

Combining Results of Multiple Search Engines in Proteo

Molecular and Cellular Proteomics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Bioinformatic Approaches to Increase Proteome Coverage. <i>Comprehensive Analytical Chemistry</i> , 2014, , 385-419.	1.3	1
2	JUMP: A Tag-based Database Search Tool for Peptide Identification with High Sensitivity and Accuracy. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3663-3673.	3.8	117
3	Machine learning applications in proteomics research: How the past can boost the future. <i>Proteomics</i> , 2014, 14, 353-366.	2.2	52
4	Quantitative label-free redox proteomics of reversible cysteine oxidation in red blood cell membranes. <i>Free Radical Biology and Medicine</i> , 2014, 71, 90-98.	2.9	15
5	<scp>MSDA</scp>, a proteomics software suite for inâ€depth <scp>M</scp>ass <scp>S</scp>pectrometry <scp>D</scp>ata <scp>A</scp>nalysis using grid computing. <i>Proteomics</i> , 2014, 14, 1014-1019.	2.2	51
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13	Analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes Using Mass Spectrometry*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3105-3117.	3.8	188
14	Effective Leveraging of Targeted Search Spaces for Improving Peptide Identification in Tandem Mass Spectrometry Based Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 5169-5178.	3.7	20
15	Peptide identification in â€shotgunâ€ proteomics using tandem mass spectrometry: Comparison of search engine algorithms. <i>Journal of Analytical Chemistry</i> , 2015, 70, 1614-1619.	0.9	2
16	Quantitative Proteomic Analysis of Histone Modifications. <i>Chemical Reviews</i> , 2015, 115, 2376-2418.	47.7	306
17	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015, 33, 22-24.	17.5	460
18	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441.	12.0	319

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20	Food Proteins and Peptides. <i>Comprehensive Analytical Chemistry</i> , 2015, 68, 309-357.	1.3	9
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