

# David C Trudgian

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

2,437  
citations

279798

23  
h-index

526287

27  
g-index

28  
all docs

28  
docs citations

28  
times ranked

4825  
citing authors

#	ARTICLE	IF	CITATIONS
1	ProteoSign: an end-user online differential proteomics statistical analysis platform. <i>Nucleic Acids Research</i> , 2017, 45, W300-W306.	14.5	32
2	Fucosylation and protein glycosylation create functional receptors for cholera toxin. <i>ELife</i> , 2015, 4, e09545.	6.0	81
3	Type VI Secretion System Toxins Horizontally Shared between Marine Bacteria. <i>PLoS Pathogens</i> , 2015, 11, e1005128.	4.7	71
4	Comprehensive identification of arginine methylation in primary T cells reveals regulatory roles in cell signalling. <i>Nature Communications</i> , 2015, 6, 6758.	12.8	129
5	Optimal Translational Termination Requires C4 Lysyl Hydroxylation of eRF1. <i>Molecular Cell</i> , 2014, 53, 645-654.	9.7	99
6	Conserved and host-specific features of influenza virion architecture. <i>Nature Communications</i> , 2014, 5, 4816.	12.8	214
7	Confetti: A Multiprotease Map of the HeLa Proteome for Comprehensive Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1573-1584.	3.8	89
8	<sc>GOAT</sc> – A simple <sc>LC</sc> – <sc>MS</sc>/<sc>MS</sc> gradient optimization tool. <i>Proteomics</i> , 2014, 14, 1467-1471.	2.2	17
9	Sulfur Amino Acids Regulate Translational Capacity and Metabolic Homeostasis through Modulation of tRNA Thiolation. <i>Cell</i> , 2013, 154, 416-429.	28.9	189
10	QuaNCAT: quantitating proteome dynamics in primary cells. <i>Nature Methods</i> , 2013, 10, 343-346.	19.0	162
11	Regulation of OSR1 and the sodium, potassium, two chloride cotransporter by convergent signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18826-18831.	7.1	27
12	Quantitative Phosphoproteome Analysis Unveils LAT as a Modulator of CD3 $\zeta$ and ZAP-70 Tyrosine Phosphorylation. <i>PLoS ONE</i> , 2013, 8, e77423.	2.5	27
13	Mapping the Phosphoproteome of Influenza A and B Viruses by Mass Spectrometry. <i>PLoS Pathogens</i> , 2012, 8, e1002993.	4.7	121
14	Detection of Multiple Autoantibodies in Patients with Ankylosing Spondylitis Using Nucleic Acid Programmable Protein Arrays. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M9.00384.	3.8	77
15	Discovery of Candidate Serum Proteomic and Metabolomic Biomarkers in Ankylosing Spondylitis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013904.	3.8	92
16	A Method for Large-scale Identification of Protein Arginine Methylation. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1489-1499.	3.8	122
17	Cloud CFP: A Shotgun Proteomics Data Analysis Pipeline Using Cloud and High Performance Computing. <i>Journal of Proteome Research</i> , 2012, 11, 6282-6290.	3.7	52
18	Oxygenase-catalyzed ribosome hydroxylation occurs in prokaryotes and humans. <i>Nature Chemical Biology</i> , 2012, 8, 960-962.	8.0	135

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19	The FIH hydroxylase is a cellular peroxide sensor that modulates HIF transcriptional activity. <i>EMBO Reports</i> , 2012, 13, 251-257.	4.5	120
20	T Cell Receptor (TCR)-induced Tyrosine Phosphorylation Dynamics Identifies THEMIS as a New TCR Signalosome Component. <i>Journal of Biological Chemistry</i> , 2011, 286, 7535-7547.	3.4	75
21	Aberrant succination of proteins in fumarate hydratase-deficient mice and HLRCC patients is a robust biomarker of mutation status. <i>Journal of Pathology</i> , 2011, 225, 4-11.	4.5	225
22	Comparative evaluation of label-free SING normalized spectral index quantitation in the central proteomics facilities pipeline. <i>Proteomics</i> , 2011, 11, 2790-2797.	2.2	120
23	Quantitative Mass Spectrometry Reveals Dynamics of Factor-inhibiting Hypoxia-inducible Factor-catalyzed Hydroxylation*. <i>Journal of Biological Chemistry</i> , 2011, 286, 33784-33794.	3.4	22
24	Protein Kinase C and NF- $\kappa$ B-Dependent CD4 Downregulation in Macrophages Induced by T Cell-Derived Soluble Factors: Consequences for HIV-1 Infection. <i>Journal of Immunology</i> , 2011, 187, 748-759.	0.8	12
25	CPFP: a central proteomics facilities pipeline. <i>Bioinformatics</i> , 2010, 26, 1131-1132.	4.1	96
26	SILACAnalyzer - A Tool for Differential Quantitation of Stable Isotope Derived Data. <i>Lecture Notes in Computer Science</i> , 2010, , 45-55.	1.3	6
27	Honing their silicoolkit for detecting protein disorder. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1260-1266.	2.5	25