Thang V Pham

List of Publications by Year
in descending order

82 papers	2,796 citations	147801 31 h-index	197818 49 g-index
85 all docs	85 docs citations	85 times ranked	5443 citing authors

#	Article	IF	Citations
1	Secreted protein markers in oral squamous cell carcinoma (OSCC). Clinical Proteomics, 2022, 19, 4.	2.1	12
2	Tumor Drug Concentration and Phosphoproteomic Profiles After Two Weeks of Treatment With Sunitinib in Patients with Newly Diagnosed Glioblastoma. Clinical Cancer Research, 2022, 28, 1595-1602.	7.0	12
3	Phosphoproteomic profiling of T cell acute lymphoblastic leukemia reveals targetable kinases and combination treatment strategies. Nature Communications, 2022, 13, 1048.	12.8	12
4	Phosphoproteomic Analysis of FLCN Inactivation Highlights Differential Kinase Pathways and Regulatory TFEB Phosphoserines. Molecular and Cellular Proteomics, 2022, 21, 100263.	3.8	1
5	Quantitative analysis of CDX2 protein expression improves its clinical utility as a prognostic biomarker in stage II and III colon cancer. European Journal of Cancer, 2021, 144, 91-100.	2.8	14
6	Proteomic and Functional Studies Reveal Detyrosinated Tubulin as Treatment Target in Sarcomere Mutation-Induced Hypertrophic Cardiomyopathy. Circulation: Heart Failure, 2021, 14, e007022.	3.9	58
7	Time dependent effect of cold ischemia on the phosphoproteome and protein kinase activity in fresh-frozen colorectal cancer tissue obtained from patients. Clinical Proteomics, 2021, 18, 8.	2.1	2
8	Feasibility of phosphoproteomics to uncover oncogenic signalling in secreted extracellular vesicles using glioblastoma-EGFRVIII cells as a model. Journal of Proteomics, 2021, 232, 104076.	2.4	5
9	Sex-Related Differences in Protein Expression in Sarcomere Mutation-Positive Hypertrophic Cardiomyopathy. Frontiers in Cardiovascular Medicine, 2021, 8, 612215.	2.4	11
10	Quantitative Phosphoproteomic Analysis Reveals Dendritic Cell- Specific STAT Signaling After Î±2-3â€“Linked Sialic Acid Ligand Binding. Frontiers in Immunology, 2021, 12, 673454.	4.8	3
11	The influence of delay in mononuclear cell isolation on acute myeloid leukemia phosphorylation profiles. Journal of Proteomics, 2021, 238, 104134.	2.4	3
12	Lipopolysaccharideâ€•regulated secretion of soluble and vesicleâ€•based proteins from a panel of colorectal cancer cell lines. Proteomics - Clinical Applications, 2021, 15, 1900119.	1.6	2
13	Prediction of response to sunitinib in patients with advanced renal cell carcinoma (RCC) using mass spectrometry-based (phospho) proteomics.. Journal of Clinical Oncology, 2021, 39, e16556-e16556.	1.6	0
14	Phosphoproteomic Characterization of Primary AML Samples and Relevance for Response Toward FLT3-inhibitors. HemaSphere, 2021, 5, e606.	2.7	12
15	Effects of Cancer Presence and Therapy on the Platelet Proteome. International Journal of Molecular Sciences, 2021, 22, 8236.	4.1	8
16	Longitudinal stability of urinary extracellular vesicle protein patterns within and between individuals. Scientific Reports, 2021, 11, 15629.	3.3	6
17	Loss of FLCN-FNIP1/2 induces a non-canonical interferon response in human renal tubular epithelial cells. ELife, 2021, 10, .	6.0	15
18	Omics Analysis of Educated Platelets in Cancer and Benign Disease of the Pancreas. Cancers, 2021, 13, 66.	3.7	20

