

# Victoria M Harman

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

636  
citations

687363

13  
h-index

794594

19  
g-index

21  
all docs

21  
docs citations

21  
times ranked

941  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies. <i>Nature Communications</i> , 2022, 13, 801.	12.8	47
2	Decoding the Absolute Stoichiometric Composition and Structural Plasticity of $\hat{1}\pm$ -Carboxysomes. <i>MBio</i> , 2022, 13, e0362921.	4.1	27
3	Monitoring recombinant protein expression in bacteria by rapid evaporative ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e8670.	1.5	8
4	Construction of $\hat{A}$ la carte QconCAT protein standards for multiplexed quantification of user-specified target proteins. <i>BMC Biology</i> , 2021, 19, 195.	3.8	8
5	Quantitative Proteomics of Enriched Esophageal and Gut Tissues from the Human Blood Fluke <i>Schistosoma mansoni</i> Pinpoints Secreted Proteins for Vaccine Development. <i>Journal of Proteome Research</i> , 2020, 19, 314-326.	3.7	17
6	PEPPI-MS: Polyacrylamide-Gel-Based Prefractionation for Analysis of Intact Proteoforms and Protein Complexes by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 3779-3791.	3.7	49
7	Decoding the stoichiometric composition and organisation of bacterial metabolosomes. <i>Nature Communications</i> , 2020, 11, 1976.	12.8	49
8	Landscape of heart proteome changes in a diet-induced obesity model. <i>Scientific Reports</i> , 2019, 9, 18050.	3.3	25
9	MEERCAT: Multiplexed Efficient Cell Free Expression of Recombinant QconCATs For Large Scale Absolute Proteome Quantification. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2169-2183.	3.8	23
10	Direct and Absolute Quantification of over 1800 Yeast Proteins via Selected Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1309-1322.	3.8	80
11	A selected reaction monitoring-based analysis of acute phase proteins in interstitial fluids from experimental equine wounds healing by secondary intention. <i>Wound Repair and Regeneration</i> , 2016, 24, 525-532.	3.0	16
12	Mass spectrometry for structural analysis and quantification of the Major Urinary Proteins of the house mouse. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 146-156.	1.5	14
13	The role of proteomics in studies of protein moonlighting. <i>Biochemical Society Transactions</i> , 2014, 42, 1698-1703.	3.4	4
14	Development of a Method for Absolute Quantification of Equine Acute Phase Proteins Using Concatenated Peptide Standards and Selected Reaction Monitoring. <i>Journal of Proteome Research</i> , 2014, 13, 5635-5647.	3.7	12
15	Quantitative analysis of chaperone network throughput in budding yeast. <i>Proteomics</i> , 2013, 13, 1276-1291.	2.2	33
16	A Software Toolkit and Interface for Performing Stable Isotope Labeling and Top3 Quantification Using Progenesis LC-MS. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 489-495.	2.0	47
17	Quantotypic Properties of QconCAT Peptides Targeting Bovine Host Response to <i>Streptococcus uberis</i> . <i>Journal of Proteome Research</i> , 2012, 11, 1832-1843.	3.7	39
18	Absolute Multiplexed Protein Quantification Using QconCAT Technology. <i>Methods in Molecular Biology</i> , 2012, 893, 267-293.	0.9	31

#	ARTICLE	IF	CITATIONS
19	Global absolute quantification of a proteome: Challenges in the deployment of a QconCAT strategy. <i>Proteomics</i> , 2011, 11, 2957-2970.	2.2	103