# VickiÂ H Wysocki

List of Publications by Year
in descending order



| 256 | 13,932 | 19657 61 | 26613 107 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 275 | 275 | 275 | 10496 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Surface-induced Dissociation Mass Spectrometry as a Structural Biology Tool. Chemical Reviews, 2022, 122, 7442-7487. | 47.7 | 31 |
| 2 | Native Mass Spectrometry and Surface Induced Dissociation Provide Insight into the Post-Translational Modifications of Tetrameric AQP0 Isolated from Bovine Eye Lens. Analytical Chemistry, 2022, 94, 1515-1519. | 6.5 | 12 |
| 3 | Native Mass Spectrometry: Recent Progress and Remaining Challenges. Annual Review of Biophysics, 2022, 51, 157-179. | 10.0 | 50 |
| 4 | A Disulfide-Stabilized AÎ² that Forms Dimers but Does Not Form Fibrils. Biochemistry, 2022, 61, 252-264. | 2.5 | 4 |
| 5 | Mechanisms of Cre recombinase synaptic complex assembly and activation illuminated by Cryo-EM. Nucleic Acids Research, 2022, 50, 1753-1769. | 14.5 | 6 |
| 6 | Optimization of proteomics sample preparation for identification of host and bacterial proteins in mouse feces. Analytical and Bioanalytical Chemistry, 2022, 414, 2317. | 3.7 | 3 |
| 7 | OUP accepted manuscript. Journal of Insect Science, 2022, 22, . | 1.5 | 2 |
| 8 | Characterization of a Salmonella Transcription Factor-DNA Complex and Identification of the Inducer by Native Mass Spectrometry. Journal of Molecular Biology, 2022, 434, 167480. | 4.2 | 4 |
| 9 | Surface-Induced Dissociation for Protein Complex Characterization. Methods in Molecular Biology, 2022, , 211-237. | 0.9 | 3 |
| 10 | Simulation of Energy-Resolved Mass Spectrometry Distributions from Surface-Induced Dissociation. Analytical Chemistry, 2022, 94, 10506-10514. | 6.5 | 2 |
| 11 | Elucidation of structureâ€“function relationships in Methanocaldococcus jannaschii RNase P, a multi-subunit catalytic ribonucleoprotein. Nucleic Acids Research, 2022, 50, 8154-8167. | 14.5 | 5 |
| 12 | De novo design of transmembrane Î² barrels. Science, 2021, 371, . | 12.6 | 83 |
| 13 | Oligomeric complexes formed by RedÎ² single strand annealing protein in its different DNA bound states. Nucleic Acids Research, 2021, 49, 3441-3460. | 14.5 | 9 |
| 14 | Surface-Induced Dissociation of Protein Complexes Selected by Trapped Ion Mobility Spectrometry. Analytical Chemistry, 2021, 93, 5513-5520. | 6.5 | 12 |
| 15 | Tandem surface-induced dissociation of protein complexes on an ultrahigh resolution platform. International Journal of Mass Spectrometry, 2021, 461, 116503. | 1.5 | 5 |
| 16 | Cellular mRNA triggers structural transformation of Ebola virus matrix protein VP40 to its essential regulatory form. Cell Reports, 2021, 35, 108986. | 6.4 | 12 |
| 17 | Transferrin receptor targeting by de novo sheet extension. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 17 |
| 18 | Variable-Temperature Electrospray Ionization for Temperature-Dependent Folding/Refolding Reactions of Proteins and Ligand Binding. Analytical Chemistry, 2021, 93, 6924-6931. | 6.5 | 33 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Surface-Induced Dissociation of Anionic vs Cationic Native-Like Protein Complexes. Journal of the American Chemical Society, 2021, 143, 7698-7706. | 13.7 | 8 |
| 20 | Characterization of Transcription Factorâ€ÐDNA Complexes Using Online Buffer Exchange Coupled to Native Mass Spectrometry. FASEB Journal, 2021, 35, . | 0.5 | 0 |
