

# David J Clark

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

3,045  
citations

218677

26  
h-index

175258

52  
g-index

56  
all docs

56  
docs citations

56  
times ranked

5307  
citing authors

#	ARTICLE	IF	CITATIONS
1	The next "sweet" spot for pancreatic ductal adenocarcinoma: Glycoprotein for early detection. <i>Mass Spectrometry Reviews</i> , 2023, 42, 822-843.	5.4	10
2	Long-term mortality in asymptomatic patients with stable ischemic heart disease undergoing percutaneous coronary intervention. <i>American Heart Journal</i> , 2022, 244, 77-85.	2.7	2
3	Impact of Magnesium on Oxytocin Receptor Function. <i>Pharmaceutics</i> , 2022, 14, 1105.	4.5	7
4	Characterization of core fucosylation via sequential enzymatic treatments of intact glycopeptides and mass spectrometry analysis. <i>Nature Communications</i> , 2022, 13, .	12.8	14
5	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189
6	Abstract 324: Unbiased proteomic and phosphoproteomic analysis identifies response signatures and novel susceptibilities after combined MEK and mTOR inhibition in BRAFV600E mutant glioma. , 2021, , .		0
7	Defining candidate mRNA and protein EV biomarkers to discriminate ccRCC and pRCC from non-malignant renal cells in vitro. <i>Medical Oncology</i> , 2021, 38, 105.	2.5	5
8	High-throughput Analyses of Glycans, Glycosites, and Intact Glycopeptides Using C4 and C18/MAX Tips and Liquid Handling System. <i>Current Protocols</i> , 2021, 1, e186.	2.9	7
9	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
10	Unbiased Proteomic and Phosphoproteomic Analysis Identifies Response Signatures and Novel Susceptibilities After Combined MEK and mTOR Inhibition in BRAFV600E Mutant Glioma. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100123.	3.8	5
11	Abstract IA-003: Proteogenomic characterizations of pancreatic ductal adenocarcinoma. , 2021, , .		0
12	Glycans, Glycosite, and Intact Glycopeptide Analysis of N-Linked Glycoproteins Using Liquid Handling Systems. <i>Analytical Chemistry</i> , 2020, 92, 1680-1686.	6.5	27
13	Glycoproteomics-based signatures for tumor subtyping and clinical outcome prediction of high-grade serous ovarian cancer. <i>Nature Communications</i> , 2020, 11, 6139.	12.8	72
14	Proteomic approaches for characterizing renal cell carcinoma. <i>Clinical Proteomics</i> , 2020, 17, 28.	2.1	8
15	High-dimensional Cytometry (ExCYT) and Mass Spectrometry of Myeloid Infiltrate in Clinically Localized Clear Cell Renal Cell Carcinoma Identifies Novel Potential Myeloid Targets for Immunotherapy. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1850-1859.	3.8	2
16	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	6.4	83
17	Impact of Increased FUT8 Expression on the Extracellular Vesicle Proteome in Prostate Cancer Cells. <i>Journal of Proteome Research</i> , 2020, 19, 2195-2205.	3.7	28
18	Protein Modifications Critical for Myonectin/Erythroferrone Secretion and Oligomer Assembly. <i>Biochemistry</i> , 2020, 59, 2684-2697.	2.5	8

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19	Deep Proteomics Using Two Dimensional Data Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 4217-4225.	6.5	23
20	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
21	Simple Tip-Based Sample Processing Method for Urinary Proteomic Analysis. <i>Analytical Chemistry</i> , 2019, 91, 5517-5522.	6.5	18
22	N-Linked Glycosylation-Dependent and -Independent Mechanisms Regulating CTRP12 Cleavage, Secretion, and Stability. <i>Biochemistry</i> , 2019, 58, 727-741.	2.5	1
23	Evaluation of NCI-7 Cell Line Panel as a Reference Material for Clinical Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2205-2215.	3.7	17
24	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography–mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661.	12.0	377
25	Reanalysis of Global Proteomic and Phosphoproteomic Data Identified a Large Number of Glycopeptides. <i>Analytical Chemistry</i> , 2018, 90, 8065-8071.	6.5	81
26	Understanding the Surgical Margin. <i>Oral and Maxillofacial Surgery Clinics of North America</i> , 2017, 29, 245-258.	1.0	23
27	Site-Specific Fucosylation Analysis Identifying Glycoproteins Associated with Aggressive Prostate Cancer Cell Lines Using Tandem Affinity Enrichments of Intact Glycopeptides Followed by Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 7623-7630.	6.5	65
28	A piRNA-like Small RNA Induces Chemoresistance to Cisplatin-Based Therapy by Inhibiting Apoptosis in Lung Squamous Cell Carcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2017, 6, 269-278.	5.1	37
29	A phosphorylation-wide sncRNA screen reveals Protein Functional Effector sncRNAs (pfeRNAs) in human lung somatic cells. <i>Cancer Letters</i> , 2017, 396, 85-93.	7.2	5
30	Overexpression of Exportin-5 Overrides the Inhibitory Effect of miRNAs Regulation Control and Stabilize Proteins via Posttranslation Modifications in Prostate Cancer. <i>Neoplasia</i> , 2017, 19, 817-829.	5.3	8
31	High-throughput analysis of N-glycans using AutoTip via glycoprotein immobilization. <i>Scientific Reports</i> , 2017, 7, 10216.	3.3	19
32	Glycoproteomic Approach Identifies KRAS as a Positive Regulator of CREG1 in Non-small Cell Lung Cancer Cells. <i>Theranostics</i> , 2016, 6, 65-77.	10.0	15
33	Triple SILAC quantitative proteomic analysis reveals differential abundance of cell signaling proteins between normal and lung cancer-derived exosomes. <i>Journal of Proteomics</i> , 2016, 133, 161-169.	2.4	112
34	A piRNA-like small RNA interacts with and modulates p-ERM proteins in human somatic cells. <i>Nature Communications</i> , 2015, 6, 7316.	12.8	88
35	Molecular margin of surgical resections—Where do we go from here?. <i>Cancer</i> , 2015, 121, 1914-1916.	4.1	26
36	Redefining the Breast Cancer Exosome Proteome by Tandem Mass Tag Quantitative Proteomics and Multivariate Cluster Analysis. <i>Analytical Chemistry</i> , 2015, 87, 10462-10469.	6.5	66

