

Michael C Fitzgerald

List of Publications by Year in descending order

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78
papers

2,600
citations

186265
28
h-index

214800
47
g-index

81
all docs

81
docs citations

81
times ranked

2060
citing authors

#	ARTICLE	IF	CITATIONS
1	Thermodynamic Analysis of Protein Stability and Ligand Binding Using a Chemical Modification- and Mass Spectrometry-Based Strategy. <i>Analytical Chemistry</i> , 2008, 80, 4175-4185.	6.5	186
2	Quantitative proteomics approach for identifying protein-drug interactions in complex mixtures using protein stability measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9078-9082.	7.1	161
3	Order out of Disorder: Working Cycle of an Intrinsically Unfolded Chaperone. <i>Cell</i> , 2012, 148, 947-957.	28.9	124
4	A General Mass Spectrometry-Based Assay for the Quantitation of Protein-Ligand Binding Interactions in Solution. <i>Journal of the American Chemical Society</i> , 2002, 124, 10256-10257.	13.7	123
5	Structural and thermodynamic characterization of a cytoplasmic dynein light chain intermediate chain complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10028-10033.	7.1	116
6	Thermodynamic analysis of protein-ligand binding interactions in complex biological mixtures using the stability of proteins from rates of oxidation. <i>Nature Protocols</i> , 2013, 8, 148-161.	12.0	96
7	Mutational Analysis of Active Site Residues in the <i>Staphylococcus aureus</i> Transpeptidase SrtA. <i>Biochemistry</i> , 2007, 46, 7269-7278.	2.5	71
8	Accuracy and Precision of a New H/D Exchange- and Mass Spectrometry-Based Technique for Measuring the Thermodynamic Properties of Protein-Peptide Complexes. <i>Biochemistry</i> , 2003, 42, 4962-4970.	2.5	66
9	The Protein Backbone Makes Important Contributions to 4-Oxalocrotonate Tautomerase Enzyme Catalysis: A Understanding from Theory and Experiment. <i>Biochemistry</i> , 2004, 43, 6885-6892.	2.5	64
10	Thermodynamic Analysis of Protein-Ligand Interactions in Complex Biological Mixtures using a Shotgun Proteomics Approach. <i>Journal of Proteome Research</i> , 2011, 10, 4948-4958.	3.7	61
11	Proteome-Wide Structural Biology: An Emerging Field for the Structural Analysis of Proteins on the Proteomic Scale. <i>Journal of Proteome Research</i> , 2018, 17, 3614-3627.	3.7	54
12	Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC)-Based Strategy for Proteome-Wide Thermodynamic Analysis of Protein-Ligand Binding Interactions. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1800-1813.	3.8	53
13	Thermodynamic stability measurements on multimeric proteins using a new H/D exchange- and matrix-assisted laser desorption/ionization (MALDI) mass spectrometry-based method. <i>Protein Science</i> , 2002, 11, 841-851.	7.6	51
14	A Solid Sample Preparation Method That Reduces Signal Suppression Effects in the MALDI Analysis of Peptides. <i>Analytical Chemistry</i> , 2001, 73, 625-631.	6.5	49
15	Measurements of Protein Stability by H/D Exchange and Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Using Picomoles of Material. <i>Analytical Chemistry</i> , 2001, 73, 3300-3304.	6.5	44
16	Analysis of protein folding and function using backbone modified proteins. <i>Bioorganic Chemistry</i> , 2004, 32, 438-449.	4.1	44
17	High-Throughput Screening Assay for the Tunable Selection of Protein Ligands. <i>ACS Combinatorial Science</i> , 2004, 6, 262-269.	3.3	43
18	H/D Exchange- and Mass Spectrometry-Based Strategy for the Thermodynamic Analysis of Protein-Ligand Binding. <i>Analytical Chemistry</i> , 2007, 79, 5869-5877.	6.5	42

