Yves Vandenbrouck

List of Publications by Year
in descending order

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	Dissecting the bacterial type VI secretion system by a genome wide in silico analysis: what can be learned from available microbial genomic resources?. BMC Genomics, 2009, 10, 104.	2.8	502
2	An accurate and interpretable model for siRNA efficacy prediction. BMC Bioinformatics, 2006, 7, 520.	2.6	248
3	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	3.7	158
4	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	12.8	152
5	Proteomic characterization of <i>Pseudomonas aeruginosa</i> PAO1 inner membrane. Proteomics, 2013, 13, 2419-2423.	2.2	98
6	Advances and Utility of the Human Plasma Proteome. Journal of Proteome Research, 2021, 20, 5241-5263.	3.7	86
7	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116.	3.7	82
8	Unbalanced expression of CK2 kinase subunits is sufficient to drive epithelial-to-mesenchymal transition by Snail1 induction. Oncogene, 2013, 32, 1373-1383.	5.9	70
9	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. Journal of Proteome Research, 2016, 15, 3998-4019.	3.7	66
10	Guidelines for reporting the use of mass spectrometry informatics in proteomics. Nature Biotechnology, 2008, 26, 862-862.	17.5	62
11	The Genexpress IMAGE Knowledge Base of the Human Brain Transcriptome: A Prototype Integrated Resource for Functional and Computational Genomics. Genome Research, 1999, 9, 195-209.	5.5	52
12	Investigating the macropinocytic proteome of <i>Dictyostelium</i> amoebae by high‑resolution mass spectrometry. Proteomics, 2012, 12, 241-245.	2.2	40
13	Uranium perturbs signaling and iron uptake response in Arabidopsis thaliana roots. Metallomics, 2014, 6, 809-821.	2.4	38
14	Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. Journal of Proteome Research, 2015, 14, 3621-3634.	3.7	35
15	Protocadherin 12 deficiency alters morphogenesis and transcriptional profile of the placenta. Physiological Genomics, 2008, 34, 193-204.	2.3	32
16	Proteomic characterization of human exhaled breath condensate. Journal of Breath Research, 2018, 12, 021001.	3.0	29
17	PepLine: A Software Pipeline for High-Throughput Direct Mapping of Tandem Mass Spectrometry Data on Genomic Sequences. Journal of Proteome Research, 2008, 7, 1873-1883.	3.7	28
18	ChloroKB: A Web Application for the Integration of Knowledge Related to Chloroplast Metabolic Network. Plant Physiology, 2017, 174, 922-934.	4.8	23

#	ARTICLE	IF	CITATIONS
19	Bioinformatics Tools and Workflow to Select Blood Biomarkers for Early Cancer Diagnosis: An Application to Pancreatic Cancer. Proteomics, 2019, 19, e1800489.	2.2	22
20	Validating Missing Proteins in Human Sperm Cells by Targeted Mass-Spectrometry- and Antibody-based Methods. Journal of Proteome Research, 2017, 16, 4340-4351.	3.7	21
21	An integrative computational model for large-scale identification of metalloproteins in microbial genomes: a focus on iron–sulfur cluster proteins. Metallomics, 2014, 6, 1913-1930.	2.4	20
22	DSIR: Assessing the Design of Highly Potent siRNA by Testing a Set of Cancer-Relevant Target Genes. PLoS ONE, 2012, 7, e48057.	2.5	18
23	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. Journal of Proteome Research, 2016, 15, 3971-3978.	3.7	15
24	The Modulation of Apolipoprotein E Gene Expression by 3,3'-5-triiodothyronine in HepG2 Cells Occurs at Transcriptional and Post-transcriptional Levels. FEBS Journal, 1994, 224, 463-471.	0.2	14
25	Thyroid Hormone Modulates Apolipoprotein-AI Gene Expression at the Post-Transcriptional Level in Hep G2 Cells. FEBS Journal, 1995, 231, 126-132.	0.2	14
26	GenoLink: a graph-based querying and browsing system for investigating the function of genes and proteins. BMC Bioinformatics, 2006, 7, 21.	2.6	12
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. PLoS ONE, 2012, 7, e51754.	2.5	12
28	Peptimapper: proteogenomics workflow for the expert annotation of eukaryotic genomes. BMC Genomics, 2019, 20, 56.	2.8	10
29	Designing an In Silico Strategy to Select Tissue-Leakage Biomarkers Using the Galaxy Framework. Methods in Molecular Biology, 2019, 1959, 275-289.	0.9	10
30	The Functionally Unannotated Proteome of Human Male Tissues: A Shared Resource to Uncover New Protein Functions Associated with Reproductive Biology. Journal of Proteome Research, 2020, 19, 4782-4794.	3.7	10
31	Thyroid Hormone Modulates Apolipoprotein-AI Gene Expression at the Post-Transcriptional Level in Hep G2 Cells. FEBS Journal, 1995, 231, 126-132.	0.2	7
32	Transcriptional regulation of apolipoprotein E expression by cyclic AMP. FEBS Letters, 1996, 397, 155-158.	2.8	7
33	GO Enrichment Analysis for Differential Proteomics Using ProteoRE. Methods in Molecular Biology, 2021, 2361, 179-196.	0.9	7
34	Integration of data and methods for genome analysis. Current Opinion in Drug Discovery & Development, 2003, 6, 346-52.	1.9	7
35	Transcriptional regulation of apolipoprotein A-I expression in Hep G2 cells by phorbol ester. FEBS Letters, 1995, 376, 99-102.	2.8	6
36	Probing Protein Interaction Networks by Combining MS-Based Proteomics and Structural Data Integration. Journal of Proteome Research, 2020, 19, 2807-2820.	3.7	6

#	Article	IF	Citations
37	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. Scientific Data, 2021, 8, 311.	5.3	6
38	Proteo3Dnet: a web server for the integration of structural information with interactomics data. Nucleic Acids Research, 2021, 49, W567-W572.	14.5	5
39	ChloroKB, a cell metabolism reconstruction of the model plant Arabidopsis thaliana. Comptes Rendus - Biologies, 2021, 344, 157-163.	0.2	5
40	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
41	Mass Spectrometry-Based Proteomics Reveal Alcohol Dehydrogenase 1B as a Blood Biomarker Candidate to Monitor Acetaminophen-Induced Liver Injury. International Journal of Molecular Sciences, 2021, 22, 11071.	4.1	1
42	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