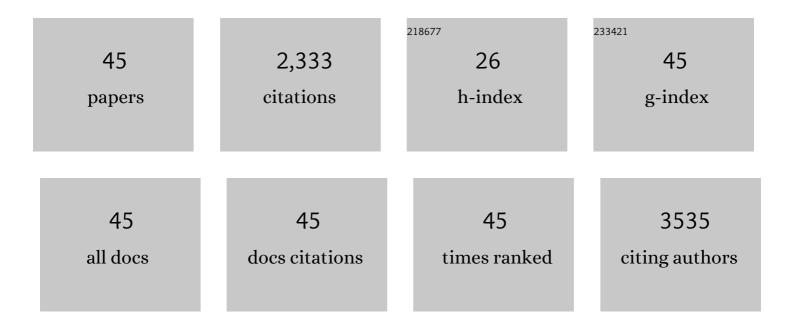
Giuseppina Maccarrone

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Prefrontal cortex shotgun proteome analysis reveals altered calcium homeostasis and immune system imbalance in schizophrenia. European Archives of Psychiatry and Clinical Neuroscience, 2009, 259, 151-163. | 3.2 | 180 |
| 2 | Proteomic analysis of dorsolateral prefrontal cortex indicates the involvement of cytoskeleton, oligodendrocyte, energy metabolism and new potential markers in schizophrenia. Journal of Psychiatric Research, 2009, 43, 978-986. | 3.1 | 165 |
| 3 | Proteome analysis of the thalamus and cerebrospinal fluid reveals glycolysis dysfunction and potential biomarkers candidates for schizophrenia. Journal of Psychiatric Research, 2010, 44, 1176-1189. | 3.1 | 158 |
| 4 | Alterations in oligodendrocyte proteins, calcium homeostasis and new potential markers in schizophrenia anterior temporal lobe are revealed by shotgun proteome analysis. Journal of Neural Transmission, 2009, 116, 275-289. | 2.8 | 137 |
| 5 | MALDI Imaging Identifies Prognostic Seven-Protein Signature of Novel Tissue Markers in Intestinal-Type Gastric Cancer. American Journal of Pathology, 2011, 179, 2720-2729. | 3.8 | 127 |
| 6 | Proteomics and Metabolomics Analysis of a Trait Anxiety Mouse Model Reveals Divergent Mitochondrial Pathways. Biological Psychiatry, 2011, 70, 1074-1082. | 1.3 | 123 |
| 7 | MALDI imaging mass spectrometry reveals COX7A2, TAGLN2 and S100-A10 as novel prognostic markers in Barrett's adenocarcinoma. Journal of Proteomics, 2012, 75, 4693-4704. | 2.4 | 90 |
| 8 | Mining the human cerebrospinal fluid proteome by immunodepletion and shotgun mass spectrometry. Electrophoresis, 2004, 25, 2402-2412. | 2.4 | 88 |
| 9 | Neddylation inhibition impairs spine development, destabilizes synapses and deteriorates cognition. Nature Neuroscience, 2015, 18, 239-251. | 14.8 | 88 |
| 10 | Proteome analysis of schizophrenia brain tissue. World Journal of Biological Psychiatry, 2010, 11, 110-120. | 2.6 | 82 |
| 11 | Cerebrospinal Fluid Biomarkers for Major Depression Confirm Relevance of Associated Pathophysiology. Neuropsychopharmacology, 2012, 37, 1013-1025. | 5.4 | 82 |
| 12 | Proteomic and Metabolomic Profiling of a Trait Anxiety Mouse Model Implicate Affected Pathways. Molecular and Cellular Proteomics, 2011, 10, M111.008110. | 3.8 | 68 |
| 13 | Different cAMP sources are critically involved in G protein–coupled receptor CRHR1 signaling. Journal of Cell Biology, 2016, 214, 181-195. | 5.2 | 61 |
| 14 | Profiling of mouse synaptosome proteome and phosphoproteome by IEF. Electrophoresis, 2010, 31, 1294-1301. | 2.4 | 60 |
| 15 | Stable Isotope Metabolic Labeling with a Novel 15N-Enriched Bacteria Diet for Improved Proteomic Analyses of Mouse Models for Psychopathologies. PLoS ONE, 2009, 4, e7821. | 2.5 | 59 |
| 16 | Psychiatric patient stratification using biosignatures based on cerebrospinal fluid protein expression clusters. Journal of Psychiatric Research, 2013, 47, 1572-1580. | 3.1 | 57 |
| 17 | Ketamine's antidepressant effect is mediated by energy metabolism and antioxidant defense system. Scientific Reports, 2017, 7, 15788. | 3.3 | 54 |
| 18 | Stress-primed secretory autophagy promotes extracellular BDNF maturation by enhancing MMP9 secretion. Nature Communications, 2021, 12, 4643. | 12.8 | 50 |

