

Fang-Jun Wang

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127
papers

3,870
citations

34
h-index

58
g-index

138
ext. papers

4,388
ext. citations

6.3
avg, IF

5.06
L-index

#	Paper	IF	Citations
127	Glycoproteomics analysis of human liver tissue by combination of multiple enzyme digestion and hydrazide chemistry. <i>Journal of Proteome Research</i> , 2009 , 8, 651-61	5.6	305
126	Recent development of monolithic stationary phases with emphasis on microscale chromatographic separation. <i>Journal of Chromatography A</i> , 2008 , 1184, 369-92	4.5	242
125	An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. <i>Journal of Proteomics</i> , 2014 , 96, 253-62	3.9	166
124	"One-pot" process for fabrication of organic-silica hybrid monolithic capillary columns using organic monomer and alkoxy silane. <i>Analytical Chemistry</i> , 2009 , 81, 3529-36	7.8	123
123	Reversed-phase-reversed-phase liquid chromatography approach with high orthogonality for multidimensional separation of phosphopeptides. <i>Analytical Chemistry</i> , 2010 , 82, 53-6	7.8	120
122	Highly efficient extraction of serum peptides by ordered mesoporous carbon. <i>Angewandte Chemie - International Edition</i> , 2011 , 50, 12218-21	16.4	111
121	Capillary trap column with strong cation-exchange monolith for automated shotgun proteome analysis. <i>Analytical Chemistry</i> , 2007 , 79, 6599-606	7.8	107
120	Preparation of monodisperse immobilized Ti(4+) affinity chromatography microspheres for specific enrichment of phosphopeptides. <i>Analytica Chimica Acta</i> , 2009 , 636, 34-41	6.6	99
119	ZnAl-Hydroxide-Supported Au Nanoclusters as Precatalysts for Chemoselective Hydrogenation of 3-Nitrostyrene. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 2709-2713	16.4	97
118	Synthesis of branched PEG brushes hybrid hydrophilic magnetic nanoparticles for the selective enrichment of N-linked glycopeptides. <i>Chemical Communications</i> , 2012 , 48, 8138-40	5.8	91
117	Coupling strong anion-exchange monolithic capillary with MALDI-TOF MS for sensitive detection of phosphopeptides in protein digest. <i>Analytical Chemistry</i> , 2010 , 82, 2907-15	7.8	87
116	Novel Features of Eukaryotic Photosystem II Revealed by Its Crystal Structure Analysis from a Red Alga. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5676-5687	5.4	84
115	Centrifugation assisted microreactor enables facile integration of trypsin digestion, hydrophilic interaction chromatography enrichment, and on-column deglycosylation for rapid and sensitive N-glycoproteome analysis. <i>Analytical Chemistry</i> , 2012 , 84, 5146-53	7.8	84
114	Gold Nanorod Photothermal Therapy Alters Cell Junctions and Actin Network in Inhibiting Cancer Cell Collective Migration. <i>ACS Nano</i> , 2018 , 12, 9279-9290	16.7	72
113	Enrichment and separation techniques for large-scale proteomics analysis of the protein post-translational modifications. <i>Journal of Chromatography A</i> , 2014 , 1372C, 1-17	4.5	72
112	Peptide profiling and the bioactivity character of yogurt in the simulated gastrointestinal digestion. <i>Journal of Proteomics</i> , 2016 , 141, 24-46	3.9	63
111	A fully automated system with online sample loading, isotope dimethyl labeling and multidimensional separation for high-throughput quantitative proteome analysis. <i>Analytical Chemistry</i> , 2010 , 82, 3007-15	7.8	62

