Xianquan Zhan

List of Publications by Year
in descending order

111 papers	3,732 citations	117625 34 h-index	161849 54 g-index
115 all docs	115 docs citations	115 times ranked	3302 citing authors

#	Article	IF	Citations
1	SOD2 Knockdown Mouse Model of Early AMD. , 2007, 48, 4407.		201
2	Novel Molecular Signaling and Classification of Human Clinically Nonfunctional Pituitary Adenomas Identified by Gene Expression Profiling and Proteomic Analyses. Cancer Research, 2005, 65, 10214-10222.	0.9	189
3	The crucial role of multiomic approach in cancer research and clinically relevant outcomes. EPMA Journal, 2018, 9, 77-102.	6.1	184
4	Chronic inflammation: key player and biomarker-set to predict and prevent cancer development and progression based on individualized patient profiles. EPMA Journal, 2019, 10, 365-381.	6.1	125
5	Pattern recognition for predictive, preventive, and personalized medicine in cancer. EPMA Journal, 2017, 8, 51-60.	6.1	119
6	Nitroproteins from a human pituitary adenoma tissue discovered with a nitrotyrosine affinity column and tandem mass spectrometry. Analytical Biochemistry, 2006, 354, 279-289.	2.4	112
7	Identification of clinical traitâ€"related lncRNA and mRNA biomarkers with weighted gene co-expression network analysis as useful tool for personalized medicine in ovarian cancer. EPMA Journal, 2019, 10, 273-290.	6.1	109
8	The human pituitary nitroproteome: detection of nitrotyrosyl-proteins with two-dimensional Western blotting, and amino acid sequence determination with mass spectrometry. Biochemical and Biophysical Research Communications, 2004, 325, 1180-1186.	2.1	91
9	Signaling pathway networks mined from human pituitary adenoma proteomics data. BMC Medical Genomics, 2010, 3, 13.	1.5	91
10	Molecular pathogenesis of human prolactinomas identified by gene expression profiling, RT-qPCR, and proteomic analyses. Pituitary, 2008, 11, 231-245.	2.9	89
11	EPMA position paper in cancer: current overview and future perspectives. EPMA Journal, 2015, 6, 9.	6.1	86
12	Exploration of variations in proteome and metabolome for predictive diagnostics and personalized treatment algorithms: Innovative approach and examples for potential clinical application. Journal of Proteomics, 2018, 188, 30-40.	2.4	76
13	The lncRNA SNHG3 regulates energy metabolism of ovarian cancer by an analysis of mitochondrial proteomes. Gynecologic Oncology, 2018, 150, 343-354.	1.4	76
14	Proteomics analysis of growth hormone isoforms in the human pituitary. Proteomics, 2005, 5, 1228-1241.	2.2	72
15	How many proteins can be identified in a 2DE gel spot within an analysis of a complex human cancer tissue proteome?. Electrophoresis, 2018, 39, 965-980.	2.4	71
16	The MAPK Pathway-Based Drug Therapeutic Targets in Pituitary Adenomas. Frontiers in Endocrinology, 2019, 10, 330.	3.5	68
17	Mass spectrometry analysis of human tear fluid biomarkers specificÂfor ocular and systemic diseases in the context of 3P medicine. EPMA Journal, 2021, 12, 449-475.	6.1	68
18	A reference map of a human pituitary adenoma proteome. Proteomics, 2003, 3, 699-713.	2.2	67

