. <i>Bioinformatics</i> , 2013, 29, 686-694.  | 1.8  | 46        |

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|----|---|-----|-----------|
| 19 | A better sequence-read simulator program for metagenomics. BMC Bioinformatics, 2014, 15, S14.   | 1.2 | 43        |
| 20 | Complete Genome Sequence of the Beer Spoilage Organism <i>Pediococcus clausenii</i> ATCC BAA-344T. Journal of Bacteriology, 2012, 194, 1271-1272.   | 1.0 | 40        |
| 21 | Identification of developmentally-specific kinotypes and mechanisms of <i>Varroa</i> mite resistance through whole-organism, kinome analysis of honeybee. Frontiers in Genetics, 2014, 5, 139.                      | 1.1 | 40        |
| 22 | DAPPLE: a pipeline for the homology-based prediction of phosphorylation sites. Bioinformatics, 2013, 29, 1693-1695.   | 1.8 | 37        |
| 23 | Divergent Immune Responses to <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Infection Correlate with Kinome Responses at the Site of Intestinal Infection. Infection and Immunity, 2013, 81, 2861-2872. | 1.0 | 33        |
| 24 | Impact of DNA source on genetic variant detection from human whole-genome sequencing data. Journal of Medical Genetics, 2019, 56, 809-817.  | 1.5 | 32        |
| 25 | A Comparison of the Chicken and Turkey Proteomes and Phosphoproteomes in the Development of Poultry-Specific Immuno-Metabolism Kinome Peptide Arrays. Frontiers in Veterinary Science, 2014, 1, 22.                 | 0.9 | 29        |
| 26 | Pentamers Not Found in the Universal Proteome Can Enhance Antigen Specific Immune Responses and Adjuvant Vaccines. PLoS ONE, 2012, 7, e43802.   | 1.1 | 28        |
| 27 | Bacterial peptides are intensively present throughout the human proteome. Self/nonself, 2010, 1, 71-74.   | 2.0 | 26        |
| 28 | Technological advances for interrogating the human kinome. Biochemical Society Transactions, 2017, 45, 65-77.   | 1.6 | 26        |
| 29 | Induction of tissue- and stressor-specific kinomic responses in chickens exposed to hot and cold stresses. Poultry Science, 2015, 94, 1333-1345.  | 1.5 | 24        |
| 30 | Concordance between RNA-sequencing data and DNA microarray data in transcriptome analysis of proliferative and quiescent fibroblasts. Royal Society Open Science, 2015, 2, 150402.                                  | 1.1 | 20        |
| 31 | DAPPLE 2: a Tool for the Homology-Based Prediction of Post-Translational Modification Sites. Journal of Proteome Research, 2016, 15, 2760-2767.   | 1.8 | 20        |
| 32 | Investigation of the cause of geographic disparities in IDEXX ELISA sensitivity in serum samples from <i>Mycobacterium bovis</i> -infected cattle. Scientific Reports, 2016, 6, 22763.                              | 1.6 | 20        |
| 33 | Genome-wide tandem repeat expansions contribute to schizophrenia risk. Molecular Psychiatry, 2022, 27, 3692-3698.   | 4.1 | 20        |
| 34 | <i>De Novo</i> Genome and Transcriptome Assembly of the Canadian Beaver (<i>Castor canadensis</i>). G3: Genes, Genomes, Genetics, 2017, 7, 755-773.   | 0.8 | 18        |
| 35 | Kinotypes: stable species- and individual-specific profiles of cellular kinase activity. BMC Genomics, 2013, 14, 854.   | 1.2 | 17        |
| 36 | Codon number shapes peptide redundancy in the universal proteome composition. Peptides, 2009, 30, 1940-1944.  | 1.2 | 16        |

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|----|---|-----|-----------|
| 37 | Rapamycin reduces fibroblast proliferation without causing quiescence and induces STAT5A/B-mediated cytokine production. <i>Nucleus</i> , 2015, 6, 490-506.   | 0.6 | 16        |
| 38 | 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        |
| 39 | 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        |
| 40 | 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        |
| 41 | Peptide Arrays for Kinome Analysis of Livestock Species. <i>Frontiers in Veterinary Science</i> , 2014, 1, 4.   | 0.9 | 11        |
| 42 | EpIC: a rational pipeline for epitope immunogenicity characterization. <i>Bioinformatics</i> , 2015, 31, 2388-2390.   | 1.8 | 11        |
| 43 | 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        |
| 44 | Analysis and comparison of the pan-genomic properties of sixteen well-characterized bacterial genera. <i>BMC Microbiology</i> , 2010, 10, 258.  | 1.3 | 9         |
| 45 | Computational Analysis of the Predicted Evolutionary Conservation of Human Phosphorylation Sites. <i>PLoS ONE</i> , 2016, 11, e0152809.   | 1.1 | 9         |
| 46 | Associations of clinical and inflammatory biomarker clusters with juvenile idiopathic arthritis categories. <i>Rheumatology</i> , 2020, 59, 1066-1075.  | 0.9 | 9         |
| 47 | Discovery of genomic variation across a generation. <i>Human Molecular Genetics</i> , 2021, 30, R174-R186.  | 1.4 | 9         |
| 48 | A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. <i>Npj Genomic Medicine</i> , 2021, 6, 91.   | 1.7 | 9         |
| 49 | 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         |
| 50 | Comparing the Similarity of Different Groups of Bacteria to the Human Proteome. <i>PLoS ONE</i> , 2012, 7, e34007.  | 1.1 | 6         |
| 51 | Conservation of kinase-phosphorylation site pairings: Evidence for an evolutionarily dynamic phosphoproteome. <i>PLoS ONE</i> , 2018, 13, e0202036.   | 1.1 | 6         |
| 52 | 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         |
| 53 | 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         |
| 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 | Equivalent input produces different output in the UniFrac significance test. BMC Bioinformatics, 2014, 15, 278.   | 1.2 | 4         |
| 56 | Biallelic PAN2 variants in individuals with a syndromic neurodevelopmental disorder and multiple congenital anomalies. European Journal of Human Genetics, 2022, 30, 611-618. | 1.4 | 4         |
| 57 | Complex Autism Spectrum Disorder with Epilepsy, Strabismus and Self-Injurious Behaviors in a Patient with a De Novo Heterozygous POLR2A Variant. Genes, 2022, 13, 470.        | 1.0 | 3         |
| 58 | Chromosomal-level reference genome assembly of the North American wolverine ( <i>Gulo gulo</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6                                       | 0.8 | 2         |