

# Sina Ghaemmaghmi

## List of Publications by Year in descending order

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45  
papers

10,246  
citations

257450

24  
h-index

223800

46  
g-index

57  
all docs

57  
docs citations

57  
times ranked

14303  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global analysis of protein expression in yeast. <i>Nature</i> , 2003, 425, 737-741.	27.8	3,407
2	Genome-Wide Analysis in Vivo of Translation with Nucleotide Resolution Using Ribosome Profiling. <i>Science</i> , 2009, 324, 218-223.	12.6	3,283
3	Single-cell proteomic analysis of <i>S. cerevisiae</i> reveals the architecture of biological noise. <i>Nature</i> , 2006, 441, 840-846.	27.8	1,434
4	Analysis of proteome dynamics in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14508-14513.	7.1	314
5	Quantitative protein stability measurement in vivo. , 2001, 8, 879-882.		154
6	Continuous Quinacrine Treatment Results in the Formation of Drug-Resistant Prions. <i>PLoS Pathogens</i> , 2009, 5, e1000673.	4.7	135
7	A Data Processing Pipeline for Mammalian Proteome Dynamics Studies Using Stable Isotope Metabolic Labeling. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010728.	3.8	124
8	A General Mass Spectrometry-Based Assay for the Quantitation of Protein-Ligand Binding Interactions in Solution. <i>Journal of the American Chemical Society</i> , 2002, 124, 10256-10257.	13.7	123
9	Discovery of 2-Aminothiazoles as Potent Antiprion Compounds. <i>Journal of Virology</i> , 2010, 84, 3408-3412.	3.4	122
10	Construction, Verification and Experimental Use of Two Epitope-Tagged Collections of Budding Yeast Strains. <i>Comparative and Functional Genomics</i> , 2005, 6, 2-16.	2.0	80
11	Cell division modulates prion accumulation in cultured cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17971-17976.	7.1	80
12	Time-resolved Analysis of Proteome Dynamics by Tandem Mass Tags and Stable Isotope Labeling in Cell Culture (TMT-SILAC) Hyperplexing. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3551-3563.	3.8	79
13	Global analysis of methionine oxidation provides a census of folding stabilities for the human proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6081-6090.	7.1	68
14	Compartment Modeling for Mammalian Protein Turnover Studies by Stable Isotope Metabolic Labeling. <i>Analytical Chemistry</i> , 2012, 84, 4014-4021.	6.5	64
15	Global Analysis of Cellular Protein Flux Quantifies the Selectivity of Basal Autophagy. <i>Cell Reports</i> , 2016, 14, 2426-2439.	6.4	57
16	Folding Kinetics of a Fluorescent Variant of Monomeric $\lambda$ Repressor. <i>Biochemistry</i> , 1998, 37, 9179-9185.	2.5	50
17	Conformational Transformation and Selection of Synthetic Prion Strains. <i>Journal of Molecular Biology</i> , 2011, 413, 527-542.	4.2	49
18	Intracerebral Infusion of Antisense Oligonucleotides Into Prion-infected Mice. <i>Molecular Therapy - Nucleic Acids</i> , 2012, 1, e9.	5.1	45

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19	Redox-mediated regulation of an evolutionarily conserved cross- $\beta^2$ structure formed by the TDP43 low complexity domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28727-28734.	7.1	44
20	Interspecies Differences in Proteome Turnover Kinetics Are Correlated With Life Spans and Energetic Demands. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100041.	3.8	44
21	Cross-species Comparison of Proteome Turnover Kinetics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 580-591.	3.8	40
22	Quantitative Analysis of in Vivo Methionine Oxidation of the Human Proteome. <i>Journal of Proteome Research</i> , 2020, 19, 624-633.	3.7	39
23	Developmentally regulated H2Av buffering via dynamic sequestration to lipid droplets in <i>Drosophila</i> embryos. <i>ELife</i> , 2018, 7, .	6.0	34
24	Convergent Replication of Mouse Synthetic Prion Strains. <i>American Journal of Pathology</i> , 2013, 182, 866-874.	3.8	33
25	A Survey of Antiprion Compounds Reveals the Prevalence of Non-PrP Molecular Targets. <i>Journal of Biological Chemistry</i> , 2011, 286, 27718-27728.	3.4	25
26	Chemical Induction of Misfolded Prion Protein Conformers in Cell Culture. <i>Journal of Biological Chemistry</i> , 2010, 285, 10415-10423.	3.4	24
27	Pharmacokinetics of Quinacrine Efflux from Mouse Brain via the P-glycoprotein Efflux Transporter. <i>PLoS ONE</i> , 2012, 7, e39112.	2.5	24
28	Proteome-wide modulation of degradation dynamics in response to growth arrest. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10329-E10338.	7.1	24
29	Successes and Challenges in Phenotype-Based Lead Discovery for Prion Diseases. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 6919-6929.	6.4	22
30	Methionine oxidation within the prion protein. <i>Prion</i> , 2020, 14, 193-205.	1.8	21
31	MicroRNA-574 regulates FAM210A expression and influences pathological cardiac remodeling. <i>EMBO Molecular Medicine</i> , 2021, 13, e12710.	6.9	21
32	Increased Degradation Rates in the Components of the Mitochondrial Oxidative Phosphorylation Chain in the Cerebellum of Old Mice. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 32.	3.4	18
33	JNK modifies neuronal metabolism to promote proteostasis and longevity. <i>Aging Cell</i> , 2019, 18, e12849.	6.7	18
34	Comprehensive Structure-Activity Profiling of Micheliolide and its Targeted Proteome in Leukemia Cells via Probe-Guided Late-Stage C-H Functionalization. <i>ACS Central Science</i> , 2021, 7, 841-857.	11.3	18
35	Antiprion compounds that reduce PrP <sup>Sc</sup> levels in dividing and stationary-phase cells. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 7999-8012.	3.0	17
36	Potential mechanisms linking SIRT activity and hypoxic 2-hydroxyglutarate generation: no role for direct enzyme (de)acetylation. <i>Biochemical Journal</i> , 2017, 474, 2829-2839.	3.7	17

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37	Kinetics of Precursor Labeling in Stable Isotope Labeling in Cell Cultures (SILAC) Experiments. <i>Analytical Chemistry</i> , 2014, 86, 11334-11341.	6.5	15
38	Protein folding stabilities are a major determinant of oxidation rates for buried methionine residues. <i>Journal of Biological Chemistry</i> , 2022, 298, 101872.	3.4	15
39	Global analysis of cellular protein flux quantifies the selectivity of basal autophagy. <i>Autophagy</i> , 2016, 12, 1411-1412.	9.1	13
40	Ion-Current-Based Temporal Proteomic Profiling of Influenza-A-Virus-Infected Mouse Lungs Revealed Underlying Mechanisms of Altered Integrity of the Lung Microvascular Barrier. <i>Journal of Proteome Research</i> , 2016, 15, 540-553.	3.7	11
41	Biology and Genetics of PrP Prion Strains. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a026922.	6.2	11
42	Strain Specificity and Drug Resistance in Anti-Prion Therapy. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 2397-2406.	2.1	11
43	Accurate Proteomewide Measurement of Methionine Oxidation in Aging Mouse Brains. <i>Journal of Proteome Research</i> , 2022, 21, 1495-1509.	3.7	10
44	Global analysis of protein degradation in prion infected cells. <i>Scientific Reports</i> , 2020, 10, 10800.	3.3	2
45	Analysis of Proteome Dynamics in Mice by Isotopic Labeling. <i>Methods in Molecular Biology</i> , 2014, 1156, 111-131.	0.9	2