| 21 | Prediction of Protein Complex Structure Using Surface-Induced Dissociation and Cryo-Electron Microscopy. Analytical Chemistry, 2021, 93, 7596-7605. | 6.5 | 13 |
| 22 | STK11/LKB1 Loss of Function Is Associated with Global DNA Hypomethylation and S-Adenosyl-Methionine Depletion in Human Lung Adenocarcinoma. Cancer Research, 2021, 81, 4194-4204. | 0.9 | 4 |
| 23 | Generation of ordered protein assemblies using rigid three-body fusion. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 25 |
| 24 | Analysis of Tagged Proteins Using Tandem Affinity-Buffer Exchange Chromatography Online with Native Mass Spectrometry. Biochemistry, 2021, 60, 1876-1884. | 2.5 | 11 |
| 25 | Protein cofactors and substrate influence Mg2+-dependent structural changes in the catalytic RNA of archaeal RNase P. Nucleic Acids Research, 2021, 49, 9444-9458. | 14.5 | 6 |
| 26 | Tunable Heteroassembly of a Plant Pseudoenzymeâ€“Enzyme Complex. ACS Chemical Biology, 2021, 16, 2315-2325. | 3.4 | 13 |
| 27 | De novo design of tyrosine and serine kinase-driven protein switches. Nature Structural and Molecular Biology, 2021, 28, 762-770. | 8.2 | 14 |
| 28 | Optimization of proteomics sample preparation for forensic analysis of skin samples. Journal of Proteomics, 2021, 249, 104360. | 2.4 | 4 |
| 29 | Rounding Out the Understanding of ACD Toxicity with the Discovery of Cyclic Forms of Actin Oligomers. International Journal of Molecular Sciences, 2021, 22, 718. | 4.1 | 6 |
| 30 | Surface-induced dissociation of protein complexes on a cyclic ion mobility spectrometer. Analyst, The, 2021, 146, 6861-6873. | 3.5 | 12 |
| 31 | Implementing Digital-Waveform Technology for Extended m/z Range Operation on a Native Dual-Quadrupole FT-IM-Orbitrap Mass Spectrometer. Journal of the American Society for Mass Spectrometry, 2021, 32, 2812-2820. | 2.8 | 9 |
| 32 | Use of tandem affinityâ€“buffer exchange chromatography online with native mass spectrometry for optimizing overexpression and purification of recombinant proteins. Methods in Enzymology, 2021, 659, 37-70. | 1.0 | 5 |
| 33 | Purification, reconstitution, and mass analysis of archaeal RNase P, a multisubunit ribonucleoprotein enzyme. Methods in Enzymology, 2021, 659, 71-103. | 1.0 | 1 |
| 34 | Solution structure of the nucleotide hydrolase BlsM: Implication of its substrate specificity. Protein Science, 2020, 29, 1760-1773. | 7.6 | 3 |
| 35 | Probing the structure of nanodiscs using surface-induced dissociation mass spectrometry. Chemical Communications, 2020, 56, 15651-15654. | 4.1 | 14 |
| 36 | Simple and Minimally Invasive SID Devices for Native Mass Spectrometry. Analytical Chemistry, 2020, 92, 11195-11203. | 6.5 | 28 |

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| 37 | Coupling 193 nm Ultraviolet Photodissociation and Ion Mobility for Sequence Characterization of Conformationally-Selected Peptides. Journal of the American Society for Mass Spectrometry, 2020, 31, 2313-2320. | 2.8 | 12 |
| 38 | HIV-1 Gag protein with or without p6 specifically dimerizes on the viral RNA packaging signal. Journal of Biological Chemistry, 2020, 295, 14391-14401. | 3.4 | 20 |
| 39 | Using SLIM-Based IMS-IMS Together with Cryogenic Infrared Spectroscopy for Glycan Analysis. Analytical Chemistry, 2020, 92, 9079-9085. | 6.5 | 45 |
| 40 | Population Distributions from Native Mass Spectrometry Titrations Reveal Nearest-Neighbor Cooperativity in the Ring-Shaped Oligomeric Protein TRAP. Biochemistry, 2020, 59, 2518-2527. | 2.5 | 8 |