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19	iq: an R package to estimate relative protein abundances from ion quantification in DIA-MS-based proteomics. Bioinformatics, 2020, 36, 2611-2613.	4.1	53
20	Proteins in stool as biomarkers for nonâ€invasive detection of colorectal adenomas with high risk of progression. Journal of Pathology, 2020, 250, 288-298.	4.5	33
21	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. Genomics, Proteomics and Bioinformatics, 2020, 18, 104-119.	6.9	51
22	Phosphotyrosine-based Phosphoproteomics for Target Identification and Drug Response Prediction in AML Cell Lines. Molecular and Cellular Proteomics, 2020, 19, 884-899.	3.8	29
23	Identification of novel cerebrospinal fluid biomarker candidates for dementia with Lewy bodies: a proteomic approach. Molecular Neurodegeneration, 2020, 15, 36.	10.8	46
24	Combined Expression of Plasma Thrombospondin-2 and CA19-9 for Diagnosis of Pancreatic Cancer and Distal Cholangiocarcinoma: A Proteome Approach. Oncologist, 2020, 25, e634-e643.	3.7	33
25	Kinase Inhibitor Treatment of Patients with Advanced Cancer Results in High Tumor Drug Concentrations and in Specific Alterations of the Tumor Phosphoproteome. Cancers, 2020, 12, 330.	3.7	11
26	Microdissected pancreatic cancer proteomes reveal tumor heterogeneity and therapeutic targets. JCI Insight, 2020, 5, .	5.0	36
27	Phospho-Proteomic Profiling of T-Cell Acute Lymphoblastic Leukemia Identifies Targetable Kinase Activities and Novel Treatment Combination Strategies. Blood, 2020, 136, 14-15.	1.4	1
28	Proteomic Analysis of miR-195 and miR-497 Replacement Reveals Potential Candidates that Increase Sensitivity to Oxaliplatin in MSI/P53wt Colorectal Cancer Cells. Cells, 2019, 8, 1111.	4.1	25
29	Human Testis Phosphoproteome Reveals Kinases as Potential Targets in Spermatogenesis and Testicular Cancer. Molecular and Cellular Proteomics, 2019, 18, S132-S144.	3.8	26
30	Proteomic analysis of gemcitabine-resistant pancreatic cancer cells reveals that microtubule-associated protein 2 upregulation associates with taxane treatment. Therapeutic Advances in Medical Oncology, 2019, 11, 175883591984123.	3.2	35
31	Tumor Heterogeneity Underlies Differential Cisplatin Sensitivity in Mouse Models of Small-Cell Lung Cancer. Cell Reports, 2019, 27, 3345-3358.e4.	6.4	42
32	<scp>INKA</scp> , an integrative data analysis pipeline for phosphoproteomic inference of active kinases. Molecular Systems Biology, 2019, 15, e8250.	7.2	53
33	Proteome analysis of non-small cell lung cancer cell line secretomes and patient sputum reveals biofluid biomarker candidates for cisplatin response prediction. Journal of Proteomics, 2019, 196, 106-119.	2.4	18
34	Changes in the urinary extracellular vesicle proteome are associated with nephronophthisis-related ciliopathies. Journal of Proteomics, 2019, 192, 27-36.	2.4	22
35	Comparison of phosphoproteomic profiles in left- and right-sided colorectal cancers.. Journal of Clinical Oncology, 2019, 37, 582-582.	1.6	0
36	O3â€14â€03: IDENTIFICATION OF NOVEL CEREBROSPINAL FLUID BIOMARKER CANDIDATES FOR DEMENTIA WITH LEWY BODIES: A PROTEOMIC APPROACH. Alzheimer's and Dementia, 2018, 14, P1060.	0.8	0