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37	FGF23 Is Endogenously Phosphorylated in Bone Cells. <i>Journal of Bone and Mineral Research</i> , 2015, 30, 449-454.	2.8	30
38	Ebp1 activates podoplanin expression and contributes to oral tumorigenesis. <i>Oncogene</i> , 2014, 33, 3839-3850.	5.9	37
39	Lysine methylation is an endogenous post-translational modification of tau protein in human brain and a modulator of aggregation propensity. <i>Biochemical Journal</i> , 2014, 462, 77-88.	3.7	102
40	Novel dimensions of piRNAs in cancer. <i>Cancer Letters</i> , 2013, 336, 46-52.	7.2	107
41	Plasma Membrane Proteomics of Tumor Spheres Identify CD166 as a Novel Marker for Cancer Stem-like Cells in Head and Neck Squamous Cell Carcinoma. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3271-3284.	3.8	74
42	Exosomal Proteome Profiling: A Potential Multi-Marker Cellular Phenotyping Tool to Characterize Hypoxia-Induced Radiation Resistance in Breast Cancer. <i>Proteomes</i> , 2013, 1, 87-108.	3.5	44
43	Proteomic View of Interactions of Shiga Toxin-Producing <i>Escherichia coli</i> with the Intestinal Environment in Gnotobiotic Piglets. <i>PLoS ONE</i> , 2013, 8, e66462.	2.5	18
44	Cancer Biomarker Discovery: Lectin-Based Strategies Targeting Glycoproteins. <i>Disease Markers</i> , 2012, 33, 1-10.	1.3	50
45	Cancer biomarker discovery: lectin-based strategies targeting glycoproteins. <i>Disease Markers</i> , 2012, 33, 1-10.	1.3	18
46	Characterizing the <i>Escherichia coli</i> O157:H7 Proteome Including Protein Associations with Higher Order Assemblies. <i>PLoS ONE</i> , 2011, 6, e26554.	2.5	20
47	Proteomic analysis of iron acquisition, metabolic and regulatory responses of <i>Yersinia pestis</i> to iron starvation. <i>BMC Microbiology</i> , 2010, 10, 30.	3.3	35
48	Using chemical derivatization and mass spectrometric analysis to characterize the post-translationally modified <i>Staphylococcus aureus</i> surface protein G. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1394-1404.	2.3	10
49	Temperature and growth phase influence the outer-membrane proteome and the expression of a type VI secretion system in <i>Yersinia pestis</i> . <i>Microbiology (United Kingdom)</i> , 2009, 155, 498-512.	1.8	77
50	The <i>Shigella dysenteriae</i> serotype 1 proteome, profiled in the host intestinal environment, reveals major metabolic modifications and increased expression of invasive proteins. <i>Proteomics</i> , 2009, 9, 5029-5045.	2.2	41
51	Comparison of two label-free global quantitation methods, APEX and 2D gel electrophoresis, applied to the <i>Shigella dysenteriae</i> proteome. <i>Proteome Science</i> , 2009, 7, 22.	1.7	28
52	Integral and peripheral association of proteins and protein complexes with <i>Yersinia pestis</i> inner and outer membranes. <i>Proteome Science</i> , 2009, 7, 5.	1.7	26
53	Characterizing the dynamic nature of the <i>Yersinia pestis</i> periplasmic proteome in response to nutrient exhaustion and temperature change. <i>Proteomics</i> , 2008, 8, 1442-1458.	2.2	32
54	Widespread Occurrence of Non-Enzymatic Deamidations of Asparagine Residues in <i>Yersinia pestis</i> Proteins Resulting from Alkaline pH Membrane Extraction Conditions. <i>The Open Proteomics Journal</i> , 2008, 1, 106-115.	0.4	5

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55	Proteomic profiling of cell envelope-associated proteins from <i>Staphylococcus aureus</i> . <i>Proteomics</i> , 2006, 6, 1530-1549.	2.2	102
56	Comparative proteomic analysis of <i>Staphylococcus aureus</i> strains with differences in resistance to the cell wall-targeting antibiotic vancomycin. <i>Proteomics</i> , 2006, 6, 4246-4258.	2.2	75