| 41 | A Tilted Surface and Ion Carpet Array for SID. Journal of the American Society for Mass Spectrometry, 2020, 31, 458-462. | 2.8 | 5 |
| 42 | De novo design of protein logic gates. Science, 2020, 368, 78-84. | 12.6 | 151 |
| 43 | Quaternary Structure of the Tryptophan Synthase Î±-Subunit Homolog BX1 from Zea mays. Journal of the American Society for Mass Spectrometry, 2020, 31, 227-233. | 2.8 | 4 |
| 44 | Characterization of [2Feâ€“2S]â€Clusterâ€Bridged Protein Complexes and Reaction Intermediates by use of Native Mass Spectrometric Methods. Angewandte Chemie, 2020, 132, 6790-6794. | 2.0 | 0 |
| 45 | Collision Cross Sections of Charge-Reduced Proteins and Protein Complexes: A Database for Collision Cross Section Calibration. Analytical Chemistry, 2020, 92, 4475-4483. | 6.5 | 32 |
| 46 | Ion Mobility and Surface Collisions: Submicrometer Capillaries Can Produce Native-like Protein Complexes. Analytical Chemistry, 2020, 92, 2460-2467. | 6.5 | 12 |
| 47 | Rapid online buffer exchange for screening of proteins, protein complexes and cell lysates by native mass spectrometry. Nature Protocols, 2020, 15, 1132-1157. | 12.0 | 88 |
| 48 | Characterization of [2Feâ€“2S]â€Clusterâ€Bridged Protein Complexes and Reaction Intermediates by use of Native Mass Spectrometric Methods. Angewandte Chemie - International Edition, 2020, 59, 6724-6728. | 13.8 | 18 |
| 49 | Comparative Structural Analysis of 20S Proteasome Ortholog Protein Complexes by Native Mass Spectrometry. ACS Central Science, 2020, 6, 573-588. | 11.3 | 37 |
| 50 | Cytoplasmic mRNA recapping has limited impact on proteome complexity. Open Biology, 2020, 10, 200313. | 3.6 | 5 |
| 51 | Chapter 11. Surface-induced Dissociation in Biomolecular Mass Spectrometry. New Developments in Mass Spectrometry, 2020, , 281-336. | 0.2 | 3 |
| 52 | Predicting Protein Complex Structure from Surface-Induced Dissociation Mass Spectrometry Data. ACS Central Science, 2019, 5, 1330-1341. | 11.3 | 37 |
| 53 | Light-Regulation of Tryptophan Synthase by Combining Protein Design and Enzymology. International Journal of Molecular Sciences, 2019, 20, 5106. | 4.1 | 8 |
| 54 | Oligomerization Affects the Ability of Human Cyclase-Associated Proteins 1 and 2 to Promote Actin Severing by Cofilins. International Journal of Molecular Sciences, 2019, 20, 5647. | 4.1 | 27 |

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| 55 | Design and Performance of a Second-Generation Surface-Induced Dissociation Cell for Fourier Transform Ion Cyclotron Resonance Mass Spectrometry of Native Protein Complexes. Analytical Chemistry, 2019, 91, 14049-14057. | 6.5 | 14 |
| 56 | Spectroscopic Evidence for Lactam Formation in Terminal Ornithine b<sub>2</sub><sup>+</sup> and b<sub>3</sub><sup>+</sup> Fragment Ions. Journal of the American Society for Mass Spectrometry, 2019, 30, 1565-1577. | 2.8 | 2 |
| 57 | Light Regulation of Enzyme Allostery through Photo-responsive Unnatural Amino Acids. Cell Chemical Biology, 2019, 26, 1501-1514.e9. | 5.2 | 25 |
| 58 | Surface-Induced Dissociation of Noncovalent Protein Complexes in an Extended Mass Range Orbitrap Mass Spectrometer. Analytical Chemistry, 2019, 91, 3611-3618. | 6.5 | 61 |
| 59 | Generation of a Standâ€Alone Tryptophan Synthase Î±â€Subunit by Mimicking an Evolutionary Blueprint. ChemBioChem, 2019, 20, 2747-2751. | 2.6 | 4 |
