

Frank Sobott

List of Publications by Year in descending order

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Version: 2024-02-01

142
papers

7,838
citations

50566

48
h-index

68831

81
g-index

160
all docs

160
docs citations

160
times ranked

10525
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel electrochemiluminescent assay for the aptamer-based detection of testosterone. <i>Talanta</i> , 2022, 239, 123121.	2.9	9
2	Pocket delipidation induced by membrane tension or modification leads to a structurally analogous mechanosensitive channel state. <i>Structure</i> , 2022, 30, 608-622.e5.	1.6	16
3	DNA binding by the antimalarial compound artemisinin. <i>Scientific Reports</i> , 2022, 12, 133.	1.6	6
4	Tuning the rate of aggregation of hIAPP into amyloid using small-molecule modulators of assembly. <i>Nature Communications</i> , 2022, 13, 1040.	5.8	23
5	High-Resolution Hydrogen-Deuterium Protection Factors from Sparse Mass Spectrometry Data Validated by Nuclear Magnetic Resonance Measurements. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 813-822.	1.2	4
6	A NAC domain mutation (E83Q) unlocks the pathogenicity of human alpha-synuclein and recapitulates its pathological diversity. <i>Science Advances</i> , 2022, 8, eabn0044.	4.7	20
7	Sizing up DNA nanostructure assembly with native mass spectrometry and ion mobility. <i>Nature Communications</i> , 2022, 13, .	5.8	6
8	Aptamer-ligand recognition studied by native ion mobility-mass spectrometry. <i>Talanta</i> , 2021, 224, 121917.	2.9	14
9	Cryo-EM structure of human mitochondrial HSPD1. <i>iScience</i> , 2021, 24, 102022.	1.9	16
10	Structural modeling of a novel membrane-bound globin-coupled sensor in <i>Geobacter sulfurreducens</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1874-1888.	1.9	1
11	Native mass spectrometry for the design and selection of protein bioreceptors for perfluorinated compounds. <i>Analyst</i> , 2021, 146, 2065-2073.	1.7	6
12	Unveiling the binding mode of perfluorooctanoic acid to human serum albumin. <i>Protein Science</i> , 2021, 30, 830-841.	3.1	25
13	Discriminative SKP2 Interactions with CDK-Cyclin Complexes Support a Cyclin A-Specific Role in p27KIP1 Degradation. <i>Journal of Molecular Biology</i> , 2021, 433, 166795.	2.0	10
14	Brazilin Removes Toxic Alpha-Synuclein and Seeding Competent Assemblies from Parkinson Brain by Altering Conformational Equilibrium. <i>Journal of Molecular Biology</i> , 2021, 433, 166878.	2.0	10
15	Structure of the endocytic adaptor complex reveals the basis for efficient membrane anchoring during clathrin-mediated endocytosis. <i>Nature Communications</i> , 2021, 12, 2889.	5.8	13
16	Profiling Dopamine-Induced Oxidized Proteoforms of α -synuclein by Top-Down Mass Spectrometry. <i>Antioxidants</i> , 2021, 10, 893.	2.2	1
17	Entropic pressure controls the oligomerization of the <i>Vibrio cholerae</i> ParD2 antitoxin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 904-920.	1.1	5
18	Analysis of the PcrA-RNA polymerase complex reveals a helicase interaction motif and a role for PcrA/UvrD helicase in the suppression of R-loops. <i>ELife</i> , 2021, 10, .	2.8	18