110	Comparative proteomic analysis of <i>Rhodospiridium toruloides</i> during lipid accumulation. <i>Yeast</i> , 2009 , 26, 553-66	3.4	62
109	Comprehensive mapping of protein N-glycosylation in human liver by combining hydrophilic interaction chromatography and hydrazide chemistry. <i>Journal of Proteome Research</i> , 2014 , 13, 1713-21	5.6	61
108	Spatially Resolved Proteome Mapping of Laser Capture Microdissected Tissue with Automated Sample Transfer to Nanodroplets. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1864-1874	7.6	58
107	Improvement of the quantification accuracy and throughput for phosphoproteome analysis by a pseudo triplex stable isotope dimethyl labeling approach. <i>Analytical Chemistry</i> , 2011 , 83, 7755-62	7.8	51
106	Monolithic capillary column based glycoproteomic reactor for high-sensitive analysis of N-glycoproteome. <i>Analytical Chemistry</i> , 2013 , 85, 2847-52	7.8	50
105	Development of glycoprotein capture-based label-free method for the high-throughput screening of differential glycoproteins in hepatocellular carcinoma. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.006445	7.6	49
104	Five-plex isotope dimethyl labeling for quantitative proteomics. <i>Chemical Communications</i> , 2014 , 50, 1708-10	5.8	46
103	Facile preparation of ordered mesoporous silica-carbon composite nanoparticles for glycan enrichment. <i>Chemical Communications</i> , 2013 , 49, 5162-4	5.8	46
102	Perspectives of comprehensive phosphoproteome analysis using shotgun strategy. <i>Analytical Chemistry</i> , 2011 , 83, 8078-85	7.8	45
101	Improve the coverage for the analysis of phosphoproteome of HeLa cells by a tandem digestion approach. <i>Journal of Proteome Research</i> , 2012 , 11, 2828-37	5.6	44
100	Multi-hierarchical profiling the structure-activity relationships of engineered nanomaterials at nano-bio interfaces. <i>Nature Communications</i> , 2018 , 9, 4416	17.4	41
99	Capture and dimethyl labeling of glycopeptides on hydrazide beads for quantitative glycoproteomics analysis. <i>Analytical Chemistry</i> , 2012 , 84, 8452-6	7.8	40
98	The proteome analysis of oleaginous yeast <i>Lipomyces starkeyi</i> . <i>FEMS Yeast Research</i> , 2011 , 11, 42-51	3.1	40
97	Phosphoric acid functionalized mesoporous organo-silica (EPO) as the adsorbent for in situ enrichment and isotope labeling of endogenous phosphopeptides. <i>Chemical Communications</i> , 2012 , 48, 961-3	5.8	36
96	Separation of intact proteins by using polyhedral oligomeric silsesquioxane based hybrid monolithic capillary columns. <i>Journal of Chromatography A</i> , 2013 , 1317, 138-47	4.5	35
95	Magnetic nanoparticles coated with maltose-functionalized polyethyleneimine for highly efficient enrichment of N-glycopeptides. <i>Journal of Chromatography A</i> , 2015 , 1425, 213-20	4.5	34
94	A proteomic analysis of engineered tendon formation under dynamic mechanical loading in vitro. <i>Biomaterials</i> , 2011 , 32, 4085-95	15.6	34
93	Development of a combined chemical and enzymatic approach for the mass spectrometric identification and quantification of aberrant N-glycosylation. <i>Journal of Proteomics</i> , 2012 , 75, 1666-74	3.9	32