| 60 | De novo design of tunable, pH-driven conformational changes. Science, 2019, 364, 658-664. | 12.6 | 109 |
| 61 | Relative interfacial cleavage energetics of protein complexes revealed by surface collisions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8143-8148. | 7.1 | 60 |
| 62 | Integrated Use of Biochemical, Native Mass Spectrometry, Computational, and Genome-Editing Methods to Elucidate the Mechanism of a deglycase. Journal of Molecular Biology, 2019, 431, 4497-4513. | 4.2 | 9 |
| 63 | Programmable design of orthogonal protein heterodimers. Nature, 2019, 565, 106-111. | 27.8 | 139 |
| 64 | Surface-Induced Dissociation: An Effective Method for Characterization of Protein Quaternary Structure. Analytical Chemistry, 2019, 91, 190-209. | 6.5 | 67 |
| 65 | Stoichiometry of triple-sieve tRNA editing complex ensures fidelity of aminoacyl-tRNA formation. Nucleic Acids Research, 2019, 47, 929-940. | 14.5 | 13 |
| 66 | Salmonella-Mediated Inflammation Eliminates Competitors for Fructose-Asparagine in the Gut. Infection and Immunity, 2018, 86, . | 2.2 | 12 |
| 67 | How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214. | 8.0 | 580 |
| 68 | Surface Induced Dissociation Coupled with High Resolution Mass Spectrometry Unveils Heterogeneity of a 211 kDa Multicopper Oxidase Protein Complex. Journal of the American Society for Mass Spectrometry, 2018, 29, 723-733. | 2.8 | 19 |
| 69 | Confirmation of intersubunit connectivity and topology of designed protein complexes by native MS. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1268-1273. | 7.1 | 60 |
| 70 | Identification of Bacterial Species That Can Utilize Fructose-Asparagine. Applied and Environmental Microbiology, 2018, 84, . | 3.1 | 15 |
| 71 | Investigation of sliding DNA clamp dynamics by single-molecule fluorescence, mass spectrometry and structure-based modeling. Nucleic Acids Research, 2018, 46, 3103-3118. | 14.5 | 11 |
| 72 | Measurement of Fructoseâ€“Asparagine Concentrations in Human and Animal Foods. Journal of Agricultural and Food Chemistry, 2018, 66, 212-217. | 5.2 | 15 |

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| 73 | The Exon Junction Complex Undergoes a Compositional Switch that Alters mRNP Structure and Nonsense-Mediated mRNA Decay Activity. Cell Reports, 2018, 25, 2431-2446.e7. | 6.4 | 59 |
| 74 | Proteogenomic Analysis of Surgically Resected Lung Adenocarcinoma. Journal of Thoracic Oncology, 2018, 13, 1519-1529. | 1.1 | 17 |
| 75 | Localization of Protein Complex Bound Ligands by Surface-Induced Dissociation High-Resolution Mass Spectrometry. Analytical Chemistry, 2018, 90, 12796-12801. | 6.5 | 27 |
| 76 | RNA-binding proteins and heat-shock protein 90 are constituents of the cytoplasmic capping enzyme interactome. Journal of Biological Chemistry, 2018, 293, 16596-16607. | 3.4 | 7 |
| 77 | Identifying Unknown Enzymeâ€“Substrate Pairs from the Cellular Milieu with Native Mass Spectrometry. ChemBioChem, 2017, 18, 613-617. | 2.6 | 9 |
| 78 | Eng1 and Exg8 Are the Major Î±-Glucanases Secreted by the Fungal Pathogen Histoplasma capsulatum. Journal of Biological Chemistry, 2017, 292, 4801-4810. | 3.4 | 46 |
| 79 | Surface induced dissociation as a tool to study membrane protein complexes. Chemical Communications, 2017, 53, 3106-3109. | 4.1 | 34 |