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19	Nanobody-aided crystallization of the transcription regulator PaaR2 from <i>Escherichia coli</i> O157:H7. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 374-384.	0.4	2
20	A model of full-length RAGE in complex with S100B. <i>Structure</i> , 2021, 29, 989-1002.e6.	1.6	5
21	On-grid and in-flow mixing for time-resolved cryo-EM. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1233-1240.	1.1	14
22	Fast Grid Preparation for Time-Resolved Cryo-Electron Microscopy. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	0
23	Cycloalkane-modified amphiphilic polymers provide direct extraction of membrane proteins for CryoEM analysis. <i>Communications Biology</i> , 2021, 4, 1337.	2.0	13
24	Further insights from structural mass spectrometry into endocytosis adaptor protein assemblies. <i>International Journal of Mass Spectrometry</i> , 2020, 447, 116240.	0.7	4
25	Styrene maleic-acid lipid particles (SMALPs) into detergent or amphipols: An exchange protocol for membrane protein characterisation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183192.	1.4	27
26	Need for Speed: Examining Protein Behavior during CryoEM Grid Preparation at Different Timescales. <i>Structure</i> , 2020, 28, 1238-1248.e4.	1.6	61
27	Metal ions shape α -synuclein. <i>Scientific Reports</i> , 2020, 10, 16293.	1.6	55
28	Software Requirements for the Analysis and Interpretation of Native Ion Mobility Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020, 92, 10881-10890.	3.2	17
29	Computational Strategies and Challenges for Using Native Ion Mobility Mass Spectrometry in Biophysics and Structural Biology. <i>Analytical Chemistry</i> , 2020, 92, 10872-10880.	3.2	24
30	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1783-1802.	1.2	67
31	Do Aptamers Always Bind? The Need for a Multifaceted Analytical Approach When Demonstrating Binding Affinity between Aptamer and Low Molecular Weight Compounds. <i>Journal of the American Chemical Society</i> , 2020, 142, 19622-19630.	6.6	63
32	Effects of Detergent on α -Synuclein Structure: A Native MS-Ion Mobility Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7884.	1.8	9
33	Extent of N-terminus exposure of monomeric alpha-synuclein determines its aggregation propensity. <i>Nature Communications</i> , 2020, 11, 2820.	5.8	99
34	The <i>Escherichia coli</i> RnIA-RnIB toxin-antitoxin complex: production, characterization and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 31-39.	0.4	2
35	Interrogating Membrane Protein Structure and Lipid Interactions by Native Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2020, 2168, 233-261.	0.4	5
36	Allosteric modulation of the GTPase activity of a bacterial LRRK2 homolog by conformation-specific Nanobodies. <i>Biochemical Journal</i> , 2020, 477, 1203-1218.	1.7	12

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37	Sample deposition onto cryo-EM grids: from sprays to jets and back. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 340-349.	1.1	23
38	Structural mechanism of synergistic activation of Aurora kinase B/C by phosphorylated INCENP. <i>Nature Communications</i> , 2019, 10, 3166.	5.8	21
39	MIND: A Double-Linear Model To Accurately Determine Monoisotopic Precursor Mass in High-Resolution Top-Down Proteomics. <i>Analytical Chemistry</i> , 2019, 91, 10310-10319.	3.2	3
40	Recommendations for reporting ion mobility Mass Spectrometry measurements. <i>Mass Spectrometry Reviews</i> , 2019, 38, 291-320.	2.8	315
41	Native Ion Mobility-Mass Spectrometry Reveals the Formation of β -Barrel Shaped Amyloid β Hexamers in a Membrane-Mimicking Environment. <i>Journal of the American Chemical Society</i> , 2019, 141, 10440-10450.	6.6	94
42	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
43	Cyclized NDGA modifies dynamic α -synuclein monomers preventing aggregation and toxicity. <i>Scientific Reports</i> , 2019, 9, 2937.	1.6	31
44	Thermodynamic Stability of the Transcription Regulator PaaR2 from <i>Escherichia coli</i> O157:H7. <i>Biophysical Journal</i> , 2019, 116, 1420-1431.	0.2	4
45	A dual role in regulation and toxicity for the disordered N-terminus of the toxin GraT. <i>Nature Communications</i> , 2019, 10, 972.	5.8	29
46	Methionine oxidation in α -synuclein inhibits its propensity for ordered secondary structure. <i>Journal of Biological Chemistry</i> , 2019, 294, 5657-5665.	1.6	25
47	Enhanced oligomerization of full-length RAGE by synergy of the interaction of its domains. <i>Scientific Reports</i> , 2019, 9, 20332.	1.6	14
48	masstodon: A Tool for Assigning Peaks and Modeling Electron Transfer Reactions in Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 1801-1807.	3.2	7
49	A cryo-EM grid preparation device for time-resolved structural studies. <i>IUCr</i> , 2019, 6, 1024-1031.	1.0	77
50	Fixed-Charge Trimethyl Pyrylium Modification for Enabling Enhanced Top-Down Mass Spectrometry Sequencing of Intact Protein Complexes. <i>Analytical Chemistry</i> , 2018, 90, 2756-2764.	3.2	19
51	Radical solutions: Principles and application of electron-based dissociation in mass spectrometry-based analysis of protein structure. <i>Mass Spectrometry Reviews</i> , 2018, 37, 750-771.	2.8	67
52	Phosphorylation decelerates conformational dynamics in bacterial translation elongation factors. <i>Science Advances</i> , 2018, 4, eaap9714.	4.7	37
53	Advances in native high-performance liquid chromatography and intact mass spectrometry for the characterization of biopharmaceutical products. <i>Journal of Separation Science</i> , 2018, 41, 125-144.	1.3	48
54	Estimation of Rates of Reactions Triggered by Electron Transfer in Top-Down Mass Spectrometry. <i>Journal of Computational Biology</i> , 2018, 25, 282-301.	0.8	2

