

Margherita Squillario

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5560021/publications.pdf>

Version: 2024-02-01

17
papers

260
citations

1163117

8
h-index

1125743

13
g-index

19
all docs

19
docs citations

19
times ranked

645
citing authors

#	ARTICLE	IF	CITATIONS
1	A Reassessment of IgM Memory Subsets in Humans. <i>Journal of Immunology</i> , 2015, 195, 3716-3724.	0.8	99
2	New miRNA Signature Heralds Human NK Cell Subsets at Different Maturation Steps: Involvement of miR-146a-5p in the Regulation of KIR Expression. <i>Frontiers in Immunology</i> , 2018, 9, 2360.	4.8	47
3	Effect of Size and Heterogeneity of Samples on Biomarker Discovery: Synthetic and Real Data Assessment. <i>PLoS ONE</i> , 2012, 7, e32200.	2.5	23
4	Different Features of Tumor-Associated NK Cells in Patients With Low-Grade or High-Grade Peritoneal Carcinomatosis. <i>Frontiers in Immunology</i> , 2019, 10, 1963.	4.8	21
5	Tracing CLL-biased stereotyped immunoglobulin gene rearrangements in normal B cell subsets using a high-throughput immunogenetic approach. <i>Molecular Medicine</i> , 2020, 26, 25.	4.4	17
6	A telescope GWAS analysis strategy, based on SNPs-genes-pathways ensemble and on multivariate algorithms, to characterize late onset Alzheimer's disease. <i>Scientific Reports</i> , 2020, 10, 12063.	3.3	11
7	A computational procedure for functional characterization of potential marker genes from molecular data: Alzheimer's as a case study. <i>BMC Medical Genomics</i> , 2011, 4, 55.	1.5	10
8	Regenerative medicine for the treatment of Teno-desmic injuries of the equine. A series of 150 horses treated with platelet-derived growth factors. <i>In Vivo</i> , 2014, 28, 1119-23.	1.3	9
9	Knowledge Driven Variable Selection (KDVS) – a new approach to enrichment analysis of gene signatures obtained from high-throughput data. <i>Source Code for Biology and Medicine</i> , 2013, 8, 2.	1.7	7
10	Effects of Chronic Arginase Inhibition with Norvaline on Tau Pathology and Brain Glucose Metabolism in Alzheimer's Disease Mice. <i>Neurochemical Research</i> , 2022, 47, 1255-1268.	3.3	6
11	Transplantation Induces Profound Changes in the Transcriptional Asset of Hematopoietic Stem Cells: Identification of Specific Signatures Using Machine Learning Techniques. <i>Journal of Clinical Medicine</i> , 2020, 9, 1670.	2.4	4
12	Enhancing Interpretability of Gene Signatures with Prior Biological Knowledge. <i>Microarrays (Basel)</i> , 2014, 3, 14.	1.4	3
13	A Machine Learning Pipeline for Discriminant Pathways Identification. <i>Lecture Notes in Computer Science</i> , 2012, , 36-48.	1.3	3
14	Identification of Pathway Signatures in Parkinson's Disease with Gene Ontology and Sparse Regularization. <i>Lecture Notes in Computer Science</i> , 2014, , 259-273.	1.3	0
15	High-Throughput Ig Sequencing of Paired Blood and Spleen Samples Allows a Redefinition of Memory IgM Subsets in Humans. <i>Blood</i> , 2014, 124, 565-565.	1.4	0
16	Adenine: A HPC-Oriented Tool for Biological Data Exploration. <i>Lecture Notes in Computer Science</i> , 2019, , 51-59.	1.3	0
17	Next Generation Sequencing and Microrna Assay in a Cohort of Patients Affected By Myelodysplastic Syndromes. an Analysis of Clinical and Genotypic Features. <i>Blood</i> , 2019, 134, 5414-5414.	1.4	0