| 80 | Infrared Multiple-Photon Dissociation Action Spectroscopy of the b<sub>2</sub><sup>+</sup> Ion from PPG: Evidence of Third Residue Affecting b<sub>2</sub><sup>+</sup> Fragment Structure. Journal of the American Society for Mass Spectrometry, 2017, 28, 1482-1488. | 2.8 | 15 |
| 81 | Chemical and pathogen-induced inflammation disrupt the murine intestinal microbiome. Microbiome, 2017, 5, 47. | 11.1 | 125 |
| 82 | Surface-Induced Dissociation of Protein Complexes in a Hybrid Fourier Transform Ion Cyclotron Resonance Mass Spectrometer. Analytical Chemistry, 2017, 89, 895-901. | 6.5 | 22 |
| 83 | Biogenic manganese oxide nanoparticle formation by a multimeric multicopper oxidase Mnx. Nature Communications, 2017, 8, 746. | 12.8 | 65 |
| 84 | Foldability of a Natural De Novo Evolved Protein. Structure, 2017, 25, 1687-1696.e4. | 3.3 | 44 |
| 85 | Human Argonaute3 has slicer activity. Nucleic Acids Research, 2017, 45, 11867-11877. | 14.5 | 86 |
| 86 | Evolutionary diversification of proteinâ€“protein interactions by interface add-ons. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8333-E8342. | 7.1 | 22 |
| 87 | A novel double kink-turn module in euryarchaeal RNase P RNAs. Nucleic Acids Research, 2017, 45, 7432-7440. | 14.5 | 22 |
| 88 | A metabolic intermediate of the fructose-asparagine utilization pathway inhibits growth of a Salmonella fraB mutant. Scientific Reports, 2016, 6, 28117. | 3.3 | 21 |
| 89 | A Protein-derived Oxygen Is the Source of the Amide Oxygen of Nitrile Hydratases. Journal of Biological Chemistry, 2016, 291, 7822-7829. | 3.4 | 6 |
| 90 | The P seudomonas aeruginosa â€… AmrZ C â€terminal domain mediates tetramerization and is required for its activator and repressor functions. Environmental Microbiology Reports, 2016, 8, 85-90. | 2.4 | 15 |

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| 91 | Use of chemical modification and mass spectrometry to identify substrate-contacting sites in proteinaceous RNase P, a tRNA processing enzyme. Nucleic Acids Research, 2016, 44, 5344-5355. | 14.5 | 14 |
| 92 | Extended Gas-Phase Trapping Followed by Surface-Induced Dissociation of Noncovalent Protein Complexes. Analytical Chemistry, 2016, 88, 1218-1221. | 6.5 | 21 |
| 93 | Possible isomers in ligand protected Ag<sub>11</sub>cluster ions identified by ion mobility mass spectrometry and fragmented by surface induced dissociation. Chemical Communications, 2016, 52, 3805-3808. | 4.1 | 39 |
| 94 | R vs. S fluoroproline ring substitution: trans/cis effects on the formation of b<sub>2</sub> ions in gas-phase peptide fragmentation. Physical Chemistry Chemical Physics, 2016, 18, 2202-2209. | 2.8 | 6 |
| 95 | Laser desorption ionization of small molecules assisted by tungsten oxide and rhenium oxide particles. Journal of Mass Spectrometry, 2015, 50, 891-898. | 1.6 | 15 |
| 96 | Resolution of Stepwise Cooperativities of Copper Binding by the Homotetrameric Copperâ€Sensitive Operon Repressor (CsoR): Impact on Structure and Stability. Angewandte Chemie - International Edition, 2015, 54, 12795-12799. | 13.8 | 11 |
| 97 | Surface-Induced Dissociation of Homotetramers with D2 Symmetry Yields their Assembly Pathways and Characterizes the Effect of Ligand Binding. Chemistry and Biology, 2015, 22, 583-592. | 6.0 | 62 |
| 98 | Low energy CID and action IRMPD provide insights into a minor subpopulation of the gas-phase conformers of triply charged bradykinin. International Journal of Mass Spectrometry, 2015, 391, 2-10. | 1.5 | 4 |