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55	Evaluation of ion mobility for the separation of glycoconjugate isomers due to different types of sialic acid linkage, at the intact glycoprotein, glycopeptide and glycan level. <i>Journal of Proteomics</i> , 2018, 173, 22-31.	1.2	24
56	Editorial and Review: 30th ASMS Sanibel Conference on Mass Spectrometry – Computational Modelling in Mass Spectrometry and Ion Mobility: Methods for Ion Structure and Reactivity Determination. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 2283-2286.	1.2	1
57	The effect of reactive oxygen and nitrogen species on the structure of cytoglobin: A potential tumor suppressor. <i>Redox Biology</i> , 2018, 19, 1-10.	3.9	31
58	Analysis of the natively unstructured RNA/protein-recognition core in the Escherichia coli RNA degradosome and its interactions with regulatory RNA/Hfq complexes. <i>Nucleic Acids Research</i> , 2018, 46, 387-402.	6.5	66
59	Hidden States within Disordered Regions of the CcdA Antitoxin Protein. <i>Journal of the American Chemical Society</i> , 2017, 139, 2693-2701.	6.6	9
60	Proton Dynamics in Protein Mass Spectrometry. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 1105-1112.	2.1	34
61	Analyzing complex mixtures of drug-like molecules: Ion mobility as an adjunct to existing liquid chromatography-(tandem) mass spectrometry methods. <i>Journal of Chromatography A</i> , 2017, 1490, 80-88.	1.8	9
62	Preprotein mature domains contain translocase targeting signals that are essential for secretion. <i>Journal of Cell Biology</i> , 2017, 216, 1357-1369.	2.3	67
63	Raman optical activity of human α -synuclein in intrinsically disordered, micelle-bound α -helical, molten globule and oligomeric β -sheet state. <i>Journal of Raman Spectroscopy</i> , 2017, 48, 910-918.	1.2	36
64	Antarctic fish versus human cytoglobins – The same but yet so different. <i>Journal of Inorganic Biochemistry</i> , 2017, 173, 66-78.	1.5	15
65	Specific sequences in the N-terminal domain of human small heat-shock protein HSPB6 dictate preferential hetero-oligomerization with the orthologue HSPB1. <i>Journal of Biological Chemistry</i> , 2017, 292, 9944-9957.	1.6	23
66	AtaT blocks translation initiation by N-acetylation of the initiator tRNA ^{fMet} . <i>Nature Chemical Biology</i> , 2017, 13, 640-646.	3.9	71
67	Phase Separation of C9orf72 Dipeptide Repeats Perturbs Stress Granule Dynamics. <i>Molecular Cell</i> , 2017, 65, 1044-1055.e5.	4.5	437
68	A homologue of the Parkinson's disease-associated protein LRRK2 undergoes a monomer-dimer transition during GTP turnover. <i>Nature Communications</i> , 2017, 8, 1008.	5.8	53
69	Apparent activation energies of protein-protein complex dissociation in the gas phase determined by electrospray mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 6549-6558.	1.9	15
70	Native Mass Spectrometry for the Characterization of Structure and Interactions of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2017, 1635, 205-232.	0.4	16
71	A broader view on ion heating in traveling-wave devices using fragmentation of Csl clusters and extent of H _E TM migration as molecular thermometers. <i>Analyst</i> , 2017, 142, 3388-3399.	1.7	7
72	Conformational Space and Stability of ETD Charge Reduction Products of Ubiquitin. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 69-76.	1.2	27