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19	Differences in the spatial and quantitative reproducibility between two second-dimensional gel electrophoresis systems. Electrophoresis, 2003, 24, 1834-1846.	2.4	57
20	Multi-parameter systematic strategies for predictive, preventive and personalised medicine in cancer. EPMA Journal, 2013, 4, 2.	6.1	57
21	Comparative proteomics analysis of human lung squamous carcinoma. Biochemical and Biophysical Research Communications, 2003, 309, 253-260.	2.1	55
22	Innovating the Concept and Practice of Two-Dimensional Gel Electrophoresis in the Analysis of Proteomes at the Proteoform Level. Proteomes, 2019, 7, 36.	3.5	53
23	Identification of pathology-specific regulators of m6A RNA modification to optimize lung cancer management in the context of predictive, preventive, and personalized medicine. EPMA Journal, 2020, 11, 485-504.	6.1	52
24	Comparative proteomics analysis of human pituitary adenomas: Current status and future perspectives. Mass Spectrometry Reviews, 2005, 24, 783-813.	5.4	51
25	Mass spectrometry analysis of nitrotyrosine–containing proteins. Mass Spectrometry Reviews, 2015, 34, 423-448.	5.4	50
26	Identification of stromal differentially expressed proteins in the colon carcinoma by quantitative proteomics. Electrophoresis, 2013, 34, 1679-1692.	2.4	46
27	Human Pituitary Adenoma Proteomics: New Progresses and Perspectives. Frontiers in Endocrinology, 2016, 7, 54.	3.5	46
28	Heterogeneity Analysis of the Human Pituitary Proteome. Clinical Chemistry, 2003, 49, 1740-1751.	3.2	44
29	Signaling pathway network alterations in human ovarian cancers identified with quantitative mitochondrial proteomics. EPMA Journal, 2019, 10, 153-172.	6.1	44
30	The use of variations in proteomes to predict, prevent, and personalize treatment for clinically nonfunctional pituitary adenomas. EPMA Journal, 2010, 1, 439-459.	6.1	43
31	Spot volume **_vs._** amount of protein loaded onto a gel: A detailed, statistical comparison of two gel electrophoresis systems. Electrophoresis, 2003, 24, 1818-1833.	2.4	41
32	Anti-parasite drug ivermectin can suppress ovarian cancer by regulating lncRNA-EIF4A3-mRNA axes. EPMA Journal, 2020, 11, 289-309.	6.1	41
33	Proteomics and Transcriptomics Analyses of Secretagogin Down-Regulation in Human Non-Functional Pituitary Adenomas. Pituitary, 2003, 6, 189-202.	2.9	40
34	Targets of Tyrosine Nitration in Diabetic Rat Retina. Molecular and Cellular Proteomics, 2008, 7, 864-874.	3.8	40
35	Multiomics-Based Signaling Pathway Network Alterations in Human Non-functional Pituitary Adenomas. Frontiers in Endocrinology, 2019, 10, 835.	3.5	40
36	Prolactin Variants in Human Pituitaries and Pituitary Adenomas Identified With Two-Dimensional Gel Electrophoresis and Mass Spectrometry. Frontiers in Endocrinology, 2018, 9, 468.	3.5	39

