

# Rovshan G Sadygov

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7942375/publications.pdf>

Version: 2024-02-01

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	A Model for Random Sampling and Estimation of Relative Protein Abundance in Shotgun Proteomics. <i>Analytical Chemistry</i> , 2004, 76, 4193-4201.	6.5	2,280
2	Shotgun identification of protein modifications from protein complexes and lens tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7900-7905.	7.1	571
3	Large-scale database searching using tandem mass spectra: Looking up the answer in the back of the book. <i>Nature Methods</i> , 2004, 1, 195-202.	19.0	375
4	MS1, MS2, and SQT—three unified, compact, and easily parsed file formats for the storage of shotgun proteomic spectra and identifications. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2162-2168.	1.5	350
5	A Correlation Algorithm for the Automated Quantitative Analysis of Shotgun Proteomics Data. <i>Analytical Chemistry</i> , 2003, 75, 6912-6921.	6.5	276
6	Code Developments to Improve the Efficiency of Automated MS/MS Spectra Interpretation. <i>Journal of Proteome Research</i> , 2002, 1, 211-215.	3.7	198
7	A Hypergeometric Probability Model for Protein Identification and Validation Using Tandem Mass Spectral Data and Protein Sequence Databases. <i>Analytical Chemistry</i> , 2003, 75, 3792-3798.	6.5	198
8	Statistical Models for Protein Validation Using Tandem Mass Spectral Data and Protein Amino Acid Sequence Databases. <i>Analytical Chemistry</i> , 2004, 76, 1664-1671.	6.5	127
9	ChromAlign: A Two-Step Algorithmic Procedure for Time Alignment of Three-Dimensional LC-MS Chromatographic Surfaces. <i>Analytical Chemistry</i> , 2006, 78, 8207-8217.	6.5	101
10	Cognitive Enhancement with Rosiglitazone Links the Hippocampal PPAR $\beta$ and ERK MAPK Signaling Pathways. <i>Journal of Neuroscience</i> , 2012, 32, 16725-16735.	3.6	99
11	On the adiabatic to diabatic states transformation in the presence of a conical intersection: A most diabatic basis from the solution to a Poisson's equation. I. <i>Journal of Chemical Physics</i> , 1998, 109, 20-25.	3.0	86
12	Assessment of cardiac proteome dynamics with heavy water: slower protein synthesis rates in interfibrillar than subsarcolemmal mitochondria. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2013, 304, H1201-H1214.	3.2	66
13	Measuring protein synthesis using metabolic 2H labeling, high-resolution mass spectrometry, and an algorithm. <i>Analytical Biochemistry</i> , 2011, 412, 47-55.	2.4	64
14	Hepatic Mitochondrial Defects in a Nonalcoholic Fatty Liver Disease Mouse Model Are Associated with Increased Degradation of Oxidative Phosphorylation Subunits. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2371-2386.	3.8	59
15	Cognitive Enhancing Treatment with a PPAR $\beta$ Agonist Normalizes Dentate Granule Cell Presynaptic Function in Tg2576 APP Mice. <i>Journal of Neuroscience</i> , 2014, 34, 1028-1036.	3.6	48
16	Altered Retinoic Acid Metabolism in Diabetic Mouse Kidney Identified by 18O Isotopic Labeling and 2D Mass Spectrometry. <i>PLoS ONE</i> , 2010, 5, e11095.	2.5	45
17	d2ome, Software for in Vivo Protein Turnover Analysis Using Heavy Water Labeling and LC-MS, Reveals Alterations of Hepatic Proteome Dynamics in a Mouse Model of NAFLD. <i>Journal of Proteome Research</i> , 2018, 17, 3740-3748.	3.7	42
18	Increased serotransferrin and ceruloplasmin turnover in diet-controlled patients with type 2 diabetes. <i>Free Radical Biology and Medicine</i> , 2017, 113, 461-469.	2.9	41

