

Moyez Dharsee

List of Publications by Year in descending order

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29
papers

2,063
citations

535685

17
h-index

799663

21
g-index

29
all docs

29
docs citations

29
times ranked

4560
citing authors

#	ARTICLE	IF	CITATIONS
1	Big Data Needs Big Governance: Best Practices From Brain-CODE, the Ontario-Brain Institute's Neuroinformatics Platform. <i>Frontiers in Genetics</i> , 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. <i>Journal of Psychiatric Research</i> , 2019, 110, 38-44.	1.5	31
3	The CAMH Neuroinformatics Platform: A Hospital-Focused Brain-CODE Implementation. <i>Frontiers in Neuroinformatics</i> , 2018, 12, 77.	1.3	8
4	Brain-CODE: A Secure Neuroinformatics Platform for Management, Federation, Sharing and Analysis of Multi-Dimensional Neuroscience Data. <i>Frontiers in Neuroinformatics</i> , 2018, 12, 28.	1.3	43
5	Designing and Implementing a Privacy Preserving Record Linkage Protocol. <i>International Journal of Population Data Science</i> , 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. <i>Scientific Reports</i> , 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. <i>BMC Psychiatry</i> , 2016, 16, 105.	1.1	114
8	miR-221/222 Are Involved in Response to Sunitinib Treatment in Metastatic Renal Cell Carcinoma. <i>Molecular Therapy</i> , 2015, 23, 1748-1758.	3.7	73
9	Exploring high dimensional data with Butterfly: a novel classification algorithm based on discrete dynamical systems. <i>Bioinformatics</i> , 2014, 30, 712-718.	1.8	15
10	MicroRNA Signature Helps Distinguish Early from Late Biochemical Failure in Prostate Cancer. <i>Clinical Chemistry</i> , 2013, 59, 1595-1603.	1.5	50
11	Identification of the IGF1/PI3K/NF- κ B/ERK gene signalling networks associated with chemotherapy resistance and treatment response in high-grade serous epithelial ovarian cancer. <i>BMC Cancer</i> , 2013, 13, 549.	1.1	95
12	Use of microRNA signature to distinguish early from late biochemical failure in prostate cancer.. <i>Journal of Clinical Oncology</i> , 2013, 31, 194-194.	0.8	0
13	Abstract 810: Integrative genomic and transcriptomic analysis in identification 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. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.012302.	2.5	57
16	EMT transcription factors snail and slug directly contribute to cisplatin resistance in ovarian cancer. <i>BMC Cancer</i> , 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 Endoplasmic Reticulum Chaperone (HSP90B1) Are Associated with Breast Cancer Metastasis and Decreased Survival. <i>PLoS ONE</i> , 2012, 7, e30992.	1.1	80

#	ARTICLE	IF	CITATIONS
19	Abstract 3004: Biomarker identification through integrative bioinformatics analysis of serous epithelial ovarian cancer tumor samples. , 2012, , .		0
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. <i>Journal of Hematology and Oncology</i> , 2010, 3, 13.	6.9	19
22	Urinary Protein Profiles in a Rat Model for Diabetic Complications. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2145-2158.	2.5	28
23	Rapid Evolution of Functional Complexity in a Domain Family. <i>Science Signaling</i> , 2009, 2, ra50.	1.6	57
24	Multiple myeloma phosphotyrosine proteomic profile associated with FGFR3 expression, ligand activation, and drug inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20127-20132.	3.3	43
25	DESIGN AND ANALYSIS OF QUANTITATIVE DIFFERENTIAL PROTEOMICS INVESTIGATIONS USING LC-MS TECHNOLOGY. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 107-123.	0.3	18
26	Large-scale mapping of human protein-protein interactions by mass spectrometry. <i>Molecular Systems Biology</i> , 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. <i>Journal of Proteome Research</i> , 2006, 5, 2701-2710.	1.8	56
29	The reproducible acquisition of comparative liquid chromatography/tandem mass spectrometry data from complex biological samples. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 1697-1710.	0.7	21