92	Proteomic reactors and their applications in biology. <i>FEBS Journal</i> , 2011 , 278, 3796-806	5.7	32
91	Biflavones from Ginkgo biloba as inhibitors of human thrombin. <i>Bioorganic Chemistry</i> , 2019 , 92, 103199	5.1	31
90	Functionalizing with glycopeptide dendrimers significantly enhances the hydrophilicity of the magnetic nanoparticles. <i>Chemical Communications</i> , 2015 , 51, 4093-6	5.8	31
89	Online multidimensional separation with biphasic monolithic capillary column for shotgun proteome analysis. <i>Journal of Proteome Research</i> , 2008 , 7, 306-10	5.6	31
88	ZnAl-Hydrotalcite-Supported Au ₂₅ Nanoclusters as Precatalysts for Chemoselective Hydrogenation of 3-Nitrostyrene. <i>Angewandte Chemie</i> , 2017 , 129, 2753-2757	3.6	30
87	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. <i>Skeletal Muscle</i> , 2012 , 2, 5	5.1	30
86	Proteomics Analysis of O-GalNAc Glycosylation in Human Serum by an Integrated Strategy. <i>Analytical Chemistry</i> , 2017 , 89, 1469-1476	7.8	29
85	Improved recovery and identification of membrane proteins from rat hepatic cells using a centrifugal proteomic reactor. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, O111.008425	7.6	29
84	A peptide N-terminal protection strategy for comprehensive glycoproteome analysis using hydrazide chemistry based method. <i>Scientific Reports</i> , 2015 , 5, 10164	4.9	28
83	A simple integrated system for rapid analysis of sialic-acid-containing N-glycopeptides from human serum. <i>Proteomics</i> , 2013 , 13, 1306-13	4.8	28
82	Isobaric cross-sequence labeling of peptides by using site-selective N-terminus dimethylation. <i>Chemical Communications</i> , 2012 , 48, 6265-7	5.8	28
81	Proteomic analysis of protein methylation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , 2015 , 114, 226-33	3.9	27
80	Comprehensive proteome quantification reveals NgBR as a new regulator for epithelial-mesenchymal transition of breast tumor cells. <i>Journal of Proteomics</i> , 2015 , 112, 38-52	3.9	27
79	Selective capture of phosphopeptides by hierarchical Ti-aluminophosphate-5 molecular sieves. <i>Chemical Communications</i> , 2012 , 48, 1802-4	5.8	26
78	Analytical aspects of proteomics: 2009-2010. <i>Analytical Chemistry</i> , 2011 , 83, 4407-26	7.8	26
77	Oncogenic AURKA-enhanced N-methyladenosine modification increases DROSHA mRNA stability to transactivate STC1 in breast cancer stem-like cells. <i>Cell Research</i> , 2021 , 31, 345-361	24.7	26
76	Preparation of capillary hybrid monolithic column with sulfonate strong cation exchanger for proteome analysis. <i>Journal of Chromatography A</i> , 2012 , 1256, 136-43	4.5	24
75	Comprehensive and reliable phosphorylation site mapping of individual phosphoproteins by combination of multiple stage mass spectrometric analysis with a target-decoy database search. <i>Analytical Chemistry</i> , 2009 , 81, 5794-805	7.8	22

74	Isolation and characterization of PSI-LHCI super-complex and their sub-complexes from a red alga <i>Cyanidioschyzon merolae</i> . <i>Photosynthesis Research</i> , 2017 , 133, 201-214	3.7	21
73	Preparation of a butyl-silica hybrid monolithic column with a "one-pot" process for bioseparation by capillary liquid chromatography. <i>Analytical and Bioanalytical Chemistry</i> , 2013 , 405, 2265-71	4.4	21
72	C-N and N-H Bond Metathesis Reactions Mediated by Carbon Dioxide. <i>ChemSusChem</i> , 2015 , 8, 2066-72	8.3	21
71	Large-scale quantification of single amino-acid variations by a variation-associated database search strategy. <i>Journal of Proteome Research</i> , 2014 , 13, 241-8	5.6	20
70	Real-Time Tracking the Synthesis and Degradation of Albumin in Complex Biological Systems with a near-Infrared Fluorescent Probe. <i>Analytical Chemistry</i> , 2017 , 89, 9884-9891	7.8	20
69	High-sensitivity N-glycoproteomic analysis of mouse brain tissue by protein extraction with a mild detergent of N-dodecyl β -D-maltoside. <i>Analytical Chemistry</i> , 2015 , 87, 2054-7	7.8	20
68	Automated injection of uncleaned samples using a ten-port switching valve and a strong cation-exchange trap column for proteome analysis. <i>Journal of Chromatography A</i> , 2007 , 1171, 56-62	4.5	20
67	Probing the Lysine Proximal Microenvironments within Membrane Protein Complexes by Active Dimethyl Labeling and Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 12060-12065	7.8	20
66	Large-scale proteome quantification of hepatocellular carcinoma tissues by a three-dimensional liquid chromatography strategy integrated with sample preparation. <i>Journal of Proteome Research</i> , 2014 , 13, 3645-54	5.6	19
65	Reductive methylation labeling, from quantitative to structural proteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2019 , 118, 771-778	14.6	18
64	Highly efficient N-glycoproteomic sample preparation by combining C(18) and graphitized carbon adsorbents. <i>Analytical and Bioanalytical Chemistry</i> , 2014 , 406, 3103-9	4.4	15
63	Enhancing the performance of LC-MS for intact protein analysis by counteracting the signal suppression effects of trifluoroacetic acid during electrospray. <i>Chemical Communications</i> , 2015 , 51, 14758-60	5.8	15
62	Fractionation of phosphopeptides on strong anion-exchange capillary trap column for large-scale phosphoproteome analysis of microgram samples. <i>Journal of Separation Science</i> , 2010 , 33, 1879-87	3.4	15
61	Prediction of ligand modulation patterns on membrane receptors via lysine reactivity profiling. <i>Chemical Communications</i> , 2019 , 55, 4311-4314	5.8	13
60	In situ sample processing approach (iSPA) for comprehensive quantitative phosphoproteome analysis. <i>Journal of Proteome Research</i> , 2014 , 13, 3896-904	5.6	12
59	Phosphoproteome analysis of an early onset mouse model (TgCRND8) of Alzheimer's disease reveals temporal changes in neuronal and glia signaling pathways. <i>Proteomics</i> , 2013 , 13, 1292-305	4.8	12
58	Combination of online enzyme digestion with stable isotope labeling for high-throughput quantitative proteome analysis. <i>Proteomics</i> , 2012 , 12, 3129-37	4.8	12
57	N-terminal labeling of peptides by trypsin-catalyzed ligation for quantitative proteomics. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 9205-9	16.4	12

