

# David M Good

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

2,602  
citations

394421

19  
h-index

580821

25  
g-index

26  
all docs

26  
docs citations

26  
times ranked

2843  
citing authors

#	ARTICLE	IF	CITATIONS
1	Naturally Occurring Human Urinary Peptides for Use in Diagnosis of Chronic Kidney Disease. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2424-2437.	3.8	434
2	Performance Characteristics of Electron Transfer Dissociation Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1942-1951.	3.8	356
3	Urinary Proteomics in Diabetes and CKD. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 1283-1290.	6.1	267
4	Body Fluid Proteomics for Biomarker Discovery: Lessons from the Past Hold the Key to Success in the Future. <i>Journal of Proteome Research</i> , 2007, 6, 4549-4555.	3.7	216
5	Urinary Proteomic Biomarkers in Coronary Artery Disease. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 290-298.	3.8	197
6	CE-MS analysis of the human urinary proteome for biomarker discovery and disease diagnostics. <i>Proteomics - Clinical Applications</i> , 2008, 2, 964-973.	1.6	178
7	Implementation of Electron-Transfer Dissociation on a Hybrid Linear Ion Trap Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2007, 79, 3525-3534.	6.5	166
8	Discovery and validation of urinary biomarkers for prostate cancer. <i>Proteomics - Clinical Applications</i> , 2008, 2, 556-570.	1.6	133
9	Identification and Validation of Urinary Biomarkers for Differential Diagnosis and Evaluation of Therapeutic Intervention in Anti-neutrophil Cytoplasmic Antibody-associated Vasculitis. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2296-2307.	3.8	100
10	Electrophoretic methods for analysis of urinary polypeptides in IgA-associated renal diseases. <i>Electrophoresis</i> , 2007, 28, 4469-4483.	2.4	83
11	The human urinary proteome reveals high similarity between kidney aging and chronic kidney disease. <i>Proteomics</i> , 2009, 9, 2108-2117.	2.2	82
12	Methionine Deprivation Induces a Targetable Vulnerability in Triple-Negative Breast Cancer Cells by Enhancing TRAIL Receptor-2 Expression. <i>Clinical Cancer Research</i> , 2015, 21, 2780-2791.	7.0	77
13	Post-acquisition ETD spectral processing for increased peptide identifications. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1435-1440.	2.8	61
14	Sequence Scrambling in Shotgun Proteomics is Negligible. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1121-1124.	2.8	48
15	Advancing proteomics with ion/ion chemistry. <i>BioTechniques</i> , 2006, 40, 783-789.	1.8	46
16	The effect of interfering ions on search algorithm performance for electron-transfer dissociation data. <i>Proteomics</i> , 2010, 10, 164-167.	2.2	35
17	A New Probabilistic Database Search Algorithm for ETD Spectra. <i>Journal of Proteome Research</i> , 2009, 8, 3198-3205.	3.7	33
18	Dual Electrospray Ion Source for Electron-Transfer Dissociation on a Hybrid Linear Ion Trap Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2007, 79, 7916-7919.	6.5	32

#	ARTICLE	IF	CITATIONS
19	Adapting mass spectrometry-based platforms for clinical proteomics applications: The capillary electrophoresis coupled mass spectrometry paradigm. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2009, 46, 129-152.	6.1	24
20	Drug Target Identification from Protein Dynamics using Quantitative Pathway Analysis. <i>Journal of Proteome Research</i> , 2011, 10, 2679-2683.	3.7	15
21	Are the majority of a2-ions cyclic?. <i>Physical Chemistry Chemical Physics</i> , 2010, 12, 13372.	2.8	9
22	Carbonyl Charge Solvation Patterns May Relate to Fragmentation Classes in Collision-Activated Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1319-1325.	2.8	3
23	In silico Proteome-wide Amino acid and Elemental Composition (PACE) Analysis of Expression Proteomics Data Provides A Fingerprint of Dominant Metabolic Processes. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 219-229.	6.9	3
24	Employment of Complementary Dissociation Techniques for Body Fluid Characterization and Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2013, 1002, 223-232.	0.9	2
25	Mass Spectrometric Analysis of Body Fluids for Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2009, 566, 277-291.	0.9	2
26	N-Terminal Peptide Sequence Repetition Influences the Kinetics of Backbone Fragmentation: A Manifestation of the Jahn-Teller Effect?. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1671-1675.	2.8	0