Rovshan G Sadygov

List of Publications by Year
in descending order

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60 papers	5,681 citations	201674 27 h-index	123424 61 g-index
61 all docs	61 docs citations	61 times ranked	6949 citing authors

#	Article	IF	Citations
1	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	6.5	6
2	Using Heavy Mass Isotopomers for Protein Turnover in Heavy Water Metabolic Labeling. Journal of Proteome Research, 2021, 20, 2035-2041.	3.7	7
3	A novel estimator of the interaction matrix in Graphical Gaussian Model of omics data using the entropy of non-equilibrium systems. Bioinformatics, 2021, 37, 837-844.	4.1	2
4	Partial Isotope Profiles Are Sufficient for Protein Turnover Analysis Using Closed-Form Equations of Mass Isotopomer Dynamics. Analytical Chemistry, 2020, 92, 14747-14753.	6.5	12
5	High-Resolution Mass Spectrometry for In Vivo Proteome Dynamics using Heavy Water Metabolic Labeling. International Journal of Molecular Sciences, 2020, 21, 7821.	4.1	5
6	Timepoint Selection Strategy for In Vivo Proteome Dynamics from Heavy Water Metabolic Labeling and LCâ€“MS. Journal of Proteome Research, 2020, 19, 2105-2112.	3.7	8
7	Proteome dynamics from heavy water metabolic labeling and peptide tandem mass spectrometry. International Journal of Mass Spectrometry, 2019, 445, 116194.	1.5	8
8	Calculation of the Protein Turnover Rate Using the Number of Incorporated 2H Atoms and Proteomics Analysis of a Single Labeled Sample. Analytical Chemistry, 2019, 91, 14340-14351.	6.5	9
9	Another look at matrix correlations. Bioinformatics, 2019, 35, 4748-4753.	4.1	2
10	Poisson Model To Generate Isotope Distribution for Biomolecules. Journal of Proteome Research, 2018, 17, 751-758.	3.7	15
11	d2ome, Software for in Vivo Protein Turnover Analysis Using Heavy Water Labeling and LCâ€“MS, Reveals Alterations of Hepatic Proteome Dynamics in a Mouse Model of NAFLD. Journal of Proteome Research, 2018, 17, 3740-3748.	3.7	42
12	Hepatic Mitochondrial Defects in a Nonalcoholic Fatty Liver Disease Mouse Model Are Associated with Increased Degradation of Oxidative Phosphorylation Subunits. Molecular and Cellular Proteomics, 2018, 17, 2371-2386.	3.8	59
13	PPARgamma agonists rescue increased phosphorylation of FGF14 at S226 in the Tg2576 mouse model of Alzheimer's disease. Experimental Neurology, 2017, 295, 1-17.	4.1	35
14	Increased serotransferrin and ceruloplasmin turnover in diet-controlled patients with type 2 diabetes. Free Radical Biology and Medicine, 2017, 113, 461-469.	2.9	41
15	Predicting the protein half-life in tissue from its cellular properties. PLoS ONE, 2017, 12, e0180428.	2.5	11
16	Gaussian Process Modeling of Protein Turnover. Journal of Proteome Research, 2016, 15, 2115-2122.	3.7	25
17	Proteome Dynamics Reveals Pro-Inflammatory Remodeling of Plasma Proteome in a Mouse Model of NAFLD. Journal of Proteome Research, 2016, 15, 3388-3404.	3.7	15
18	Integrative proteomic analysis reveals reprograming tumor necrosis factor signaling in epithelial mesenchymal transition. Journal of Proteomics, 2016, 148, 126-138.	2.4	29

