

Peter B Mcgarvey

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

9,590
citations

471509

17
h-index

501196

28
g-index

35
all docs

35
docs citations

35
times ranked

14834
citing authors

#	ARTICLE	IF	CITATIONS
1	UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489.	14.5	4,709
2	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. <i>Bioinformatics</i> , 2015, 31, 926-932.	4.1	1,223
3	UniRef: comprehensive and non-redundant UniProt reference clusters. <i>Bioinformatics</i> , 2007, 23, 1282-1288.	4.1	1,144
4	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
5	Infrastructure for the life sciences: design and implementation of the UniProt website. <i>BMC Bioinformatics</i> , 2009, 10, 136.	2.6	405
6	The CPTAC Data Portal: A Resource for Cancer Proteomics Research. <i>Journal of Proteome Research</i> , 2015, 14, 2707-2713.	3.7	309
7	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
8	Expression of the Rabies Virus Glycoprotein in Transgenic Tomatoes. <i>Nature Biotechnology</i> , 1995, 13, 1484-1487.	17.5	210
9	Distinct lymphocyte antigens 6 (Ly6) family members Ly6D, Ly6E, Ly6K and Ly6H drive tumorigenesis and clinical outcome. <i>Oncotarget</i> , 2016, 7, 11165-11193.	1.8	76
10	A crowdsourcing open platform for literature curation in UniProt. <i>PLoS Biology</i> , 2021, 19, e3001464.	5.6	74
11	A comprehensive protein-centric ID mapping service for molecular data integration. <i>Bioinformatics</i> , 2011, 27, 1190-1191.	4.1	70
12	ClinGen Allele Registry links information about genetic variants. <i>Human Mutation</i> , 2018, 39, 1690-1701.	2.5	48
13	UniProt genomic mapping for deciphering functional effects of missense variants. <i>Human Mutation</i> , 2019, 40, 694-705.	2.5	29
14	iTextMine: integrated text-mining system for large-scale knowledge extraction from the literature. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	22
15	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. <i>BMC Immunology</i> , 2014, 15, 61.	2.2	21
16	Protein networks in induced sputum from smokers and COPD patients. <i>International Journal of COPD</i> , 2015, 10, 1957.	2.3	21
17	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput Omics Data. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-19.	5.7	19
18	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. <i>PLoS ONE</i> , 2009, 4, e7162.	2.5	18

#	ARTICLE	IF	CITATIONS
19	eGARD: Extracting associations between genomic anomalies and drug responses from text. PLoS ONE, 2017, 12, e0189663.	2.5	14
20	ClinGen Cancer Somatic Working Group - standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 247-258.	0.7	13
21	ClinGen Cancer Somatic Working Group " standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. , 2018, , .		12
22	De novo assembly and annotation of transcriptomes from two cultivars of Cannabis sativa with different cannabinoid profiles. Gene, 2020, 762, 145026.	2.2	11
23	Informatics and data quality at collaborative multicenter Breast and Colon Cancer Family Registries. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e125-e128.	4.4	10
24	Initiation of rrn transcription in chloroplasts of Euglena gracilis bacillaris. Current Genetics, 1988, 14, 493-500.	1.7	9
25	Eye-Tracking Study to Enhance Usability of Molecular Diagnostics Reports in Cancer Precision Medicine. JCO Precision Oncology, 2018, 2, 1-11.	3.0	6
26	Processing of chloroplast ribosomal RNA transcripts in Euglena gracilis bacillaris. Current Genetics, 1989, 15, 363-370.	1.7	5
27	Future of Evidence Synthesis in Precision Oncology: Between Systematic Reviews and Biocuration. JCO Precision Oncology, 2018, 2, 1.	3.0	5
28	Computational clustering for viral reference proteomes: Table 1.. Bioinformatics, 2016, 32, 2041-2043.	4.1	3
29	Protein-Centric Data Integration for Functional Analysis of Comparative Proteomics Data. Methods in Molecular Biology, 2011, 694, 323-339.	0.9	3
30	Protein bioinformatics. , 2008, , 203-222.		1
31	Design and Implementation of the UniProt Website. Nature Precedings, 2008, , .	0.1	0
32	In silico Analysis of Vaccination Adverse Events. Journal of Allergy and Clinical Immunology, 2015, 135, AB104.	2.9	0
33	Cloud-based Semantic Integration and Knowledge Discovery Systems in Precision Medicine. , 2018, , .		0