| # | Article | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Tau Deletion Prevents Stress-Induced Dendritic Atrophy in Prefrontal Cortex: Role of Synaptic Mitochondria. Cerebral Cortex, 2017, 27, bhw057. | 2.9 | 49 |
| 20 | Methylglyoxalâ€mediated anxiolysis involves increased protein modification and elevated expression of glyoxalase 1 in the brain. Journal of Neurochemistry, 2010, 113, 1240-1251. | 3.9 | 45 |
| 21 | Proteomic and metabolomic profiling reveals time-dependent changes in hippocampal metabolism upon paroxetine treatment and biomarker candidates. Journal of Psychiatric Research, 2013, 47, 289-298. | 3.1 | 44 |
| 22 | Multi-omics analysis identifies mitochondrial pathways associated with anxiety-related behavior. PLoS Genetics, 2019, 15, e1008358. | 3.5 | 43 |
| 23 | FKBP5 Gene Expression Predicts Antidepressant Treatment Outcome in Depression. International Journal of Molecular Sciences, 2019, 20, 485. | 4.1 | 40 |
| 24 | QuantiSpec — Quantitative mass spectrometry data analysis of 15N-metabolically labeled proteins. Journal of Proteomics, 2009, 71, 601-608. | 2.4 | 28 |
| 25 | Shotgun Mass Spectrometry Workflow Combining IEF and LC-MALDI-TOF/TOF. Protein Journal, 2010, 29, 99-102. | 1.6 | 27 |
| 26 | The ¹⁵ N isotope effect in <i>Escherichia coli</i> : A neutron can make the difference. Proteomics, 2012, 12, 3121-3128. | 2.2 | 27 |
| 27 | B-Raf and CRHR1 Internalization Mediate Biphasic ERK1/2 Activation by CRH in Hippocampal HT22 Cells. Molecular Endocrinology, 2013, 27, 491-510. | 3.7 | 27 |
| 28 | MALDI imaging mass spectrometry analysis—A new approach for protein mapping in multiple sclerosis brain lesions. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1047, 131-140. | 2.3 | 26 |
| 29 | Regulation of proteins mediating neurodegeneration in experimental autoimmune encephalomyelitis and multiple sclerosis. Proteomics - Clinical Applications, 2009, 3, 1273-1287. | 1.6 | 25 |
| 30 | Blood Mononuclear Cell Proteome Suggests Integrin and Ras Signaling as Critical Pathways for Antidepressant Treatment Response. Biological Psychiatry, 2014, 76, e15-e17. | 1.3 | 22 |
| 31 | The quest for brain disorder biomarkers. Journal of Medical Investigation, 2005, 52, 231-235. | 0.5 | 21 |
| 32 | Shotgun mass spectrometry analysis of the human thalamus proteome. Journal of Separation Science, 2009, 32, 1231-1236. | 2.5 | 21 |
| 33 | A MS data search method for improved ¹⁵ Nâ€labeled protein identification. Proteomics, 2009, 9, 4265-4270. | 2.2 | 21 |
| 34 | Phosphopeptide enrichment by IEF. Electrophoresis, 2006, 27, 4585-4595. | 2.4 | 19 |
| 35 | Characterization of a Protein Interactome by Co-Immunoprecipitation and Shotgun Mass Spectrometry. Methods in Molecular Biology, 2017, 1546, 223-234. | 0.9 | 17 |
| 36 | Proteome profiling of peripheral mononuclear cells from human blood. Proteomics, 2013, 13, 893-897. | 2.2 | 16 |

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|----|--|-----|-----------|
| 37 | Ketamine's Effects on the Glutamatergic and GABAergic Systems: A Proteomics and Metabolomics Study in Mice. Molecular Neuropsychiatry, 2019, 5, 42-51. | 2.9 | 15 |
| 38 | In-depth analysis of the human CSF proteome using protein prefractionation. Clinical Proteomics, 2004, 1, 333-364. | 2.1 | 14 |
| 39 | The ¹⁵ <scp>N</scp> isotope effect as a means for correlating phenotypic alterations and affected pathways in a trait anxiety mouse model. Proteomics, 2012, 12, 2421-2427. | 2.2 | 14 |
| 40 | Brain Quantitative Proteomics Combining GeLC-MS and Isotope-Coded Protein Labeling (ICPL). Methods in Molecular Biology, 2014, 1156, 175-185. | 0.9 | 12 |
| 41 | 15N metabolic labeling: Evidence for a stable isotope effect on plasma protein levels and peptide chromatographic retention times. Journal of Proteomics, 2013, 88, 27-33. | 2.4 | 11 |
| 42 | Stable isotope metabolic labeling suggests differential turnover of the DPYSL protein family. Proteomics - Clinical Applications, 2016, 10, 1269-1272. | 1.6 | 8 |
| 43 | Variability assessment of ¹⁵ N metabolic labeling-based proteomics workflow in mouse plasma and brain. Molecular BioSystems, 2015, 11, 1536-1542. | 2.9 | 6 |
| 44 | Using 15N-Metabolic Labeling for Quantitative Proteomic Analyses. Methods in Molecular Biology, 2017, 1546, 235-243. | 0.9 | 4 |
| 45 | Protein Profiling and Phosphoprotein Analysis by Isoelectric Focusing. Methods in Molecular Biology, 2015, 1295, 293-303. | 0.9 | 2 |