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73	The structural basis for dynamic DNA binding and bridging interactions which condense the bacterial centromere. <i>ELife</i> , 2017, 6, .	2.8	64
74	Estimation of Rates of Reactions Triggered by Electron Transfer in Top-Down Mass Spectrometry. <i>Lecture Notes in Computer Science</i> , 2017, , 96-107.	1.0	0
75	Covalent adducts of melphalan with free amino acids and a model peptide studied by liquid chromatography/tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2016, 30, 719-730.	0.7	4
76	The preferential heterodimerization of human small heat shock proteins HSPB1 and HSPB6 is dictated by the N-terminal domain. <i>Archives of Biochemistry and Biophysics</i> , 2016, 610, 41-50.	1.4	19
77	Opposite Structural Effects of Epigallocatechin-3-gallate and Dopamine Binding to α -Synuclein. <i>Analytical Chemistry</i> , 2016, 88, 8468-8475.	3.2	61
78	ATP and autophosphorylation driven conformational changes of HipA kinase revealed by ion mobility and crosslinking mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 5925-5933.	1.9	6
79	Gas-phase microsolvation of ubiquitin: investigation of crown ether complexation sites using ion mobility-mass spectrometry. <i>Analyst, The</i> , 2016, 141, 5502-5510.	1.7	19
80	Lipids modulate the conformational dynamics of a secondary multidrug transporter. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 744-751.	3.6	111
81	Development of a novel antibody-tetrazine conjugate for bioorthogonal pretargeting. <i>Organic and Biomolecular Chemistry</i> , 2016, 14, 7544-7551.	1.5	38
82	Combining density functional theory (DFT) and collision cross-section (CCS) calculations to analyze the gas-phase behaviour of small molecules and their protonation site isomers. <i>Analyst, The</i> , 2016, 141, 4044-4054.	1.7	74
83	Top-down mass spectrometry of intact membrane protein complexes reveals oligomeric state and sequence information in a single experiment. <i>Protein Science</i> , 2015, 24, 1292-1300.	3.1	42
84	Electron transfer dissociation provides higher-order structural information of native and partially unfolded protein complexes. <i>Proteomics</i> , 2015, 15, 2813-2822.	1.3	57
85	Specific and non-specific interactions of ParB with DNA: implications for chromosome segregation. <i>Nucleic Acids Research</i> , 2015, 43, 719-731.	6.5	68
86	Characterization of top-down ETD in a travelling-wave ion guide. <i>Methods</i> , 2015, 89, 22-29.	1.9	21
87	Bouncing off the Walls: Excited Protein Complexes Tell Their Story. <i>Chemistry and Biology</i> , 2015, 22, 563-564.	6.2	3
88	Signal loss due to oligomerization in ELISA analysis of amyloid-beta can be recovered by a novel sample pre-treatment method. <i>MethodsX</i> , 2015, 2, 112-123.	0.7	19
89	Extensive Charge Reduction and Dissociation of Intact Protein Complexes Following Electron Transfer on a Quadrupole-Ion Mobility-Time-of-Flight MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1068-1076.	1.2	53
90	Protomers of Benzocaine: Solvent and Permittivity Dependence. <i>Journal of the American Chemical Society</i> , 2015, 137, 4236-4242.	6.6	172

