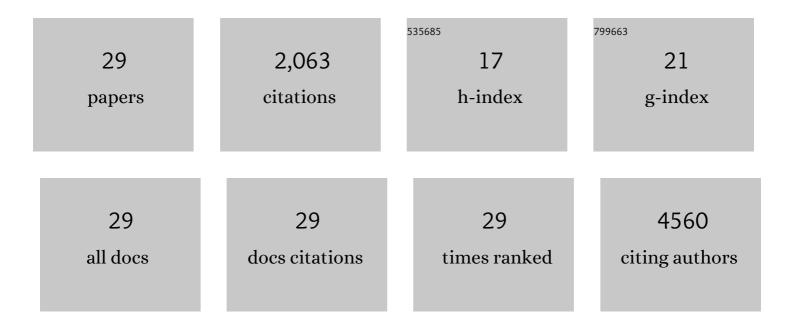
Moyez Dharsee

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4394756/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Big Data Needs Big Governance: Best Practices From Brain-CODE, the Ontario-Brain Institute's Neuroinformatics Platform. Frontiers in Genetics, 2019, 10, 191.	1.1	11
2	Plasma microRNA expression levels and their targeted pathways in patients with major depressive disorder who are responsive to duloxetine treatment. Journal of Psychiatric Research, 2019, 110, 38-44.	1.5	31
3	The CAMH Neuroinformatics Platform: A Hospital-Focused Brain-CODE Implementation. Frontiers in Neuroinformatics, 2018, 12, 77.	1.3	8
4	Brain-CODE: A Secure Neuroinformatics Platform for Management, Federation, Sharing and Analysis of Multi-Dimensional Neuroscience Data. Frontiers in Neuroinformatics, 2018, 12, 28.	1.3	43
5	Designing and Implementing a Privacy Preserving Record Linkage Protocol. International Journal of Population Data Science, 2018, 3, .	0.1	1
6	Standardization of electroencephalography for multi-site, multi-platform and multi-investigator studies: insights from the canadian biomarker integration network in depression. Scientific Reports, 2017, 7, 7473.	1.6	28
7	Discovering biomarkers for antidepressant response: protocol from the Canadian biomarker integration network in depression (CAN-BIND) and clinical characteristics of the first patient cohort. BMC Psychiatry, 2016, 16, 105.	1.1	114
8	miR-221/222 Are Involved in Response to Sunitinib Treatment in Metastatic Renal Cell Carcinoma. Molecular Therapy, 2015, 23, 1748-1758.	3.7	73
9	Exploring high dimensional data with Butterfly: a novel classification algorithm based on discrete dynamical systems. Bioinformatics, 2014, 30, 712-718.	1.8	15
10	MicroRNA Signature Helps Distinguish Early from Late Biochemical Failure in Prostate Cancer. Clinical Chemistry, 2013, 59, 1595-1603.	1.5	50
11	Identification of the IGF1/PI3K/NF κB/ERK gene signalling networks associated with chemotherapy resistance and treatment response in high-grade serous epithelial ovarian cancer. BMC Cancer, 2013, 13, 549.	1.1	95
12	Use of microRNA signature to distinguish early from late biochemical failure in prostate cancer Journal of Clinical Oncology, 2013, 31, 194-194.	0.8	0
13	Abstract 810: Integrative genomic and transcriptomic analysis in idenfitication of biomarkers of chemoresistance in serous epithelial ovarian cancer , 2013, , .		0
14	Abstract A53: Biomarkers of chemotherapy resistance in serous epithelial ovarian cancer identified by integrative genomic and transcriptomic analysis. , 2013, , .		0
15	Proteomics Analyses of Human Optic Nerve Head Astrocytes Following Biomechanical Strain. Molecular and Cellular Proteomics, 2012, 11, M111.012302.	2.5	57
16	EMT transcription factors snail and slug directly contribute to cisplatin resistance in ovarian cancer. BMC Cancer, 2012, 12, 91.	1.1	325
17	Proteomics Analyses of Activated Human Optic Nerve Head Lamina Cribrosa Cells following Biomechanical Strain. , 2012, 53, 3806.		40
18	Proteomic Analyses Reveal High Expression of Decorin and Endoplasmin (HSP90B1) Are Associated with Breast Cancer Metastasis and Decreased Survival. PLoS ONE, 2012, 7, e30992.	1.1	80

MOYEZ DHARSEE

#	Article	IF	CITATIONS
19	Abstract 3004: Biomarker identification through integrative bioinformatics analysis of serous epithelial ovarian cancer tumor samples. , 2012, , .		Ο
20	Abstract 3645: Integrative molecular profiling in serous epithelial ovarian cancer for identification of biomarkers of chemoresistance. , 2012, , .		0
21	Applying mass spectrometry based proteomic technology to advance the understanding of multiple myeloma. Journal of Hematology and Oncology, 2010, 3, 13.	6.9	19
22	Urinary Protein Profiles in a Rat Model for Diabetic Complications. Molecular and Cellular Proteomics, 2009, 8, 2145-2158.	2.5	28
23	Rapid Evolution of Functional Complexity in a Domain Family. Science Signaling, 2009, 2, ra50.	1.6	57
24	Multiple myeloma phosphotyrosine proteomic profile associated with FGFR3 expression, ligand activation, and drug inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20127-20132.	3.3	43
25	DESIGN AND ANALYSIS OF QUANTITATIVE DIFFERENTIAL PROTEOMICS INVESTIGATIONS USING LC-MS TECHNOLOGY. Journal of Bioinformatics and Computational Biology, 2008, 06, 107-123.	0.3	18
26	Largeâ€scale mapping of human protein–protein interactions by mass spectrometry. Molecular Systems Biology, 2007, 3, 89.	3.2	850
27	A High-Throughput Bioinformatics Platform for Mass Spectrometry-Based Proteomics. , 2007, , 71-88.		0
28	Differential Analysis of Membrane Proteins in Mouse Fore- and Hindbrain Using a Label-Free Approach. Journal of Proteome Research, 2006, 5, 2701-2710.	1.8	56
29	The reproducible acquisition of comparative liquid chromatography/tandem mass spectrometry data from complex biological samples. Rapid Communications in Mass Spectrometry, 2004, 18, 1697-1710.	0.7	21