

Frank Suits

List of Publications by Year in descending order

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44
papers

3,035
citations

279798

23
h-index

315739

38
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45
all docs

45
docs citations

45
times ranked

3685
citing authors

#	ARTICLE	IF	CITATIONS
1	Pipelines and Systems for Threshold-Avoiding Quantification of LC-MS/MS Data. <i>Analytical Chemistry</i> , 2021, 93, 11215-11224.	6.5	6
2	MSIWarp: A General Approach to Mass Alignment in Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2020, 92, 16138-16148.	6.5	7
3	Dynamic Edge Fabric Environment: Seamless and Automatic Switching among Resources at the Edge of IoT Network and Cloud. , 2019, , .		14
4	Optimal Operation of Energy Storage Systems Considering Forecasts and Battery Degradation. <i>IEEE Transactions on Smart Grid</i> , 2018, 9, 2086-2096.	9.0	109
5	Cognitive IoT Gateways. , 2017, , .		30
6	Greening IoT with Fog: A Survey. , 2017, , .		38
7	Optimal power purchase agreements in PV-rich communities. , 2017, , .		2
8	Interconnecting Fog computing and microgrids for greening IoT. , 2016, , .		39
9	Proteogenomics: Key Driver for Clinical Discovery and Personalized Medicine. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 21-47.	1.6	17
10	Identification of Analytical Factors Affecting Complex Proteomics Profiles Acquired in a Factorial Design Study with Analysis of Variance: Simultaneous Component Analysis. <i>Analytical Chemistry</i> , 2016, 88, 4229-4238.	6.5	10
11	Inversion of peak elution order prevents uniform time alignment of complex liquid-chromatography coupled to mass spectrometry datasets. <i>Journal of Chromatography A</i> , 2014, 1373, 61-72.	3.7	4
12	Parallelisation study of a three-dimensional environmental flow model. <i>Computers and Geosciences</i> , 2014, 64, 96-103.	4.2	20
13	Queries of MALDI-imaging global datasets identifying ion mass signatures associated with tissue compartments. <i>Proteomics</i> , 2014, 14, 862-871.	2.2	10
14	A Critical Assessment of Feature Selection Methods for Biomarker Discovery in Clinical Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 263-276.	3.8	120
15	Correlation Queries for Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2013, 85, 4398-4404.	6.5	14
16	msCompare: A Framework for Quantitative Analysis of Label-free LC-MS Data for Comparative Candidate Biomarker Studies. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015974.	3.8	39
17	Surface flow dynamics within an exposed wind-driven bay: Combined HF radar observations and model simulations. , 2012, , .		5
18	Profiling and Identification of Cerebrospinal Fluid Proteins in a Rat EAE Model of Multiple Sclerosis. <i>Journal of Proteome Research</i> , 2012, 11, 2048-2060.	3.7	51

#	ARTICLE	IF	CITATIONS
19	Threshold-Avoiding Proteomics Pipeline. <i>Analytical Chemistry</i> , 2011, 83, 7786-7794.	6.5	18
20	The Impact of Delayed Storage on the Measured Proteome and Metabolome of Human Cerebrospinal Fluid. <i>Clinical Chemistry</i> , 2011, 57, 1703-1711.	3.2	59
21	A high-throughput processing service for retention time alignment of complex proteomics and metabolomics LC-MS data. <i>Bioinformatics</i> , 2011, 27, 1176-1178.	4.1	9
22	Time Alignment Algorithms Based on Selected Mass Traces for Complex LC-MS Data. <i>Journal of Proteome Research</i> , 2010, 9, 1483-1495.	3.7	52
23	The Effect of Preanalytical Factors on Stability of the Proteome and Selected Metabolites in Cerebrospinal Fluid (CSF). <i>Journal of Proteome Research</i> , 2009, 8, 5511-5522.	3.7	102
24	Further aspects of the roaming mechanism in formaldehyde dissociation. <i>Chemical Physics</i> , 2008, 347, 288-299.	1.9	45
25	Two-Dimensional Method for Time Aligning Liquid Chromatography-Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2008, 80, 3095-3104.	6.5	44
26	Optimized Time Alignment Algorithm for LC-MS Data: Correlation Optimized Warping Using Component Detection Algorithm-Selected Mass Chromatograms. <i>Analytical Chemistry</i> , 2008, 80, 7012-7021.	6.5	79
27	A noise model for mass spectrometry based proteomics. <i>Bioinformatics</i> , 2008, 24, 1070-1077.	4.1	59
28	Chip-LC-MS for label-free profiling of human serum. <i>Electrophoresis</i> , 2007, 28, 4493-4505.	2.4	31
29	Magnitude and spatial orientation of the hydrophobic moments of multi-domain proteins. <i>International Journal of Bioinformatics Research and Applications</i> , 2006, 2, 161.	0.2	2
30	The roaming atom pathway in formaldehyde decomposition. <i>Journal of Chemical Physics</i> , 2006, 125, 044303.	3.0	83
31	Blue Matter: Strong Scaling of Molecular Dynamics on Blue Gene/L. <i>Lecture Notes in Computer Science</i> , 2006, , 846-854.	1.3	38
32	Blue matter on blue gene/L. , 2005, , .		21
33	Molecular dynamics investigation of the structural properties of phosphatidylethanolamine lipid bilayers. <i>Journal of Chemical Physics</i> , 2005, 122, 244714.	3.0	37
34	Role of Cholesterol and Polyunsaturated Chains in Lipid-Protein Interactions: A Molecular Dynamics Simulation of Rhodopsin in a Realistic Membrane Environment. <i>Journal of the American Chemical Society</i> , 2005, 127, 4576-4577.	13.7	134
35	Molecular dynamics investigation of dynamical properties of phosphatidylethanolamine lipid bilayers. <i>Journal of Chemical Physics</i> , 2005, 122, 244715.	3.0	36
36	Molecular-Level Organization of Saturated and Polyunsaturated Fatty Acids in a Phosphatidylcholine Bilayer Containing Cholesterol. <i>Biochemistry</i> , 2004, 43, 15318-15328.	2.5	168

#	ARTICLE	IF	CITATIONS
37	Describing Protein Folding Kinetics by Molecular Dynamics Simulations. 1. Theory. Journal of Physical Chemistry B, 2004, 108, 6571-6581.	2.6	391
38	Describing Protein Folding Kinetics by Molecular Dynamics Simulations. 2. Example Applications to Alanine Dipeptide and a β^2 -Hairpin Peptide. Journal of Physical Chemistry B, 2004, 108, 6582-6594.	2.6	171
39	Blue Matter, an application framework for molecular simulation on Blue Gene. Journal of Parallel and Distributed Computing, 2003, 63, 759-773.	4.1	62
40	Blue Gene: A vision for protein science using a petaflop supercomputer. IBM Systems Journal, 2001, 40, 310-327.	3.0	211
41	Poincare sphere interpretation of Kerr-effect measurements using a photoelastic modulator. IEEE Transactions on Magnetism, 1992, 28, 2976-2978.	2.1	2
42	Bilayer Permalloy films grown in orthogonal applied fields. IEEE Transactions on Magnetism, 1990, 26, 2353-2355.	2.1	5
43	Bloch line influence on wall motion response in thin-film heads. Journal of Applied Physics, 1988, 63, 4033-4035.	2.5	18
44	Optical constants of organic tholins produced in a simulated Titanian atmosphere: From soft x-ray to microwave frequencies. Icarus, 1984, 60, 127-137.	2.5	609