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37	Quantitative analysis of the mitochondrial proteome in human ovarian carcinomas. Endocrine-Related Cancer, 2018, 25, 909-931.	3.1	38
38	Nitroproteins in Human Astrocytomas Discovered by Gel Electrophoresis and Tandem Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2015, 26, 2062-2076.	2.8	37
39	Heterogeneity analysis of the proteomes in clinically nonfunctional pituitary adenomas. BMC Medical Genomics, 2014, 7, 69.	1.5	36
40	Linear ion-trap mass spectrometric characterization of human pituitary nitrotyrosine-containing proteins. International Journal of Mass Spectrometry, 2007, 259, 96-104.	1.5	34
41	Mitochondrial proteomics of nasopharyngeal carcinoma metastasis. BMC Medical Genomics, 2012, 5, 62.	1.5	34
42	10th Anniversary of the European Association for Predictive, Preventive and Personalised (3P) MedicineÂ- EPMA World Congress Supplement 2020. EPMA Journal, 2020, 11, 1-133.	6.1	34
43	Quantitative proteomics reveals a broadâ€spectrum antiviral property of ivermectin, benefiting for COVIDâ€19 treatment. Journal of Cellular Physiology, 2021, 236, 2959-2975.	4.1	34
44	Exploration of Molecular Network Variations in Different Subtypes of Human Non-functional Pituitary Adenomas. Frontiers in Endocrinology, 2016, 7, 13.	3.5	33
45	MASS SPECTROMETRYâ€BASED PERSONALIZED DRUG THERAPY. Mass Spectrometry Reviews, 2020, 39, 523-552.	5.4	31
46	Mitochondrial Dysfunction Pathway Networks and Mitochondrial Dynamics in the Pathogenesis of Pituitary Adenomas. Frontiers in Endocrinology, 2019, 10, 690.	3.5	28
47	Identification of differentially expressed proteins in the spinal cord of neuropathic pain models with PKCgamma silence by proteomic analysis. Brain Research, 2012, 1440, 34-46.	2.2	27
48	Identification of the proteomic variations of invasive relative to nonâ€invasive nonâ€functional pituitary adenomas. Electrophoresis, 2014, 35, 2184-2194.	2.4	27
49	Pituitary Adenoma Nitroproteomics: Current Status and Perspectives. Oxidative Medicine and Cellular Longevity, 2013, 2013, 1-16.	4.0	26
50	Proteomic and functional profiles of a follicleâ€stimulating hormone positive human nonfunctional pituitary adenoma. Electrophoresis, 2015, 36, 1289-1304.	2.4	26
51	Quantitative Analysis of Ubiquitinated Proteins in Human Pituitary and Pituitary Adenoma Tissues. Frontiers in Endocrinology, 2019, 10, 328.	3.5	26
52	Mass Spectrometric Identification of In Vivo Nitrotyrosine Sites in the Human Pituitary Tumor Proteome. Methods in Molecular Biology, 2009, 566, 137-163.	0.9	26
53	Two-dimensional Gel Electrophoresis Coupled with Mass Spectrometry Methods for an Analysis of Human Pituitary Adenoma Tissue Proteome. Journal of Visualized Experiments, 2018, , .	0.3	25
54	Targeting Nrf2-Mediated Oxidative Stress Response Signaling Pathways as New Therapeutic Strategy for Pituitary Adenomas. Frontiers in Pharmacology, 2021, 12, 565748.	3.5	23

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55	Comprehensive Analysis of Alteration Landscape and Its Clinical Significance of Mitochondrial Energy Metabolism Pathway-Related Genes in Lung Cancers. Oxidative Medicine and Cellular Longevity, 2021, 2021, 1-12.	4.0	22
56	MALDI-induced fragmentation of leucine enkephalin, nitro-Tyr-leucine enkaphalin, and d5-Phe-nitro-Tyr-leucine enkaphalin. International Journal of Mass Spectrometry, 2009, 287, 77-86.	1.5	21
57	Protein Tyrosine Nitration in Lung Cancer: Current Research Status and Future Perspectives. Current Medicinal Chemistry, 2018, 25, 3435-3454.	2.4	21
58	Quantitative proteomics revealed energy metabolism pathway alterations in human epithelial ovarian carcinoma and their regulation by the antiparasite drug ivermectin: data interpretation in the context of 3P medicine. EPMA Journal, 2020, 11, 661-694.	6.1	20
59	Identification of Immune-Related Gene Signatures in Lung Adenocarcinoma and Lung Squamous Cell Carcinoma. Frontiers in Immunology, 2021, 12, 752643.	4.8	19
60	TMT-based quantitative proteomics revealed follicle-stimulating hormone (FSH)-related molecular characterizations for potentially prognostic assessment and personalized treatment of FSH-positive non-functional pituitary adenomas. EPMA Journal, 2019, 10, 395-414.	6.1	18
61	Label-free quantitative identification of abnormally ubiquitinated proteins as useful biomarkers for human lung squamous cell carcinomas. EPMA Journal, 2020, 11, 73-94.	6.1	17
62	Quantitative analysis of the human ovarian carcinoma mitochondrial phosphoproteome. Aging, 2019, 11, 6449-6468.	3.1	17
63	Cancer Stemness-Based Prognostic Immune-Related Gene Signatures in Lung Adenocarcinoma and Lung Squamous Cell Carcinoma. Frontiers in Endocrinology, 2021, 12, 755805.	3.5	17
64	Editorial: Systems Biological Aspects of Pituitary Tumors. Frontiers in Endocrinology, 2016, 7, 86.	3.5	16
65	Integration of quantitative phosphoproteomics and transcriptomics revealed phosphorylation-mediated molecular events as useful tools for a potential patient stratification and personalized treatment of human nonfunctional pituitary adenomas. EPMA Journal, 2020, 11, 419-467.	6.1	15
66	MASS SPECTROMETRYâ€BASED MITOCHONDRIAL PROTEOMICS IN HUMAN OVARIAN CANCERS. Mass Spectrometry Reviews, 2020, 39, 471-498.	5.4	15
67	Comprehensive Analysis of Tumor Microenvironment Identified Prognostic Immune-Related Gene Signature in Ovarian Cancer. Frontiers in Genetics, 2021, 12, 616073.	2.3	15
68	The use of mass spectrometry in a proteomeâ€centered multiomics study of human pituitary adenomas. Mass Spectrometry Reviews, 2022, 41, 964-1013.	5.4	14
69	Identification of Glioblastoma Phosphotyrosine-Containing Proteins with Two-Dimensional Western Blotting and Tandem Mass Spectrometry. BioMed Research International, 2015, 2015, 1-21.	1.9	13
70	Mass spectrometry-based proteomics analyses of post-translational modifications and proteoforms in human pituitary adenomas. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140584.	2.3	13
71	Quantitative Analysis of Proteome in Non-functional Pituitary Adenomas: Clinical Relevance and Potential Benefits for the Patients. Frontiers in Endocrinology, 2019, 10, 854.	3.5	12
72	Human growth hormone proteoform pattern changes in pituitary adenomas: Potential biomarkers for 3P medical approaches. EPMA Journal, 2021, 12, 67-89.	6.1	12