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19	Tracer-based estimates of protein flux in cases of incomplete product renewal: evidence and implications of heterogeneity in collagen turnover. American Journal of Physiology - Endocrinology and Metabolism, 2015, 309, E115-E121.	3.5	16
20	Using SEQUEST with Theoretically Complete Sequence Databases. Journal of the American Society for Mass Spectrometry, 2015, 26, 1858-1864.	2.8	10
21	Mixed-effects model of epithelialâ€“mesenchymal transition reveals rewiring of signaling networks. Cellular Signalling, 2015, 27, 1413-1425.	3.6	25
22	Current Bioinformatics Challenges in Proteome Dynamics using Heavy Water-based Metabolic Labeling. Journal of Data Mining in Genomics & Proteomics, 2014, 05, e112.	0.5	2
23	The Cancer Drug Tamoxifen: A Potential Therapeutic Treatment for Spinal Cord Injury. Journal of Neurotrauma, 2014, 31, 268-283.	3.4	37
24	Cognitive Enhancing Treatment with a PPARÎ³ Agonist Normalizes Dentate Granule Cell Presynaptic Function in Tg2576 APP Mice. Journal of Neuroscience, 2014, 34, 1028-1036.	3.6	48
25	Cardiac mitochondrial proteome dynamics with heavy water reveals stable rate of mitochondrial protein synthesis in heart failure despite decline in mitochondrial oxidative capacity. Journal of Molecular and Cellular Cardiology, 2014, 75, 88-97.	1.9	34
26	Use of singular value decomposition analysis to differentiate phosphorylated precursors in strong cation exchange fractions. Electrophoresis, 2014, 35, 3498-3503.	2.4	5
27	Use of Theoretical Peptide Distributions in Phosphoproteome Analysis. Journal of Proteome Research, 2013, 12, 3207-3214.	3.7	1
28	Assessment of cardiac proteome dynamics with heavy water: slower protein synthesis rates in interfibrillar than subsarcolemmal mitochondria. American Journal of Physiology - Heart and Circulatory Physiology, 2013, 304, H1201-H1214.	3.2	66
29	Detection of Structural and Metabolic Changes in Traumatically Injured Hippocampus by Quantitative Differential Proteomics. Journal of Neurotrauma, 2013, 30, 775-788.	3.4	32
30	High Mass Accuracy Phosphopeptide Identification Using Tandem Mass Spectra. International Journal of Proteomics, 2012, 2012, 1-5.	2.0	4
31	Cognitive Enhancement with Rosiglitazone Links the Hippocampal PPARÎ³ and ERK MAPK Signaling Pathways. Journal of Neuroscience, 2012, 32, 16725-16735.	3.6	99
32	Improved Mass Defect Model for Theoretical Tryptic Peptides. Analytical Chemistry, 2012, 84, 3026-3032.	6.5	11
33	Generalized linear and mixed models for label-free shotgun proteomics. Statistics and Its Interface, 2012, 5, 89-98.	0.3	6
34	Examining Troughs in the Mass Distribution of All Theoretically Possible Tryptic Peptides. Journal of Proteome Research, 2011, 10, 4150-4157.	3.7	25
35	SVM Model for Quality Assessment of Medium Resolution Mass Spectra from¹⁸O-Water Labeling Experiments. Journal of Proteome Research, 2011, 10, 2095-2103.	3.7	7
36	A parallel method for enumerating amino acid compositions and masses of all theoretical peptides. BMC Bioinformatics, 2011, 12, 432.	2.6	11

