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dbGSH: a database of S-glutathionylation

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#	Paper	IF	Citations
49	S-glutathionylation reactions in mitochondrial function and disease. <i>Frontiers in Cell and Developmental Biology</i> , 2014 , 2, 68	5.7	80
48	Glutathionylation of the aquaporin-2 water channel: a novel post-translational modification modulated by the oxidative stress. <i>Journal of Biological Chemistry</i> , 2014 , 289, 27807-13	5.4	25
47	Glutathione: new roles in redox signaling for an old antioxidant. Frontiers in Pharmacology, 2014 , 5, 196	5.6	368
46	Characterization and identification of protein O-GlcNAcylation sites with substrate specificity. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 16, S1	3.6	23
45	Glutathione in Cellular Redox Homeostasis: Association with the Excitatory Amino Acid Carrier 1 (EAAC1). <i>Molecules</i> , 2015 , 20, 8742-58	4.8	74
44	Teaching the fundamentals of electron transfer reactions in mitochondria and the production and detection of reactive oxygen species. <i>Redox Biology</i> , 2015 , 4, 381-98	11.3	155
43	Characterization and identification of ubiquitin conjugation sites with E3 ligase recognition specificities. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 1, S1	3.6	16
42	PGluS: prediction of protein S-glutathionylation sites with multiple features and analysis. <i>Molecular BioSystems</i> , 2015 , 11, 923-9		19
41	MDD-SOH: exploiting maximal dependence decomposition to identify S-sulfenylation sites with substrate motifs. <i>Bioinformatics</i> , 2016 , 32, 165-72	7.2	17
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37	Proteomic approaches to quantify cysteine reversible modifications in aging and neurodegenerative diseases. <i>Proteomics - Clinical Applications</i> , 2016 , 10, 1159-1177	3.1	23
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35	SOHSite: incorporating evolutionary information and physicochemical properties to identify protein S-sulfenylation sites. <i>BMC Genomics</i> , 2016 , 17 Suppl 1, 9	4.5	35
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33	Regulation of DJ-1 by Glutaredoxin 1 in Vivo: Implications for Parkinson Disease. <i>Biochemistry</i> , 2016 , 55, 4519-32	3.2	22

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32	dbPTM 2016: 10-year anniversary of a resource for post-translational modification of proteins. <i>Nucleic Acids Research</i> , 2016 , 44, D435-46	20.1	125
31	Photodynamic treatment with hexyl-aminolevulinate mediates reversible thiol oxidation in core oxidative stress signaling proteins. <i>Molecular BioSystems</i> , 2016 , 12, 796-805		5
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29	Redox Proteomics Applied to the Thiol Secretome. <i>Antioxidants and Redox Signaling</i> , 2017 , 26, 299-312	8.4	13
28	Mechanism of ROS scavenging and antioxidant signalling by redox metallic and fullerene nanomaterials: Potential implications in ROS associated degenerative disorders. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 802-813	4	79
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26	ROS and RNS signalling: adaptive redox switches through oxidative/nitrosative protein modifications. <i>Free Radical Research</i> , 2018 , 52, 507-543	4	142
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10	A global map of associations between types of protein posttranslational modifications and human genetic diseases. <i>IScience</i> , 2021 , 24, 102917	6.1	2
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8	Analysis of Cysteine Redox Post-Translational Modifications in Cell Biology and Drug Pharmacology. <i>Methods in Molecular Biology</i> , 2017 , 1558, 191-212	1.4	5
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7	SwissPalm: Protein Palmitoylation database. <i>F1000Research</i> , 2015 , 4, 261 A global map of the impact of deletion of Post-Translational Modification sites in genetic diseases.	3.6	133
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6	A global map of the impact of deletion of Post-Translational Modification sites in genetic diseases.		· · ·
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6 5 4	A global map of the impact of deletion of Post-Translational Modification sites in genetic diseases. Hsp70 in Redox Homeostasis <i>Cells</i> , 2022 , 11, Profiling the Site of Protein CoAlation and Coenzyme A Stabilization Interactions. <i>Antioxidants</i> , 2022 , 11, 1362 Targeting the YXXIMotifs of the SARS Coronaviruses 1 and 2 ORF3a Peptides by In Silico Analysis	7.9	7