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19	Painting proteins with covalent labels: Whatâ€™s in the picture?. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1193-1206.	2.8	41
20	Chemical Denaturation and Protein Precipitation Approach for Discovery and Quantitation of Proteinâ€“Drug Interactions. <i>Analytical Chemistry</i> , 2018, 90, 9249-9255.	6.5	40
21	Concentration and Desalting of Protein Samples for Mass Spectrometry Analysis. <i>Analytical Biochemistry</i> , 1998, 262, 83-85.	2.4	39
22	SUPREX (Stability of Unpurified Proteins from Rates of H/D Exchange) Analysis of the Thermodynamics of Synergistic Anion Binding by Ferric-Binding Protein (FbpA), a Bacterial Transferrinâ€. <i>Biochemistry</i> , 2004, 43, 15767-15774.	2.5	39
23	Analysis of human serum proteins by liquid phase isoelectric focusing and matrix-assisted laser desorption/ionization-mass spectrometry. <i>Proteomics</i> , 2003, 3, 1661-1666.	2.2	38
24	<i>Plasmodium</i> chaperonin TRiC/CCT identified as a target of the antihistamine clemastine using parallel chemoproteomic strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5810-5817.	7.1	37
25	SILAC-Pulse Proteolysis: A Mass Spectrometry-Based Method for Discovery and Cross-Validation in Proteome-Wide Studies of Ligand Binding. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 2073-2083.	2.8	35
26	The Energetic Contribution of BackboneâˆBackbone Hydrogen Bonds to the Thermodynamic Stability of a Hyperstable P22 Arc Repressor Mutant. <i>Journal of the American Chemical Society</i> , 2001, 123, 7709-7710.	13.7	34
27	Characterization of the <i>Saccharomyces cerevisiae</i> ATP-Interactome using the iTRAQ-SPROX Technique. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 233-243.	2.8	34
28	Conserved thermodynamic contributions of backbone hydrogen bonds in a protein fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2600-2604.	7.1	30
29	Large-Scale Analysis of Breast Cancer-Related Conformational Changes in Proteins Using Limited Proteolysis. <i>Journal of Proteome Research</i> , 2016, 15, 4666-4674.	3.7	30
30	Global Analysis of Protein Folding Thermodynamics for Disease State Characterization. <i>Journal of Proteome Research</i> , 2015, 14, 2287-2297.	3.7	28
31	A New H/D Exchange- and Mass Spectrometry-Based Method for Thermodynamic Analysis of Protein-DNA Interactions. <i>Chemistry and Biology</i> , 2003, 10, 1205-1213.	6.0	27
32	Discovery of Manassantin A Protein Targets Using Large-Scale Protein Folding and Stability Measurements. <i>Journal of Proteome Research</i> , 2016, 15, 2688-2696.	3.7	27
33	Thermodynamic Analysis of Subunit Interactions in <i>Escherichia coli</i> Molybdopterin Synthaseâ€. <i>Biochemistry</i> , 2005, 44, 2595-2601.	2.5	26
34	Mass Spectrometry-Based Thermal Shift Assay for ProteinâˆLigand Binding Analysis. <i>Analytical Chemistry</i> , 2010, 82, 5573-5581.	6.5	26
35	Protein Folding Stability Changes Across the Proteome Reveal Targets of Cu Toxicity in <i>E. coli</i> . <i>ACS Chemical Biology</i> , 2021, 16, 214-224.	3.4	26
36	Slow Histidine H/D Exchange Protocol for Thermodynamic Analysis of Protein Folding and Stability Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 1653-1660.	6.5	25

