

Yves Vandembrouck

List of Publications by Year in descending order

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42
papers

2,039
citations

394421

19
h-index

289244

40
g-index

43
all docs

43
docs citations

43
times ranked

3563
citing authors

#	ARTICLE	IF	CITATIONS
1	GO Enrichment Analysis for Differential Proteomics Using ProteoRE. <i>Methods in Molecular Biology</i> , 2021, 2361, 179-196.	0.9	7
2	Proteo3Dnet: a web server for the integration of structural information with interactomics data. <i>Nucleic Acids Research</i> , 2021, 49, W567-W572.	14.5	5
3	ChloroKB, a cell metabolism reconstruction of the model plant <i>Arabidopsis thaliana</i> . <i>Comptes Rendus - Biologies</i> , 2021, 344, 157-163.	0.2	5
4	Mass Spectrometry-Based Proteomics Reveal Alcohol Dehydrogenase 1B as a Blood Biomarker Candidate to Monitor Acetaminophen-Induced Liver Injury. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11071.	4.1	1
5	Advances and Utility of the Human Plasma Proteome. <i>Journal of Proteome Research</i> , 2021, 20, 5241-5263.	3.7	86
6	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. <i>Scientific Data</i> , 2021, 8, 311.	5.3	6
7	The Functionally Unannotated Proteome of Human Male Tissues: A Shared Resource to Uncover New Protein Functions Associated with Reproductive Biology. <i>Journal of Proteome Research</i> , 2020, 19, 4782-4794.	3.7	10
8	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	12.8	152
9	Probing Protein Interaction Networks by Combining MS-Based Proteomics and Structural Data Integration. <i>Journal of Proteome Research</i> , 2020, 19, 2807-2820.	3.7	6
10	Bioinformatics Tools and Workflow to Select Blood Biomarkers for Early Cancer Diagnosis: An Application to Pancreatic Cancer. <i>Proteomics</i> , 2019, 19, e1800489.	2.2	22
11	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. <i>Journal of Proteome Research</i> , 2019, 18, 4108-4116.	3.7	82
12	Peptimapper: proteogenomics workflow for the expert annotation of eukaryotic genomes. <i>BMC Genomics</i> , 2019, 20, 56.	2.8	10
13	Designing an In Silico Strategy to Select Tissue-Leakage Biomarkers Using the Galaxy Framework. <i>Methods in Molecular Biology</i> , 2019, 1959, 275-289.	0.9	10
14	Proteomic characterization of human exhaled breath condensate. <i>Journal of Breath Research</i> , 2018, 12, 021001.	3.0	29
15	ChloroKB: A Web Application for the Integration of Knowledge Related to Chloroplast Metabolic Network. <i>Plant Physiology</i> , 2017, 174, 922-934.	4.8	23
16	Validating Missing Proteins in Human Sperm Cells by Targeted Mass-Spectrometry- and Antibody-based Methods. <i>Journal of Proteome Research</i> , 2017, 16, 4340-4351.	3.7	21
17	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970.	3.7	158
18	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. <i>Journal of Proteome Research</i> , 2016, 15, 3971-3978.	3.7	15

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19	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. <i>Journal of Proteome Research</i> , 2016, 15, 3998-4019.	3.7	66
20	Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. <i>Journal of Proteome Research</i> , 2015, 14, 3621-3634.	3.7	35
21	Uranium perturbs signaling and iron uptake response in <i>Arabidopsis thaliana</i> roots. <i>Metallomics</i> , 2014, 6, 809-821.	2.4	38
22	An integrative computational model for large-scale identification of metalloproteins in microbial genomes: a focus on iron-sulfur cluster proteins. <i>Metallomics</i> , 2014, 6, 1913-1930.	2.4	20
23	Unbalanced expression of CK2 kinase subunits is sufficient to drive epithelial-to-mesenchymal transition by Snail1 induction. <i>Oncogene</i> , 2013, 32, 1373-1383.	5.9	70
24	Proteomic characterization of <i>Pseudomonas aeruginosa</i> PAO1 inner membrane. <i>Proteomics</i> , 2013, 13, 2419-2423.	2.2	98
25	Abstract 3419: A multiplexed enzymatic repair assay on biochip reveals a functional DNA repair signature in cancer cell lines exposed to cytotoxic anticancer drugs.. , 2013, , .		0
26	DSIR: Assessing the Design of Highly Potent siRNA by Testing a Set of Cancer-Relevant Target Genes. <i>PLoS ONE</i> , 2012, 7, e48057.	2.5	18
27	Functional DNA Repair Signature of Cancer Cell Lines Exposed to a Set of Cytotoxic Anticancer Drugs Using a Multiplexed Enzymatic Repair Assay on Biochip. <i>PLoS ONE</i> , 2012, 7, e51754.	2.5	12
28	Investigating the macropinocytic proteome of <i>Dictyostelium</i> amoebae by high-resolution mass spectrometry. <i>Proteomics</i> , 2012, 12, 241-245.	2.2	40
29	Exploring the Plant Response to Cadmium Exposure by Transcriptomic, Proteomic and Metabolomic Approaches: Potentiality of High-Throughput Methods, Promises of Integrative Biology. , 2012, , 119-142.		3
30	Dissecting the bacterial type VI secretion system by a genome wide in silico analysis: what can be learned from available microbial genomic resources?. <i>BMC Genomics</i> , 2009, 10, 104.	2.8	502
31	Guidelines for reporting the use of mass spectrometry informatics in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 862-862.	17.5	62
32	PepLine: A Software Pipeline for High-Throughput Direct Mapping of Tandem Mass Spectrometry Data on Genomic Sequences. <i>Journal of Proteome Research</i> , 2008, 7, 1873-1883.	3.7	28
33	Protocadherin 12 deficiency alters morphogenesis and transcriptional profile of the placenta. <i>Physiological Genomics</i> , 2008, 34, 193-204.	2.3	32
34	GenoLink: a graph-based querying and browsing system for investigating the function of genes and proteins. <i>BMC Bioinformatics</i> , 2006, 7, 21.	2.6	12
35	An accurate and interpretable model for siRNA efficacy prediction. <i>BMC Bioinformatics</i> , 2006, 7, 520.	2.6	248
36	Integration of data and methods for genome analysis. <i>Current Opinion in Drug Discovery & Development</i> , 2003, 6, 346-52.	1.9	7

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37	The Genexpress IMAGE Knowledge Base of the Human Brain Transcriptome: A Prototype Integrated Resource for Functional and Computational Genomics. <i>Genome Research</i> , 1999, 9, 195-209.	5.5	52
38	Transcriptional regulation of apolipoprotein E expression by cyclic AMP. <i>FEBS Letters</i> , 1996, 397, 155-158.	2.8	7
39	Thyroid Hormone Modulates Apolipoprotein-AI Gene Expression at the Post-Transcriptional Level in Hep G2 Cells. <i>FEBS Journal</i> , 1995, 231, 126-132.	0.2	7
40	Transcriptional regulation of apolipoprotein A-I expression in Hep G2 cells by phorbol ester. <i>FEBS Letters</i> , 1995, 376, 99-102.	2.8	6
41	Thyroid Hormone Modulates Apolipoprotein-AI Gene Expression at the Post-Transcriptional Level in Hep G2 Cells. <i>FEBS Journal</i> , 1995, 231, 126-132.	0.2	14
42	The Modulation of Apolipoprotein E Gene Expression by 3,3'-5-triiodothyronine in HepG2 Cells Occurs at Transcriptional and Post-transcriptional Levels. <i>FEBS Journal</i> , 1994, 224, 463-471.	0.2	14