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73	VE-statin/Egfl7 expression in malignant glioma and its relevant molecular network. International Journal of Clinical and Experimental Pathology, 2014, 7, 1022-31.	0.5	12
74	Proteomic and Bioinformatics Analyses of Mouse Liver Microsomes. International Journal of Proteomics, 2012, 2012, 1-24.	2.0	11
75	HSP60 Regulates Lipid Metabolism in Human Ovarian Cancer. Oxidative Medicine and Cellular Longevity, 2021, 2021, 1-21.	4.0	11
76	Mitochondrial Dysfunction Pathway Alterations Offer Potential Biomarkers and Therapeutic Targets for Ovarian Cancer. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-22.	4.0	11
77	Proteomic Identification of an Upregulated Isoform of Annexin A3 in the Spinal Cords of Rats in a Neuropathic Pain Model. Frontiers in Neuroscience, 2017, 11, 484.	2.8	10
78	Revival of 2DE-LC/MS in Proteomics and Its Potential for Large-Scale Study of Human Proteoforms. Med One, 2018, , .	1.0	10
79	VE-statin/Egfl7 siRNA inhibits angiogenesis in malignant glioma in vitro. International Journal of Clinical and Experimental Pathology, 2014, 7, 1077-84.	0.5	10
80	The differentially mitochondrial proteomic dataset in human ovarian cancer relative to control tissues. Data in Brief, 2018, 20, 459-462.	1.0	6
81	SILAC quantitative proteomics analysis of ivermectinâ€related proteomic profiling and molecular network alterations in human ovarian cancer cells. Journal of Mass Spectrometry, 2021, 56, e4659.	1.6	6
82	Quantitative Acetylomics Revealed Acetylation-Mediated Molecular Pathway Network Changes in Human Nonfunctional Pituitary Neuroendocrine Tumors. Frontiers in Endocrinology, 2021, 12, 753606.	3.5	6
83	Muti-omics integration analysis revealed molecular network alterations in human nonfunctional pituitary neuroendocrine tumors in the framework of 3P medicine. EPMA Journal, 2022, 13, 9-37.	6.1	6
84	Editorial: Molecular Network Study of Pituitary Adenomas. Frontiers in Endocrinology, 2020, 11, 26.	3.5	5
85	Phosphorylation-Mediated Molecular Pathway Changes in Human Pituitary Neuroendocrine Tumors Identified by Quantitative Phosphoproteomics. Cells, 2021, 10, 2225.	4.1	5
86	Integrated genomic analysis of proteasome alterations across 11,057 patients with 33 cancer types: clinically relevant outcomes in framework of 3P medicine. EPMA Journal, 2021, 12, 605-627.	6.1	5
87	Current Status of Two-Dimensional Gel Electrophoresis and Multi-Dimensional Liquid Chromatography as Proteomic Separation Techniques. Annals of Chromatography and Separation Techniques, 2015, 1, 1-3.	0.3	5
88	Machine Learning Identifies Pan-Cancer Landscape of Nrf2 Oxidative Stress Response Pathway-Related Genes. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-30.	4.0	5
89	Tangled quest of post-COVID-19 infection-caused neuropathology and what 3P nano-bio-medicine can solve?. EPMA Journal, 2022, 13, 261-284.	6.1	5
90	Energy Metabolism Heterogeneity-Based Molecular Biomarkers for Ovarian Cancer. , 0, , .		4