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37	Selection of Protein Kinase Inhibitors Based on Tumor Tissue Kinase Activity Profiles in Patients with Refractory Solid Malignancies: An Interventional Molecular Profiling Study. Oncologist, 2018, 23, 1135.	3.7	2
38	Cancer cells copy migratory behavior and exchange signaling networks via extracellular vesicles. EMBO Journal, 2018, 37, .	7.8	58
39	Phosphotyrosine-based-phosphoproteomics scaled-down to biopsy level for analysis of individual tumor biology and treatment selection. Journal of Proteomics, 2017, 162, 99-107.	2.4	31
40	Feasibility of urinary extracellular vesicle proteome profiling using a robust and simple, clinically applicable isolation method. Journal of Extracellular Vesicles, 2017, 6, 1313091.	12.2	51
41	Identification of Differentially Expressed Splice Variants by the Proteogenomic Pipeline Splicify. Molecular and Cellular Proteomics, 2017, 16, 1850-1863.	3.8	33
42	[P2â€“242]: PROTEOMICS IDENTIFICATION OF NOVEL CEREBROSPINAL FLUID BIOMARKER CANDIDATES OF DEMENTIA WITH LEWY BODIES. Alzheimer's and Dementia, 2017, 13, P704.	0.8	0
43	Novel Stool-Based Protein Biomarkers for Improved Colorectal Cancer Screening. Annals of Internal Medicine, 2017, 167, 855.	3.9	39
44	Response and toxicity prediction by MALDIâ€TOFâ€MS serum peptide profiling in patients with nonâ€small cell lung cancer. Proteomics - Clinical Applications, 2016, 10, 743-749.	1.6	4
45	Peptide-mediated â€˜miniprepâ€™ isolation of extracellular vesicles is suitable for high-throughput proteomics. EuPA Open Proteomics, 2016, 11, 11-15.	2.5	28
46	Sunitinib activates Axl signaling in renal cell cancer. International Journal of Cancer, 2016, 138, 3002-3010.	5.1	32
47	Evaluation of potential circulating biomarkers for prediction of response to chemoradiation in patients with glioblastoma. Journal of Neuro-Oncology, 2016, 129, 221-230.	2.9	13
48	O1â€06â€03: Proteomic Analysis of Extracellular Vesicles in Alzheimerâ€™s Disease Cerebrospinal FLUID. Alzheimer's and Dementia, 2016, 12, P186.	0.8	0
49	Exosomes Secreted by Apoptosis-Resistant Acute Myeloid Leukemia (AML) Blasts Harbor Regulatory Network Proteins Potentially Involved in Antagonism of Apoptosis. Molecular and Cellular Proteomics, 2016, 15, 1281-1298.	3.8	90
50	Novel diagnostic cerebrospinal fluid biomarkers for pathologic subtypes of frontotemporal dementia identified by proteomics. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2016, 2, 86-94.	2.4	68
51	Secretome proteomics reveals candidate non-invasive biomarkers of BRCA1 deficiency in breast cancer. Oncotarget, 2016, 7, 63537-63548.	1.8	14
52	Mass spectrometry-based phosphoproteomics of tumor needle biopsies from patients (pts) with advanced solid tumors during treatment with protein kinase inhibitors.. Journal of Clinical Oncology, 2016, 34, 11609-11609.	1.6	0
53	Feasibility of label-free phosphoproteomics and application to base-line signaling of colorectal cancer cell lines. Journal of Proteomics, 2015, 127, 247-258.	2.4	45
54	Evaluation of different phospho-tyrosine antibodies for label-free phosphoproteomics. Journal of Proteomics, 2015, 127, 259-263.	2.4	43