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37	Thermodynamic Analysis of Protein Folding and Stability Using a Tryptophan Modification Protocol. <i>Analytical Chemistry</i> , 2014, 86, 7041-7048.	6.5	24
38	Discovery of Tamoxifen and <i>N</i> -Desmethyl Tamoxifen Protein Targets in MCF-7 Cells Using Large-Scale Protein Folding and Stability Measurements. <i>Journal of Proteome Research</i> , 2017, 16, 4073-4085.	3.7	24
39	Mass Spectrometry- and Lysine Amidination-Based Protocol for Thermodynamic Analysis of Protein Folding and Ligand Binding Interactions. <i>Analytical Chemistry</i> , 2011, 83, 3555-3562.	6.5	23
40	Discovery of Age-Related Protein Folding Stability Differences in the Mouse Brain Proteome. <i>Journal of Proteome Research</i> , 2016, 15, 4731-4741.	3.7	22
41	Large-Scale Analysis of Breast Cancer-Related Conformational Changes in Proteins Using SILAC-SPROX. <i>Journal of Proteome Research</i> , 2017, 16, 3277-3286.	3.7	22
42	Comparative Analysis of Mass-Spectrometry-Based Proteomic Methods for Protein Target Discovery Using a One-Pot Approach. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 217-226.	2.8	22
43	Accuracy of SUPREX (stability of unpurified proteins from rates of H/D exchange) and MALDI mass spectrometry-derived protein unfolding free energies determined under non-EX2 exchange conditions. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1535-1542.	2.8	21
44	Thermodynamic Analysis of the Geldanamycin-Hsp90 Interaction in a Whole Cell Lysate Using a Mass Spectrometry-Based Proteomics Approach. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1670-1676.	2.8	20
45	Pathogenic Mutations Induce Partial Structural Changes in the Native β -Sheet Structure of Transthyretin and Accelerate Aggregation. <i>Biochemistry</i> , 2017, 56, 4808-4818.	2.5	20
46	Thermodynamic Analysis of Cyclosporin A Binding to Cyclophilin A in a Lung Tumor Tissue Lysate. <i>Analytical Chemistry</i> , 2004, 76, 4343-4348.	6.5	19
47	H/D Exchange and Mass Spectrometry-Based Method for Biophysical Analysis of Multidomain Proteins at the Domain Level. <i>Analytical Chemistry</i> , 2007, 79, 8728-8739.	6.5	19
48	Synthesis and Biological Evaluation of Manassantin Analogues for Hypoxia-Inducible Factor 1 α Inhibition. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 7659-7671.	6.4	19
49	Identification of an Essential Backbone Amide Bond in the Folding and Stability of a Multimeric Enzyme. <i>Journal of the American Chemical Society</i> , 2000, 122, 8105-8111.	13.7	18
50	Protocol for the Thermodynamic Analysis of Some Proteins Using an H/D Exchange- and Mass Spectrometry-Based Technique. <i>Analytical Chemistry</i> , 2005, 77, 693-697.	6.5	18
51	Throughput and efficiency of a mass spectrometry-based screening assay for protein-Ligand binding detection. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1303-1311.	2.8	18
52	Chemo-Selection Strategy for Limited Proteolysis Experiments on the Proteomic Scale. <i>Analytical Chemistry</i> , 2018, 90, 14039-14047.	6.5	18
53	Comparative Analysis of Two Different Amide-to-Ester Bond Mutations in the β -Sheet of 4-Oxalocrotonate Tautomerase. <i>Biochemistry</i> , 2003, 42, 6620-6630.	2.5	16
54	<i>Ex Vivo</i> Analysis of Synergistic Anion Binding to FbpA in Gram-Negative Bacteria. <i>Biochemistry</i> , 2008, 47, 4298-4305.	2.5	16