| 99 | Refining the Structural Model of a Heterohexameric Protein Complex: Surface Induced Dissociation and Ion Mobility Provide Key Connectivity and Topology Information. ACS Central Science, 2015, 1, 477-487. | 11.3 | 57 |
| 100 | Bound in flight. Nature Chemistry, 2015, 7, 189-190. | 13.6 | 1 |
| 101 | Mutant Poisoning Demonstrates a Nonsequential Mechanism for Digestion of Double-Stranded DNA by Î» Exonuclease Trimers. Biochemistry, 2015, 54, 942-951. | 2.5 | 4 |
| 102 | A Dimer Interface Mutation in Glyceraldehyde-3-Phosphate Dehydrogenase Regulates Its Binding to AU-rich RNA. Journal of Biological Chemistry, 2015, 290, 1770-1785. | 3.4 | 47 |
| 103 | Label-free detection and identification of protein ligands captured by receptors in a polymerized planar lipid bilayer using MALDI-TOF MS. Analytical and Bioanalytical Chemistry, 2015, 407, 2777-2789. | 3.7 | 3 |
| 104 | Surface induced dissociation yields substructure of Methanosarcina thermophila 20S proteasome complexes. International Journal of Mass Spectrometry, 2015, 377, 201-204. | 1.5 | 13 |
| 105 | Top-Down-Assisted Bottom-Up Method for Homologous Protein Sequencing: Hemoglobin from 33 Bird Species. Journal of the American Society for Mass Spectrometry, 2015, 26, 1875-1884. | 2.8 | 5 |
| 106 | Illustration of SID-IM-SID (surface-induced dissociation-ion mobility-SID) mass spectrometry: homo and hetero model protein complexes. Analyst, The, 2015, 140, 7012-7019. | 3.5 | 18 |
| 107 | Surface-Induced Dissociation Mass Spectra as a Tool for Distinguishing Different Structural Forms of Gas-Phase Multimeric Protein Complexes. Analytical Chemistry, 2015, 87, 11879-11886. | 6.5 | 52 |
| 108 | Probing the Run-On Oligomer of Activated SgrAI Bound to DNA. PLoS ONE, 2015, 10, e0124783. | 2.5 | 12 |

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| 109 | Shotgun Proteomic Analysis of Protein Expression in Mosquito Ovaries Post Blood Meal. FASEB Journal, 2015, 29, 567.13. | 0.5 | 0 |
| 110 | Mass Spectrometry in Structural Biology: Surfaceâ€induced Dissociation/Ion Mobility of Protein Complexes. FASEB Journal, 2015, 29, 360.3. | 0.5 | 1 |
| 111 | Gene regulation by substoichiometric heterocomplex formation of undecameric TRAP and trimeric anti-TRAP. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3442-3447. | 7.1 | 13 |
| 112 | Surface Induced Dissociation: Dissecting Noncovalent Protein Complexes in the Gas phase. Accounts of Chemical Research, 2014, 47, 1010-1018. | 15.6 | 112 |
| 113 | Human Defensins Facilitate Local Unfolding of Thermodynamically Unstable Regions of Bacterial Protein Toxins. Immunity, 2014, 41, 709-721. | 14.3 | 71 |
| 114 | Uncovering the Stoichiometry of Pyrococcus furiosus RNaseâ€‰P, a Multiâ€Subunit Catalytic Ribonucleoprotein Complex, by Surfaceâ€induced Dissociation and Ion Mobility Mass Spectrometry. Angewandte Chemie - International Edition, 2014, 53, 11483-11487. | 13.8 | 32 |
| 115 | Gas-Phase Helical Peptides Mimic Solution-Phase Behavior. Journal of the American Chemical Society, 2014, 136, 14173-14183. | 13.7 | 11 |
| 116 | Histone H1 Phosphorylation in Breast Cancer. Journal of Proteome Research, 2014, 13, 2453-2467. | 3.7 | 38 |
| 117 | Investigations of the Mechanism of the â€œProline Effectâ€•in Tandem Mass Spectrometry Experiments: The â€œPipecolic Acid Effectâ€• Journal of the American Society for Mass Spectrometry, 2014, 25, 1705-1715. | 2.8 | 24 |
| 118 | Paper Spray Ionization of Noncovalent Protein Complexes. Analytical Chemistry, 2014, 86, 1342-1346. | 6.5 | 70 |
