

Elien Vandermarliere

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/245881/publications.pdf>

Version: 2024-02-01

25
papers

566
citations

687363

13
h-index

677142

22
g-index

31
all docs

31
docs citations

31
times ranked

990
citing authors

#	ARTICLE	IF	CITATIONS
1	Bcl-xL acts as an inhibitor of IP3R channels, thereby antagonizing Ca ²⁺ -driven apoptosis. <i>Cell Death and Differentiation</i> , 2022, 29, 788-805.	11.2	41
2	Sensitive and Specific Spectral Library Searching with CompOmics Spectral Library Searching Tool and Percolator. <i>Journal of Proteome Research</i> , 2022, 21, 1365-1370.	3.7	6
3	Massively parallel interrogation of protein fragment secretability using SECRIFY reveals features influencing secretory system transit. <i>Nature Communications</i> , 2021, 12, 6414.	12.8	5
4	COSS: A Fast and User-Friendly Tool for Spectral Library Searching. <i>Journal of Proteome Research</i> , 2020, 19, 2786-2793.	3.7	18
5	The CEP5 Peptide Promotes Abiotic Stress Tolerance, As Revealed by Quantitative Proteomics, and Attenuates the AUX/IAA Equilibrium in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1248-1262.	3.8	35
6	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. <i>Journal of Proteome Research</i> , 2020, 19, 3478-3486.	3.7	19
7	Bcl-2 and IP3 compete for the ligand-binding domain of IP3Rs modulating Ca ²⁺ signaling output. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 3843-3859.	5.4	31
8	Scop3D: Online Visualization of Mutation Rates on Protein Structure. <i>Journal of Proteome Research</i> , 2019, 18, 765-769.	3.7	2
9	A double point mutation at residues Ile14 and Val15 of Bcl-2 uncovers a role for the BH4 domain in both protein stability and function. <i>FEBS Journal</i> , 2018, 285, 127-145.	4.7	16
10	Cross-linked peptide identification: A computational forest of algorithms. <i>Mass Spectrometry Reviews</i> , 2018, 37, 738-749.	5.4	27
11	The study of degradation mechanisms of glyco-engineered plant produced anti-rabies monoclonal antibodies E559 and 62-71-3. <i>PLoS ONE</i> , 2018, 13, e0209373.	2.5	3
12	Differences in antigenic sites and other functional regions between genotype A and G mumps virus surface proteins. <i>Scientific Reports</i> , 2018, 8, 13337.	3.3	22
13	The mutational landscape of MYCN, Lin28b and ALK driven murine neuroblastoma mimics human disease. <i>Oncotarget</i> , 2018, 9, 8334-8349.	1.8	6
14	Methods to Calculate Spectrum Similarity. <i>Methods in Molecular Biology</i> , 2017, 1549, 75-100.	0.9	18
15	A Pipeline for Differential Proteomics in Unsequenced Species. <i>Journal of Proteome Research</i> , 2016, 15, 1963-1970.	3.7	10
16	Xlmass: A New Approach toward the Identification of Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016, 88, 9949-9957.	6.5	25
17	The Lyssavirus glycoprotein: A key to cross-immunity. <i>Virology</i> , 2016, 498, 250-256.	2.4	11
18	Resolution of protein structure by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2016, 35, 653-665.	5.4	15

#	ARTICLE	IF	CITATIONS
19	Ryanodine receptors are targeted by anti-apoptotic Bcl-XL involving its BH4 domain and Lys87 from its BH3 domain. Scientific Reports, 2015, 5, 9641.	3.3	30
20	Scop3D: Three-dimensional visualization of sequence conservation. Proteomics, 2015, 15, 1448-1452.	2.2	11
21	PepShell: Visualization of Conformational Proteomics Data. Journal of Proteome Research, 2015, 14, 1987-1990.	3.7	2
22	Limited Proteolysis Combined with Stable Isotope Labeling Reveals Conformational Changes in Protein (Pseudo)kinases upon Binding Small Molecules. Journal of Proteome Research, 2015, 14, 4179-4193.	3.7	7
23	Unraveling the specificities of the different human methionine sulfoxide reductases. Proteomics, 2014, 14, 1990-1998.	2.2	7
24	Protein structure as a means to triage proposed <sc>PTM</sc> sites. Proteomics, 2013, 13, 1028-1035.	2.2	31
25	Getting intimate with trypsin, the leading protease in proteomics. Mass Spectrometry Reviews, 2013, 32, 453-465.	5.4	164