56	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. <i>Journal of Separation Science</i> , 2008 , 31, 2589-97	3.4	12
55	Modulating the selectivity of affinity absorbents to multi-phosphopeptides by a competitive substitution strategy. <i>Journal of Chromatography A</i> , 2016 , 1461, 35-41	4.5	12
54	A one step approach for preparation of an octadecylsilica hybrid monolithic column via a non-hydrolytic sol-gel (NHSG) method. <i>RSC Advances</i> , 2013 , 3, 22160	3.7	11
53	A six-plex proteome quantification strategy reveals the dynamics of protein turnover. <i>Scientific Reports</i> , 2013 , 3, 1827	4.9	11
52	Improvement of proteome coverage using hydrophobic monolithic columns in shotgun proteome analysis. <i>Journal of Chromatography A</i> , 2009 , 1216, 3887-94	4.5	11
51	Detecting Proteins Glycosylation by a Homogeneous Reaction System with Zwitterionic Gold Nanoclusters. <i>Analytical Chemistry</i> , 2017 , 89, 4339-4343	7.8	10
50	Analysis of human serum phosphopeptidome by a focused database searching strategy. <i>Journal of Proteomics</i> , 2013 , 78, 389-97	3.9	10
49	Highly Efficient Extraction of Serum Peptides by Ordered Mesoporous Carbon. <i>Angewandte Chemie</i> , 2011 , 123, 12426-12429	3.6	10
48	Integration of monolithic frit into the particulate capillary (IMFPC) column in shotgun proteome analysis. <i>Analytica Chimica Acta</i> , 2009 , 652, 324-30	6.6	10
47	Phosphorylation of PP1 Regulator Sds22 by PLK1 Ensures Accurate Chromosome Segregation. <i>Journal of Biological Chemistry</i> , 2016 , 291, 21123-21136	5.4	10
46	Global Quantification of Intact Proteins via Chemical Isotope Labeling and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2019 , 18, 2185-2194	5.6	9
45	Proteomic analysis reveals the protective effects of emodin on severe acute pancreatitis induced lung injury by inhibiting neutrophil proteases activity. <i>Journal of Proteomics</i> , 2020 , 220, 103760	3.9	9
44	Comprehensive analysis of the N and C terminus of endogenous serum peptides reveals a highly conserved cleavage site pattern derived from proteolytic enzymes. <i>Protein and Cell</i> , 2012 , 3, 669-74	7.2	9
43	Unusual zymogen activation patterns in the protein corona of Ca-zeolites. <i>Nature Catalysis</i> , 2021 , 4, 607-614	6.4	9
42	Protein digestomic analysis reveals the bioactivity of deer antler velvet in simulated gastrointestinal digestion. <i>Food Research International</i> , 2017 , 96, 182-190	7	8
41	Enhancing the Mass Spectrometry Sensitivity for Oligonucleotide Detection by Organic Vapor Assisted Electrospray. <i>Analytical Chemistry</i> , 2017 , 89, 10256-10263	7.8	8
40	Water-soluble Au nanoclusters for multiplexed mass spectrometry imaging. <i>Chemical Communications</i> , 2017 , 53, 12688-12691	5.8	8
39	Quantitative Lysine Reactivity Profiling Reveals Conformational Inhibition Dynamics and Potency of Aurora A Kinase Inhibitors. <i>Analytical Chemistry</i> , 2019 , 91, 13222-13229	7.8	7