| 119 | Interfacial Residues Promote an Optimal Alignment of the Catalytic Center in Human Soluble Guanylate Cyclase: Heterodimerization Is Required but Not Sufficient for Activity. Biochemistry, 2014, 53, 2153-2165. | 2.5 | 39 |
| 120 | Surface Induced Dissociation Yields Quaternary Substructure of Refractory Noncovalent Phosphorylase B and Glutamate Dehydrogenase Complexes. Journal of the American Society for Mass Spectrometry, 2014, 25, 368-379. | 2.8 | 34 |
| 121 | Ligand binding and unfolding of tryptophan synthase revealed by ion mobility-tandem mass spectrometry employing collision and surface induced dissociation. International Journal for Ion Mobility Spectrometry, 2013, 16, 133-143. | 1.4 | 12 |
| 122 | High-resolution identification of human adiponectin oligomers and regulation by pioglitazone in type 2 diabetic patients. Analytical Biochemistry, 2013, 437, 150-160. | 2.4 | 8 |
| 123 | Influence of N-terminal Residue Composition on the Structure of Proline-Containing b2+ Ions. Journal of Physical Chemistry A, 2013, 117, 1291-1298. | 2.5 | 25 |
| 124 | Impact of charge state on gas-phase behaviors of noncovalent protein complexes in collision induced dissociation and surface induced dissociation. Analyst, The, 2013, 138, 1353. | 3.5 | 74 |
| 125 | A polymetamorphic protein. Protein Science, 2013, 22, 641-649. | 7.6 | 7 |
| 126 | Molecular Model of a Soluble Guanylyl Cyclase Fragment Determined by Small-Angle X-ray Scattering and Chemical Cross-Linking. Biochemistry, 2013, 52, 1568-1582. | 2.5 | 56 |

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| 127 | An Unusual Dimeric Small Heat Shock Protein Provides Insight into the Mechanism of This Class of Chaperones. Journal of Molecular Biology, 2013, 425, 1683-1696. | 4.2 | 54 |
| 128 | Structural Analysis of Activated SgrAIâ€“DNA Oligomers Using Ion Mobility Mass Spectrometry. Biochemistry, 2013, 52, 4373-4381. | 2.5 | 20 |
| 129 | Low Mass MS/MS Fragments of Protonated Amino Acids Used for Distinction of Their <sup>13</sup>C-Isotopomers in Metabolic Studies. Journal of the American Society for Mass Spectrometry, 2013, 24, 622-631. | 2.8 | 10 |
| 130 | Dissecting the Large Noncovalent Protein Complex GroEL with Surface-Induced Dissociation and Ion Mobilityâ€“Mass Spectrometry. Analytical Chemistry, 2013, 85, 8262-8267. | 6.5 | 82 |
| 131 | Survival of Host Blood Proteins in <I>Ixodes scapularis</I> (Acari: Ixodidae) Ticks: A Time Course Study. Journal of Medical Entomology, 2013, 50, 1282-1290. | 1.8 | 13 |
| 132 | SQID-XLink: implementation of an intensity-incorporated algorithm for cross-linked peptide identification. Bioinformatics, 2012, 28, 2548-2550. | 4.1 | 10 |
| 133 | ETD fragmentation features improve algorithm. Expert Review of Proteomics, 2012, 9, 241-243. | 3.0 | 0 |
| 134 | Molecular Structure and Function of the Novel BrnT/BrnA Toxin-Antitoxin System of Brucella abortus. Journal of Biological Chemistry, 2012, 287, 12098-12110. | 3.4 | 75 |
| 135 | PCRâ€“Electrospray Ionization Mass Spectrometry. Journal of Molecular Diagnostics, 2012, 14, 295-304. | 2.8 | 89 |
| 136 | The influence glutamic acid in protonated b3â†’b2 formation from VGEIG and related analogs. International Journal of Mass Spectrometry, 2012, 325-327, 139-149. | 1.5 | 5 |
| 137 | N-Terminal Region of CusB Is Sufficient for Metal Binding and Metal Transfer with the Metallochaperone CusF. Biochemistry, 2012, 51, 6767-6775. | 2.5 | 37 |