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55	Genome-wide siRNA Screen Identifies the Radiosensitizing Effect of Downregulation of MASTL and FOXM1 in NSCLC. Molecular Cancer Therapeutics, 2015, 14, 1434-1444.	4.1	32
56	Colorectal cancer derived organotypic spheroids maintain essential tissue characteristics but adapt their metabolism in culture. Proteome Science, 2014, 12, 39.	1.7	40
57	Proteomic analysis of cerebrospinal fluid extracellular vesicles: A comprehensive dataset. Journal of Proteomics, 2014, 106, 191-204.	2.4	222
58	Colorectal cancer candidate biomarkers identified by tissue secretome proteome profiling. Journal of Proteomics, 2014, 99, 26-39.	2.4	81
59	Mass Spectrometry-Based Serum and Plasma Peptidome Profiling for Prediction of Treatment Outcome in Patients With Solid Malignancies. Oncologist, 2014, 19, 1028-1039.	3.7	21
60	Decoration of Outer Membrane Vesicles with Multiple Antigens by Using an Autotransporter Approach. Applied and Environmental Microbiology, 2014, 80, 5854-5865.	3.1	95
61	Proteomics of differential extraction fractions enriched for chromatin-binding proteins from colon adenoma and carcinoma tissues. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1034-1043.	2.3	8
62	Mass spectrometry-based serum and plasma peptide profiling for prediction of treatment outcome in patients with cancer.. Journal of Clinical Oncology, 2014, 32, e22221-e22221.	1.6	0
63	Proteomics of Genetically Engineered Mouse Mammary Tumors Identifies Fatty Acid Metabolism Members as Potential Predictive Markers for Cisplatin Resistance. Molecular and Cellular Proteomics, 2013, 12, 1319-1334.	3.8	24
64	Differential Detergent Extraction of Mycobacterium marinum Cell Envelope Proteins Identifies an Extensively Modified Threonine-Rich Outer Membrane Protein with Channel Activity. Journal of Bacteriology, 2013, 195, 2050-2059.	2.2	25
65	Proteomic Profiling of Mycobacterium tuberculosis Identifies Nutrient-starvation-responsive Toxinâ€“antitoxin Systems. Molecular and Cellular Proteomics, 2013, 12, 1180-1191.	3.8	148
66	An accurate paired sample test for count data. Bioinformatics, 2012, 28, i596-i602.	4.1	63
67	Label-free mass spectrometry-based proteomics for biomarker discovery and validation. Expert Review of Molecular Diagnostics, 2012, 12, 343-359.	3.1	46
68	Proteomics of Mouse BRCA1-deficient Mammary Tumors Identifies DNA Repair Proteins with Potential Diagnostic and Prognostic Value in Human Breast Cancer. Molecular and Cellular Proteomics, 2012, 11, M111.013334-1-M111.013334-19.	3.8	23
69	Proximal Fluid Proteome Profiling of Mouse Colon Tumors Reveals Biomarkers for Early Diagnosis of Human Colorectal Cancer. Clinical Cancer Research, 2012, 18, 2613-2624.	7.0	46
70	The Proteome of the Locus Ceruleus in Parkinson's Disease: Relevance to Pathogenesis. Brain Pathology, 2012, 22, 485-498.	4.1	53
71	Response prediction by MALDI-TOF-MS serum peptide profiling of combination treatment with sorafenib and erlotinib in patients with non-small cell lung cancer.. Journal of Clinical Oncology, 2012, 30, e18094-e18094.	1.6	0
72	Workflow Comparison for Label-Free, Quantitative Secretome Proteomics for Cancer Biomarker Discovery: Method Evaluation, Differential Analysis, and Verification in Serum. Journal of Proteome Research, 2010, 9, 1913-1922.	3.7	126

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73	On the beta-binomial model for analysis of spectral count data in label-free tandem mass spectrometry-based proteomics. Bioinformatics, 2010, 26, 363-369.	4.1	153
74	Comparative Protein Profiling Reveals Minichromosome Maintenance (MCM) Proteins As Novel Potential Tumor Markers for Meningiomas. Journal of Proteome Research, 2010, 9, 485-494.	3.7	59
75	iTRAQ-based Proteomics Profiling Reveals Increased Metabolic Activity and Cellular Cross-talk in Angiogenic Compared with Invasive Glioblastoma Phenotype. Molecular and Cellular Proteomics, 2009, 8, 2595-2612.	3.8	65
76	Prediction of outcome of non-small cell lung cancer patients treated with chemotherapy and bortezomib by time-course MALDI-TOF-MS serum peptide profiling. Proteome Science, 2009, 7, 34.	1.7	32
77	Quadratic boosting. Pattern Recognition, 2008, 41, 331-341.	8.1	9
78	High-throughput and targeted in-depth mass spectrometry-based approaches for biofluid profiling and biomarker discovery. Biomarkers in Medicine, 2007, 1, 541-565.	1.4	30
79	Sparse representation for coarse and fine object recognition. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2006, 28, 555-567.	13.9	19
80	Learning spatial relations in object recognition. Pattern Recognition Letters, 2006, 27, 1673-1684.	4.2	17
81	Object recognition with uncertain geometry and uncertain part detection. Computer Vision and Image Understanding, 2005, 99, 241-258.	4.7	14
82	Face detection by aggregated Bayesian network classifiers. Pattern Recognition Letters, 2002, 23, 451-461.	4.2	41