38	Automation of nanoflow liquid chromatography-tandem mass spectrometry for proteome and peptide profiling analysis by using a monolithic analytical capillary column. <i>Electrophoresis</i> , 2008 , 29, 1612-8	3.6	7
37	Probing conformational hotspots for the recognition and intervention of protein complexes by lysine reactivity profiling. <i>Chemical Science</i> , 2020 , 12, 1451-1457	9.4	7
36	Small-Molecule Antagonist Targeting Exportin-1 via Rational Structure-Based Discovery. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 3881-3895	8.3	6
35	Differential analysis of N-glycoproteome between hepatocellular carcinoma and normal human liver tissues by combination of multiple protease digestion and solid phase based labeling. <i>Clinical Proteomics</i> , 2014 , 11, 26	5	6
34	Reversed Phase Monolithic Column Based Enzyme Reactor for Protein Analysis. <i>Chinese Journal of Analytical Chemistry</i> , 2013 , 41, 10-14	1.6	6
33	Probing the Proteomics Dark Regions by VAILase Cleavage at Aliphatic Amino Acids. <i>Analytical Chemistry</i> , 2020 , 92, 2770-2777	7.8	6
32	Inactivating SARS-CoV-2 by electrochemical oxidation. <i>Science Bulletin</i> , 2021 , 66, 720-726	10.6	6
31	High specific phosphopeptides enrichment by titanium silicalite with post-treatment of desilication. <i>Analytical Methods</i> , 2013 , 5, 2939	3.2	5
30	Single-Atom Pt Derived from the Laser Dissociation of a Platinum Cluster: Insights into Nonoxidative Alkane Conversion. <i>Journal of Physical Chemistry Letters</i> , 2020 , 11, 5987-5991	6.4	4
29	Specific mixing facilitates the comparative quantification of phosphorylation sites with significant dysregulations. <i>Analytica Chimica Acta</i> , 2017 , 950, 129-137	6.6	4
28	Elucidating the Molecular Mechanism of Dynamic Photodamage of Photosystem II Membrane Protein Complex by Integrated Proteomics Strategy. <i>CCS Chemistry</i> , 443-454	7.2	4
27	Electrospray ionization in concentrated acetonitrile vapor improves the performance of mass spectrometry for proteomic analyses. <i>Journal of Chromatography A</i> , 2017 , 1483, 101-109	4.5	3
26	Elucidating the various multi-phosphorylation statuses of protein functional regions by 193-nm ultraviolet photodissociation. <i>Chinese Chemical Letters</i> , 2018 , 29, 694-698	8.1	3
25	Highly efficient artificial blood coagulation shortcut confined on Ca-zeolite surface. <i>Nano Research</i> , 2021 , 14, 3309-3318	10	3
24	Identification of pyridoxal phosphate-modified proteins using mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2018 , 32, 195-200	2.2	3
23	Inhibition of human thrombin by the constituents of licorice: inhibition kinetics and mechanistic insights through and studies.. <i>RSC Advances</i> , 2020 , 10, 3626-3635	3.7	2
22	Nano LC-MS Based Proteomic Analysis as a Predicting Approach to Study Cellular Responses of Carbon Nanotubes. <i>Journal of Nanoscience and Nanotechnology</i> , 2016 , 16, 2350-9	1.3	2
21	A strategy with label-free quantification of the targeted peptides for quantitative peptidome analysis of human serum. <i>Science China Chemistry</i> , 2010 , 53, 759-767	7.9	2