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55	Guanidine-Induced Equilibrium Unfolding of a Homo-Hexameric Enzyme 4-Oxalocrotonate Tautomerase (4-OT). <i>Biochemistry</i> , 2001, 40, 4493-4502.	2.5	15
56	Are dust mite allergens more abundant and/or more stable than other Dermatophagoides pteronyssinus proteins?. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1030-1032.e1.	2.9	15
57	Proteases of Dermatophagoides pteronyssinus. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1204.	4.1	14
58	Proteome-Wide Characterization of Phosphorylation-Induced Conformational Changes in Breast Cancer. <i>Journal of Proteome Research</i> , 2018, 17, 1129-1137.	3.7	14
59	Energetics-Based Methods for Protein Folding and Stability Measurements. <i>Annual Review of Analytical Chemistry</i> , 2014, 7, 209-228.	5.4	13
60	Hydrogen/Deuterium Exchange- and Protease Digestion-Based Screening Assay for Protein-Ligand Binding Detection. <i>Analytical Chemistry</i> , 2009, 81, 6860-6867.	6.5	12
61	The accuracy and precision of a new H/D exchange- and mass spectrometry-based technique for measuring the thermodynamic stability of proteins. <i>Analytica Chimica Acta</i> , 2003, 496, 225-232.	5.4	11
62	Discovery of Novel Cyclophilin A Ligands Using an H/D Exchange and Mass Spectrometry-Based Strategy. <i>Journal of Biomolecular Screening</i> , 2010, 15, 1051-1062.	2.6	11
63	Stable Isotope Labeling Strategy for Protein-Ligand Binding Analysis in Multi-Component Protein Mixtures. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 418-430.	2.8	11
64	False-Positive Rate Determination of Protein Target Discovery using a Covalent Modification- and Mass Spectrometry-Based Proteomics Platform. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 132-140.	2.8	11
65	Targeted Mass Spectrometry-Based Approach for Protein-Ligand Binding Analyses in Complex Biological Mixtures Using a Phenacyl Bromide Modification Strategy. <i>Analytical Chemistry</i> , 2016, 88, 10987-10993.	6.5	11
66	Facile chemical synthesis and equilibrium unfolding properties of CopG. <i>Protein Science</i> , 2004, 13, 1918-1926.	7.6	8
67	Direct Analysis of Backbone-Bone Hydrogen Bond Formation in Protein Folding Transition States. <i>Journal of Molecular Biology</i> , 2006, 363, 506-519.	4.2	8
68	Thermodynamic Analysis of a Molecular Chaperone Binding to Unfolded Protein Substrates. <i>Biochemistry</i> , 2010, 49, 1346-1353.	2.5	8
69	Chemoproteomics for <i>Plasmodium</i> Parasite Drug Target Discovery. <i>ChemBioChem</i> , 2021, 22, 2591-2599.	2.6	8
70	Are allergens more abundant and/or more stable than other proteins in pollens and dust?. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 1267-1269.	5.7	7
71	Characterising phase variations in MALDI-TOF data and correcting them by peak alignment. <i>Cancer Informatics</i> , 2005, 1, 32-40.	1.9	7
72	Discovery of the Xenon-Protein Interactome Using Large-Scale Measurements of Protein Folding and Stability. <i>Journal of the American Chemical Society</i> , 2022, 144, 3925-3938.	13.7	7

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73	Characterising phase variations in MALDI-TOF data and correcting them by peak alignment. <i>Cancer Informatics</i> , 2005, 1, 117693510500100.	1.9	6
74	Chemoproteomic-enabled characterization of small GTPase Rab1a as a target of an <i>N</i> -arylbenzimidazole ligand's rescue of Parkinson's-associated cell toxicity. <i>RSC Chemical Biology</i> , 2022, 3, 96-111.	4.1	5
75	Analysis of Brain Protein Stability Changes in Mouse Models of Normal Aging and α -Synucleinopathy Reveals Age- and Disease-Related Differences. <i>Journal of Proteome Research</i> , 2021, 20, 5156-5168.	3.7	4
76	Total chemical synthesis of the B1 domain of protein L from <i>Peptostreptococcus magnus</i> . <i>Bioorganic Chemistry</i> , 2006, 34, 131-141.	4.1	3
77	Chapter 6 Thermodynamic Analysis of Protein Folding and Ligand Binding by SUPREX. <i>Comprehensive Analytical Chemistry</i> , 2008, 52, 127-149.	1.3	1
78	Bet v 1 and other birch allergens are more resistant to proteolysis and more abundant than other birch pollen proteins. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 1307-1309.	5.7	0