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91	Comprehensive analysis of spliceosome genes and their mutants across 27 cancer types in 9070 patients: clinically relevant outcomes in the context of 3P medicine. EPMA Journal, 2022, 13, 335-350.	6.1	4
92	Mapping the interactome of overexpressed RAF kinase inhibitor protein in a gastric cancer cell line. BMC Cancer, 2013, 13, 536.	2.6	3
93	Nitroproteins Identified in Human Ex-smoker Bronchoalveolar Lavage Fluid. , 2011, 2, 100-15.		3
94	Preparation of Mitochondria from Ovarian Cancer Tissues and Control Ovarian Tissues for Quantitative Proteomics Analysis. Journal of Visualized Experiments, 2019, , .	0.3	2
95	Application of Two-Dimensional Gel Electrophoresis in Combination with Mass Spectrometry in the Study of Hormone Proteoforms. , 0, , .		1
96	Prolactin Proteoform Pattern Changed in Human Pituitary Adenoma Relative to Control Pituitary Tissues. , 2020, , .		1
97	A Review on Innovating the Concept and Practice of Two-Dimensional Gel Electrophoresis in the Analysis of Proteomes at the Proteoform Level. , 2021, , 135-152.		1
98	Abnormal Ubiquitination of Ubiquitin-Proteasome System in Lung Squamous Cell Carcinomas. , 0, , .		1
99	The comparison between 2DE–MS and bottom–up LC–MS demands high–end techniques for both technologies. Electrophoresis, 2022, 43, 1242-1245.	2.4	1
100	The human pituitary proteome: clinical applications. , 2008, , 425-458.		0
101	Detection of Nitrotyrosine-Containing Proteins. Springer Protocols, 2009, , 1467-1490.	0.3	0
102	Back Cover: How many proteins can be identified in a 2DE gel spot within an analysis of a complex human cancer tissue proteome?. Electrophoresis, 2018, 39, NA-NA.	2.4	0
103	The Use of Gel Electrophoresis and Mass Spectrometry to Identify Nitroproteins in Nervous System Tumors. , 2018, , .		0
104	Invasiveness-Related Proteomic Variations and Molecular Network Changes in Human Nonfunctional Pituitary Adenomas. , 2019, , .		0
105	Mitochondrial Proteomic and Molecular Network Alterations in Human Ovarian Cancers. , 0, , .		0
106	Introductory Chapter: Proteoforms. , 0, , .		0
107	EDITORIAL: A SPECIAL ISSUE DEDICATED TO THE PROFESSIONAL CONTRIBUTIONS OF DOMINIC M. DESIDERIO. Mass Spectrometry Reviews, 2020, 39, 415-416.	5.4	0
108	The Anti-Cancer Effects of Anti-Parasite Drug Ivermectin in Ovarian Cancer. , 0, , .		0

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109	Introductory Chapter: Metabolomics. , 0, , .		0
110	Multiomics-based energy metabolism heterogeneity and its regulation by antiparasite drug ivermectin.. Journal of Clinical Oncology, 2020, 38, e18080-e18080.	1.6	0
111	The Use of Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC) to Study Ivermectin-Mediated Molecular Pathway Changes in Human Ovarian Cancer Cells. Biochemistry, 0, , .	1.2	0