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37	Measuring protein synthesis using metabolic 2H labeling, high-resolution mass spectrometry, and an algorithm. Analytical Biochemistry, 2011, 412, 47-55.	2.4	64
38	Bioinformatics Tools for Mass Spectrometry-Based High-Throughput Quantitative Proteomics Platforms. Current Proteomics, 2011, 8, 125-137.	0.3	6
39	Comparison of Programmatic Approaches for Efficient Accessing to mzML Files. Journal of Data Mining in Genomics & Proteomics, 2011, 02, .	0.5	4
40	Altered Retinoic Acid Metabolism in Diabetic Mouse Kidney Identified by 18O Isotopic Labeling and 2D Mass Spectrometry. PLoS ONE, 2010, 5, e11095.	2.5	45
41	Using Power Spectrum Analysis to Evaluate18O-Water Labeling Data Acquired from Low Resolution Mass Spectrometers. Journal of Proteome Research, 2010, 9, 4306-4312.	3.7	23
42	A New Probabilistic Database Search Algorithm for ETD Spectra. Journal of Proteome Research, 2009, 8, 3198-3205.	3.7	33
43	Charger:Â Combination of Signal Processing and Statistical Learning Algorithms for Precursor Charge-State Determination from Electron-Transfer Dissociation Spectra. Analytical Chemistry, 2008, 80, 376-386.	6.5	18
44	Assigning in vivo carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching. International Journal of Mass Spectrometry, 2007, 259, 161-173.	1.5	11
45	ChromAlign:Â A Two-Step Algorithmic Procedure for Time Alignment of Three-Dimensional LCâ^'MS Chromatographic Surfaces. Analytical Chemistry, 2006, 78, 8207-8217.	6.5	101
46	Central Limit Theorem as an Approximation for Intensity-Based Scoring Function. Analytical Chemistry, 2006, 78, 89-95.	6.5	31
47	Large-scale database searching using tandem mass spectra: Looking up the answer in the back of the book. Nature Methods, 2004, 1, 195-202.	19.0	375
48	MS1, MS2, and SQTâ€"three unified, compact, and easily parsed file formats for the storage of shotgun proteomic spectra and identifications. Rapid Communications in Mass Spectrometry, 2004, 18, 2162-2168.	1.5	350
49	Statistical Models for Protein Validation Using Tandem Mass Spectral Data and Protein Amino Acid Sequence Databases. Analytical Chemistry, 2004, 76, 1664-1671.	6.5	127
50	A Model for Random Sampling and Estimation of Relative Protein Abundance in Shotgun Proteomics. Analytical Chemistry, 2004, 76, 4193-4201.	6.5	2,280
51	A Hypergeometric Probability Model for Protein Identification and Validation Using Tandem Mass Spectral Data and Protein Sequence Databases. Analytical Chemistry, 2003, 75, 3792-3798.	6.5	198
52	A Correlation Algorithm for the Automated Quantitative Analysis of Shotgun Proteomics Data. Analytical Chemistry, 2003, 75, 6912-6921.	6.5	276
53	Shotgun identification of protein modifications from protein complexes and lens tissue. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7900-7905.	7.1	571
54	Code Developments to Improve the Efficiency of Automated MS/MS Spectra Interpretation. Journal of Proteome Research, 2002, 1, 211-215.	3.7	198

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55	Dynamics of primary charge separation in bacterial photosynthesis using the multilevel Redfield-Davies secular approach. International Journal of Quantum Chemistry, 2002, 87, 254-263.	2.0	3
56	Unusual conical intersections in the Jahnâ€“Teller effect: The electronically excited states of Li3. Journal of Chemical Physics, 1999, 110, 3639-3642.	3.0	38
57	On the adiabatic to diabatic states transformation in the presence of a conical intersection: A most diabatic basis from the solution to a Poissonâ€™s equation. I. Journal of Chemical Physics, 1998, 109, 20-25.	3.0	86
58	Electronic structure aspects of the spin-forbidden reaction CH3(Xâ€‰2A2â€³)+N(4S)â†’HCN(Xâ€‰1Î£+)+H2(Xâ€‰1Î£g+). Journal of Chemical Physics, 1997, 107, 4994-4999.	3.0	28
59	Resonances in the predissociation of the Aâ€‰2Îˆ© state of MgBr. Journal of Chemical Physics, 1997, 106, 4091-4101.	3.0	13
60	A theoretical study of the structure and energetics of stacked dimers of polycyclic aromatic hydrocarbons. Application of INDO 1/S method to singlet excimers of naphthalene and phenanthrene. Chemical Physics Letters, 1994, 225, 441-447.	2.6	30