| 138 | Surface-Induced Dissociation of Ion Mobility-Separated Noncovalent Complexes in a Quadrupole/Time-of-Flight Mass Spectrometer. Analytical Chemistry, 2012, 84, 6016-6023. | 6.5 | 72 |
| 139 | Study of the fragmentation of arginine isobutyl ester applied to arginine quantification in Aedes aegypti mosquito excreta. Journal of Mass Spectrometry, 2012, 47, 1364-1371. | 1.6 | 11 |
| 140 | Development of a host blood meal database: de novo sequencing of hemoglobin from nine small mammals using mass spectrometry. Biological Chemistry, 2012, 393, 195-201. | 2.5 | 18 |
| 141 | Structural Influences on Preferential Oxazolone versus Diketopiperazine b<sub>2</sub><sup>+</sup> Ion Formation for Histidine Analogue-Containing Peptides. Journal of Physical Chemistry A, 2012, 116, 4296-4304. | 2.5 | 33 |
| 142 | Protein Subunits Released by Surface Collisions of Noncovalent Complexes: Nativelike Compact Structures Revealed by Ion Mobility Mass Spectrometry. Angewandte Chemie - International Edition, 2012, 51, 4336-4339. | 13.8 | 89 |
| 143 | Influence of a gamma amino acid on the structures and reactivity of peptide a3 ions. International Journal of Mass Spectrometry, 2012, 316-318, 259-267. | 1.5 | 4 |
| 144 | Activation by Oligomerization of an Allosteric Sequence Specific Endonuclease. FASEB Journal, 2012, 26, lb91. | 0.5 | 0 |

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| 145 | Characterization of a novel Aedes aegypti ferritin subunit identified utilizing proteomic techniques. FASEB Journal, 2012, 26, 985.4. | 0.5 | 0 |
| 146 | Use of PCR Coupled with Electrospray Ionization Mass Spectrometry for Rapid Identification of Bacterial and Yeast Bloodstream Pathogens from Blood Culture Bottles. Journal of Clinical Microbiology, 2011, 49, 345-353. | 3.9 | 100 |
| 147 | Determinants of Gas-Phase Disassembly Behavior in Homodimeric Protein Complexes with Related Yet Divergent Structures. Analytical Chemistry, 2011, 83, 3881-3889. | 6.5 | 25 |
| 148 | Statistical Analysis of Electron Transfer Dissociation Pairwise Fragmentation Patterns. Analytical Chemistry, 2011, 83, 9540-9545. | 6.5 | 32 |
| 149 | Interactions between CusF and CusB Identified by NMR Spectroscopy and Chemical Cross-Linking Coupled to Mass Spectrometry. Biochemistry, 2011, 50, 2559-2566. | 2.5 | 51 |
| 150 | Revealing the Quaternary Structure of a Heterogeneous Noncovalent Protein Complex through Surface-Induced Dissociation. Analytical Chemistry, 2011, 83, 2862-2865. | 6.5 | 78 |
| 151 | SQID: An Intensity-Incorporated Protein Identification Algorithm for Tandem Mass Spectrometry. Journal of Proteome Research, 2011, 10, 1593-1602. | 3.7 | 55 |
| 152 | Comparative Analysis of PCRâ€“Electrospray Ionization/Mass Spectrometry (MS) and MALDI-TOF/MS for the Identification of Bacteria and Yeast from Positive Blood Culture Bottles. Clinical Chemistry, 2011, 57, 1057-1067. | 3.2 | 99 |
| 153 | The role of proton bridges in selective cleavage of Ser-, Thr-, Cys-, Met-, Asp-, and Asn-containing peptides. International Journal of Mass Spectrometry, 2011, 300, 108-117. | 1.5 | 9 |
| 154 | Proteomics Analyses of the Opportunistic PathogenBurkholderia vietnamiensisUsing Protein Fractionations and Mass Spectrometry. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-10. | 3.0 | 12 |
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