20	Profiling the short-lived cationic species generated during catalytic dehydration of short-chain alcohols. <i>Communications Chemistry</i> , 2018 , 1,	6.3	2
19	Analysis of oligonucleotides by ion-pair reversed-phase liquid chromatography coupled with positive mode electrospray ionization mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2019 , 411, 4167-4173	4.4	1
18	Enrichment of peptides containing consensus sequence by an enzymatic approach for targeted analysis of proteins. <i>Proteomics</i> , 2011 , 11, 3578-81	4.8	1
17	Chloride-Mediated Peroxide-Free Photochemical Oxidation of Proteins (PPOP) in Mass Spectrometry-Based Structural Analysis.. <i>Analytical Chemistry</i> , 2021 ,	7.8	1
16	Lysine reactivity profiling reveals molecular insights into human serum albumin-small-molecule drug interactions. <i>Analytical and Bioanalytical Chemistry</i> , 2021 , 413, 7431-7440	4.4	1
15	Photochemical bromination and iodination of peptides and proteins by photoexcitation of aqueous halides. <i>Chemical Communications</i> , 2021 , 57, 11972-11975	5.8	1
14	Improving the performance of proteomic analysis via VAILase cleavage and 193-nm ultraviolet photodissociation. <i>Analytica Chimica Acta</i> , 2021 , 1155, 338340	6.6	1
13	Size-Selective VAILase Proteolysis Provides Dynamic Insights into Protein Structures. <i>Analytical Chemistry</i> , 2021 , 93, 10653-10660	7.8	1
12	Self-Adaptable Quinone-Quinol Exchange Mechanism of Photosystem II. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 10478-10489	3.4	1
11	In-situ generation and global property profiling of metal nanoclusters by ultraviolet laser dissociation-mass spectrometry. <i>Science China Chemistry</i> ,	7.9	1
10	6-Shogaol Inhibits Oxidative Stress-Induced Rat Vascular Smooth Muscle Cell Apoptosis by Regulating OXR1-p53 Axis.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 808162	5.6	0
9	Elucidating the molecular mechanisms of perfluorooctanoic acid-serum protein interactions by structural mass spectrometry. <i>Chemosphere</i> , 2021 , 132945	8.4	0
8	Comprehensive proteomic analysis of sea cucumbers (<i>Stichopus japonicus</i>) in thermal processing by HPLC-MS/MS. <i>Food Chemistry</i> , 2022 , 373, 131368	8.5	0
7	Characterization and manipulation of the photosystem II-semiconductor interfacial molecular interactions in solar-to-chemical energy conversion. <i>Journal of Energy Chemistry</i> , 2022 , 70, 437-443	12	0
6	The interfacial interactions of nanomaterials with human serum albumin.. <i>Analytical and Bioanalytical Chemistry</i> , 2022 , 1	4.4	0
5	N-Terminal Labeling of Peptides by Trypsin-Catalyzed Ligation for Quantitative Proteomics. <i>Angewandte Chemie</i> , 2013 , 125, 9375-9379	3.6	
4	Online Sample Injection and Multidimensional Chromatography Separation by Using Strong-Cation Exchange Monolithic Column. <i>Springer Theses</i> , 2014 , 7-33	0.1	
3	Large-Scale Proteome and Phosphoproteome Quantification by Using Dimethylation Isotope Labeling. <i>Springer Theses</i> , 2014 , 67-94	0.1	

- 2 Development of Polymer-Based Hydrophobic Monolithic Columns and Their Applications in Proteome Analysis. *Springer Theses*, **2014**, 35-65 0.1
- 1 Catalyst-free Photochemical Bromination of Unprotected Aromatic Amino Acid Derivatives by Using a Rotating Ultraviolet Photoreactor. *Chemical Research in Chinese Universities*,1 2.2