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91	Biophysical Studies on Interactions and Assembly of Full-size E3 Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2015, 290, 4178-4191.	1.6	24
92	Extending native mass spectrometry approaches to integral membrane proteins. <i>Biological Chemistry</i> , 2015, 396, 991-1002.	1.2	31
93	Differences in the Elemental Isotope Definition May Lead to Errors in Modern Mass-Spectrometry-Based Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 10747-10754.	3.2	6
94	Understanding reaction pathways in top-down ETD by dissecting isotope distributions: A mammoth task. <i>International Journal of Mass Spectrometry</i> , 2015, 390, 146-154.	0.7	20
95	Molecular Basis for Structural Heterogeneity of an Intrinsically Disordered Protein Bound to a Partner by Combined ESI-IM-MS and Modeling. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 472-481.	1.2	45
96	Type III restriction endonucleases are heterotrimeric: comprising one helicase-nuclease subunit and a dimeric methyltransferase that binds only one specific DNA. <i>Nucleic Acids Research</i> , 2014, 42, 5139-5150.	6.5	29
97	The Intrinsically Disordered Domain of the Antitoxin Phd Chaperones the Toxin Doc against Irreversible Inactivation and Misfolding. <i>Journal of Biological Chemistry</i> , 2014, 289, 34013-34023.	1.6	10
98	Global structural changes of an ion channel during its gating are followed by ion mobility mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17170-17175.	3.3	63
99	ETD Allows for Native Surface Mapping of a 150 kDa Noncovalent Complex on a Commercial Q-TWIMS-TOF Instrument. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 343-350.	1.2	78
100	LptA Assembles into Rod-Like Oligomers Involving Disorder-to-Order Transitions. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1593-1602.	1.2	29
101	Travelling wave ion mobility and negative ion fragmentation for the structural determination of N-linked glycans. <i>Electrophoresis</i> , 2013, 34, 2368-2378.	1.3	49
102	Structural plasticity of histones H3-H4 facilitates their allosteric exchange between RbAp48 and ASF1. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 29-35.	3.6	57
103	Organization of the BcgI restriction-modification protein for the transfer of one methyl group to DNA. <i>Nucleic Acids Research</i> , 2013, 41, 405-417.	6.5	9
104	Hfq binding changes the structure of <i>Escherichia coli</i> small noncoding RNAs OxyS and RprA, which are involved in the riboregulation of <i>rpoS</i> . <i>Rna</i> , 2013, 19, 1089-1104.	1.6	38
105	Organization of the BcgI restriction-modification protein for the cleavage of eight phosphodiester bonds in DNA. <i>Nucleic Acids Research</i> , 2013, 41, 391-404.	6.5	12
106	Contactin-associated protein-2 antibodies in non-paraneoplastic cerebellar ataxia. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2012, 83, 437-440.	0.9	105
107	The low-resolution solution structure of <i>Vibrio cholerae</i> Hfq in complex with Qrr1 sRNA. <i>Nucleic Acids Research</i> , 2012, 40, 8698-8710.	6.5	25
108	Characterization of <i>Vibrio cholerae</i> Hfq Provides Novel Insights into the Role of the Hfq C-Terminal Region. <i>Journal of Molecular Biology</i> , 2012, 420, 56-69.	2.0	27

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109	Metal and redox selectivity of protoporphyrin binding to the heme chaperone CcmE. <i>Metallomics</i> , 2011, 3, 363.	1.0	4
110	Compaction Properties of an Intrinsically Disordered Protein: Sic1 and Its Kinase-Inhibitor Domain. <i>Biophysical Journal</i> , 2011, 100, 2243-2252.	0.2	62
111	Ion Mobility Mass Spectrometry for Extracting Spectra of N-Glycans Directly from Incubation Mixtures Following Glycan Release: Application to Glycans from Engineered Glycoforms of Intact, Folded HIV gp120. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 568-581.	1.2	65
112	Characterization of β 2-microglobulin conformational intermediates associated to different fibrillation conditions. <i>Journal of Mass Spectrometry</i> , 2011, 46, 734-741.	0.7	13
113	DNA Nanomachines Investigated By Non-Denaturing Mass Spectrometry. <i>Biophysical Journal</i> , 2010, 98, 9a.	0.2	1
114	Comparison of CID versus ETD based MS/MS fragmentation for the analysis of protein ubiquitination. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1652-1659.	1.2	69
115	Quadrupole-Time-of-Flight Mass Spectrometer Modified for Higher-Energy Dissociation Reduces Protein Assemblies to Peptide Fragments. <i>Analytical Chemistry</i> , 2009, 81, 1270-1274.	3.2	50
116	Application of a Proteolysis/Mass Spectrometry Method for Investigating the Effects of Inhibitors on Hydroxylase Structure. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 2799-2805.	2.9	43
117	Structure of the Human Protein Kinase MPSK1 Reveals an Atypical Activation Loop Architecture. <i>Structure</i> , 2008, 16, 115-124.	1.6	38
118	Codon optimization can improve expression of human genes in <i>Escherichia coli</i> : A multi-gene study. <i>Protein Expression and Purification</i> , 2008, 59, 94-102.	0.6	273
119	The centaurin β -1 GTPase-like domain functions as an NTPase. <i>Biochemical Journal</i> , 2007, 401, 679-688.	1.7	29
120	Structural and Functional Characterization of the Human Protein Kinase ASK1. <i>Structure</i> , 2007, 15, 1215-1226.	1.6	98
121	Understanding Protein Interactions and Their Representation in the Gas Phase of the Mass Spectrometer. , 2006, , 147-175.		5
122	The Co-chaperone p23 Arrests the Hsp90 ATPase Cycle to Trap Client Proteins. <i>Journal of Molecular Biology</i> , 2006, 356, 746-758.	2.0	179
123	Structure of an Hsp90-Cdc37-Cdk4 Complex. <i>Molecular Cell</i> , 2006, 23, 697-707.	4.5	288
124	Tandem Mass Spectrometry Reveals the Quaternary Organization of Macromolecular Assemblies. <i>Chemistry and Biology</i> , 2006, 13, 597-605.	6.2	206
125	Structural basis for protein-protein interactions in the 14-3-3 protein family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17237-17242.	3.3	340
126	The flight of macromolecular complexes in a mass spectrometer. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2005, 363, 379-391.	1.6	70