#	ARTICLE	IF	CITATIONS
19	Unusual conical intersections in the Jahn-Teller effect: The electronically excited states of Li <sub>3</sub> . Journal of Chemical Physics, 1999, 110, 3639-3642.	3.0	38
20	The Cancer Drug Tamoxifen: A Potential Therapeutic Treatment for Spinal Cord Injury. Journal of Neurotrauma, 2014, 31, 268-283.	3.4	37
21	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
22	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
23	A New Probabilistic Database Search Algorithm for ETD Spectra. Journal of Proteome Research, 2009, 8, 3198-3205.	3.7	33
24	Detection of Structural and Metabolic Changes in Traumatically Injured Hippocampus by Quantitative Differential Proteomics. Journal of Neurotrauma, 2013, 30, 775-788.	3.4	32
25	Central Limit Theorem as an Approximation for Intensity-Based Scoring Function. Analytical Chemistry, 2006, 78, 89-95.	6.5	31
26	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
27	Integrative proteomic analysis reveals reprogramming tumor necrosis factor signaling in epithelial mesenchymal transition. Journal of Proteomics, 2016, 148, 126-138.	2.4	29
28	Electronic structure aspects of the spin-forbidden reaction CH <sub>3</sub> (X <sup>2A2</sup> ) + N(4S) → HCN(X <sup>1Σ+</sup> ) + H <sub>2</sub> (X <sup>1Σg+</sup> ). Journal of Chemical Physics, 1997, 107, 4994-4999.	3.0	28
29	Examining Troughs in the Mass Distribution of All Theoretically Possible Tryptic Peptides. Journal of Proteome Research, 2011, 10, 4150-4157.	3.7	25
30	Mixed-effects model of epithelial-mesenchymal transition reveals rewiring of signaling networks. Cellular Signalling, 2015, 27, 1413-1425.	3.6	25
31	Gaussian Process Modeling of Protein Turnover. Journal of Proteome Research, 2016, 15, 2115-2122.	3.7	25
32	Using Power Spectrum Analysis to Evaluate <sup>18</sup> O-Water Labeling Data Acquired from Low Resolution Mass Spectrometers. Journal of Proteome Research, 2010, 9, 4306-4312.	3.7	23
33	Charger: A 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
34	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
35	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
36	Poisson Model To Generate Isotope Distribution for Biomolecules. Journal of Proteome Research, 2018, 17, 751-758.	3.7	15

#	ARTICLE	IF	CITATIONS
37	Resonances in the predissociation of the $\tilde{X}^1\Sigma^+$ state of MgBr. <i>Journal of Chemical Physics</i> , 1997, 106, 4091-4101.	3.0	13
38	Partial Isotope Profiles Are Sufficient for Protein Turnover Analysis Using Closed-Form Equations of Mass Isotopomer Dynamics. <i>Analytical Chemistry</i> , 2020, 92, 14747-14753.	6.5	12
39	Assigning in vivo carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching. <i>International Journal of Mass Spectrometry</i> , 2007, 259, 161-173.	1.5	11
40	A parallel method for enumerating amino acid compositions and masses of all theoretical peptides. <i>BMC Bioinformatics</i> , 2011, 12, 432.	2.6	11
41	Improved Mass Defect Model for Theoretical Tryptic Peptides. <i>Analytical Chemistry</i> , 2012, 84, 3026-3032.	6.5	11
42	Predicting the protein half-life in tissue from its cellular properties. <i>PLoS ONE</i> , 2017, 12, e0180428.	2.5	11
43	Using SEQUEST with Theoretically Complete Sequence Databases. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1858-1864.	2.8	10
44	Calculation of the Protein Turnover Rate Using the Number of Incorporated $^2\text{H}$ Atoms and Proteomics Analysis of a Single Labeled Sample. <i>Analytical Chemistry</i> , 2019, 91, 14340-14351.	6.5	9
45	Proteome dynamics from heavy water metabolic labeling and peptide tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2019, 445, 116194.	1.5	8
46	Timepoint Selection Strategy for In Vivo Proteome Dynamics from Heavy Water Metabolic Labeling and LC-MS. <i>Journal of Proteome Research</i> , 2020, 19, 2105-2112.	3.7	8
47	SVM Model for Quality Assessment of Medium Resolution Mass Spectra from $^{18}\text{O}$ -Water Labeling Experiments. <i>Journal of Proteome Research</i> , 2011, 10, 2095-2103.	3.7	7
48	Using Heavy Mass Isotopomers for Protein Turnover in Heavy Water Metabolic Labeling. <i>Journal of Proteome Research</i> , 2021, 20, 2035-2041.	3.7	7
49	Bioinformatics Tools for Mass Spectrometry-Based High-Throughput Quantitative Proteomics Platforms. <i>Current Proteomics</i> , 2011, 8, 125-137.	0.3	6
50	Generalized linear and mixed models for label-free shotgun proteomics. <i>Statistics and Its Interface</i> , 2012, 5, 89-98.	0.3	6
51	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	6.5	6
52	Use of singular value decomposition analysis to differentiate phosphorylated precursors in strong cation exchange fractions. <i>Electrophoresis</i> , 2014, 35, 3498-3503.	2.4	5
53	High-Resolution Mass Spectrometry for In Vivo Proteome Dynamics using Heavy Water Metabolic Labeling. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7821.	4.1	5
54	High Mass Accuracy Phosphopeptide Identification Using Tandem Mass Spectra. <i>International Journal of Proteomics</i> , 2012, 2012, 1-5.	2.0	4

#	ARTICLE	IF	CITATIONS
55	Comparison of Programmatic Approaches for Efficient Accessing to mzML Files. Journal of Data Mining in Genomics & Proteomics, 2011, 02, .	0.5	4
56	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
57	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
58	Another look at matrix correlations. Bioinformatics, 2019, 35, 4748-4753.	4.1	2
59	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
60	Use of Theoretical Peptide Distributions in Phosphoproteome Analysis. Journal of Proteome Research, 2013, 12, 3207-3214.	3.7	1