

Ivan Matic

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

5,576
citations

159585

30
h-index

302126

39
g-index

45
all docs

45
docs citations

45
times ranked

6570
citing authors

#	ARTICLE	IF	CITATIONS
1	ADP-ribose transferases, an update on function and nomenclature. FEBS Journal, 2022, 289, 7399-7410.	4.7	150
2	Serine-ubiquitination regulates Golgi morphology and the secretory pathway upon Legionella infection. Cell Death and Differentiation, 2021, 28, 2957-2969.	11.2	23
3	Structural basis for protein glutamylation by the Legionella pseudokinase SidJ. Nature Communications, 2021, 12, 6174.	12.8	8
4	The 2021 FASEB science research conference on NAD metabolism and signaling. Aging, 2021, 13, 24924-24930.	3.1	1
5	An HPF1/PARP1-Based Chemical Biology Strategy for Exploring ADP-Ribosylation. Cell, 2020, 183, 1086-1102.e23.	28.9	64
6	Specificity of reversible ADP-ribosylation and regulation of cellular processes. Critical Reviews in Biochemistry and Molecular Biology, 2018, 53, 64-82.	5.2	82
7	Interplay of Histone Marks with Serine ADP-Ribosylation. Cell Reports, 2018, 24, 3488-3502.e5.	6.4	76
8	Serine is the major residue for ADP-ribosylation upon DNA damage. ELife, 2018, 7, .	6.0	167
9	Nonlocalized Searching of HCD Data for Fast and Sensitive Identification of ADP-Ribosylated Peptides. Methods in Molecular Biology, 2018, 1813, 255-269.	0.9	1
10	Serine ADP-Ribosylation Depends on HPF1. Molecular Cell, 2017, 65, 932-940.e6.	9.7	249
11	Mass spectrometry for serine ADP-ribosylation? Think o-glycosylation!. Nucleic Acids Research, 2017, 45, 6259-6264.	14.5	42
12	Mitotic post-translational modifications of histones promote chromatin compaction <i>in vitro</i> . Open Biology, 2017, 7, 170076.	3.6	56
13	Serine ADP-ribosylation reversal by the hydrolase ARH3. ELife, 2017, 6, .	6.0	163
14	Phosphoribosylation of Ubiquitin Promotes Serine Ubiquitination and Impairs Conventional Ubiquitination. Cell, 2016, 167, 1636-1649.e13.	28.9	234
15	Serine is a new target residue for endogenous ADP-ribosylation on histones. Nature Chemical Biology, 2016, 12, 998-1000.	8.0	189
16	Disruption of Macrodomain Protein SCO6735 Increases Antibiotic Production in Streptomyces coelicolor. Journal of Biological Chemistry, 2016, 291, 23175-23187.	3.4	16
17	Processing of protein ADP-ribosylation by Nudix hydrolases. Biochemical Journal, 2015, 468, 293-301.	3.7	113
18	Identification of a Class of Protein ADP-Ribosylating Sirtuins in Microbial Pathogens. Molecular Cell, 2015, 59, 309-320.	9.7	79

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19	Proteome-wide identification of SUMO modification sites by mass spectrometry. <i>Nature Protocols</i> , 2015, 10, 1374-1388.	12.0	56
20	Proteome-Wide Identification of SUMO2 Modification Sites. <i>Science Signaling</i> , 2014, 7, rs2.	3.6	174
21	Family-wide analysis of poly(ADP-ribose) polymerase activity. <i>Nature Communications</i> , 2014, 5, 4426.	12.8	386
22	Deficiency of terminal ADP-ribose protein glycohydrolase TARG1/C6orf130 in neurodegenerative disease. <i>EMBO Journal</i> , 2013, 32, 1225-1237.	7.8	263
23	Detection and Quantitation of SUMO Chains by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2012, 832, 239-247.	0.9	8
24	Mediator Phosphorylation Prevents Stress Response Transcription During Non-stress Conditions. <i>Journal of Biological Chemistry</i> , 2012, 287, 44017-44026.	3.4	33
25	The ubiquitin E1 enzyme Ube1 mediates NEDD8 activation under diverse stress conditions. <i>Cell Cycle</i> , 2012, 11, 1142-1150.	2.6	108
26	Reanalysis of phosphoproteomics data uncovers ADP-ribosylation sites. <i>Nature Methods</i> , 2012, 9, 771-772.	19.0	79
27	Absolute SILAC-Compatible Expression Strain Allows Sumo-2 Copy Number Determination in Clinical Samples. <i>Journal of Proteome Research</i> , 2011, 10, 4869-4875.	3.7	39
28	Comparative Proteomic Analysis Identifies a Role for SUMO in Protein Quality Control. <i>Science Signaling</i> , 2011, 4, rs4.	3.6	153
29	Purification and identification of endogenous polySUMO conjugates. <i>EMBO Reports</i> , 2011, 12, 142-148.	4.5	155
30	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010, 6, 450.	7.2	324
31	Regulation of Translesion Synthesis DNA Polymerase ϵ by Monoubiquitination. <i>Molecular Cell</i> , 2010, 37, 396-407.	9.7	148
32	Site-Specific Identification of SUMO-2 Targets in Cells Reveals an Inverted SUMOylation Motif and a Hydrophobic Cluster SUMOylation Motif. <i>Molecular Cell</i> , 2010, 39, 641-652.	9.7	255
33	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	12.0	769
34	System-Wide Changes to SUMO Modifications in Response to Heat Shock. <i>Science Signaling</i> , 2009, 2, ra24.	3.6	415
35	Identification of SUMO Target Proteins by Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2009, 497, 19-31.	0.9	27
36	Phosphorylation of SUMO-1 Occurs <i>in Vivo</i> and Is Conserved through Evolution. <i>Journal of Proteome Research</i> , 2008, 7, 4050-4057.	3.7	36

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37	In Vivo Identification of Human Small Ubiquitin-like Modifier Polymerization Sites by High Accuracy Mass Spectrometry and an in Vitro to in Vivo Strategy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 132-144.	3.8	251
38	The Ubiquitin-Proteasome System Is a Key Component of the SUMO-2/3 Cycle. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2107-2122.	3.8	143
39	Proteomic-based analysis of nuclear signaling: PLC β 1 affects the expression of the splicing factor SRp20 in Friend erythroleukemia cells. <i>Proteomics</i> , 2006, 6, 5725-5734.	2.2	30