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127	Heptameric (L12) ₆ /L10 rather than canonical pentameric complexes are found by tandem MS of intact ribosomes from thermophilic bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8192-8197.	3.3	134
128	Characterising electrosprayed biomolecules using tandem-MS – the noncovalent GroEL chaperonin assembly. International Journal of Mass Spectrometry, 2004, 236, 25-32.	0.7	102
129	Tandem Mass Spectrometry Defines the Stoichiometry and Quaternary Structural Arrangement of Tryptophan Molecules in the Multiprotein Complex TRAP. Journal of the American Chemical Society, 2004, 126, 5950-5951.	6.6	62
130	Biochemical and Structural Studies of the Interaction of Cdc37 with Hsp90. Journal of Molecular Biology, 2004, 340, 891-907.	2.0	82
131	Gas-phase dissociation pathways of a tetrameric protein complex. International Journal of Mass Spectrometry, 2003, 230, 193-200.	0.7	57
132	Reactions of gold cluster cations Au _n ⁺ (n=1-12) with H ₂ S and H ₂ . Journal of Chemical Physics, 2003, 118, 7808-7816.	1.2	72
133	Thermal Dissociation of Multimeric Protein Complexes by Using Nanoelectrospray Mass Spectrometry. Analytical Chemistry, 2003, 75, 2208-2214.	3.2	161
134	Subunit Exchange of Multimeric Protein Complexes. Journal of Biological Chemistry, 2002, 277, 38921-38929.	1.6	180
135	A Tandem Mass Spectrometer for Improved Transmission and Analysis of Large Macromolecular Assemblies. Analytical Chemistry, 2002, 74, 1402-1407.	3.2	481
136	Protein complexes gain momentum. Current Opinion in Structural Biology, 2002, 12, 729-734.	2.6	138
137	Detection of intact hemoglobin from aqueous solution with laser desorption mass spectrometry. , 2000, 14, 859-861.		28
138	Speciation in Solution: Silicate Oligomers in Aqueous Solutions Detected by Mass Spectrometry. Angewandte Chemie - International Edition, 2000, 39, 3901-3905.	7.2	78
139	Ionic clathrates from aqueous solutions detected with laser induced liquid beam ionization/desorption mass spectrometry. International Journal of Mass Spectrometry, 1999, 185-187, 271-279.	0.7	51
140	Examination of Condensation Products of Group 4 Alkoxides with Laser-Induced Liquid Beam Ionization/Desorption Mass Spectrometry. Chemistry - A European Journal, 1998, 4, 2353-2359.	1.7	21
141	Laser desorption mass spectrometry on thin liquid jets. Fresenius' Journal of Analytical Chemistry, 1998, 360, 745-749.	1.5	19
142	Cation Selectivity of Natural and Synthetic Ionophores Probed with Laser-Induced Liquid Beam Mass Spectrometry. Analytical Chemistry, 1997, 69, 3587-3594.	3.2	50