Christine Hoogland

List of Publications by Year
in descending order

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39 papers	5,658 citations	346980 22 h-index	355658 38 g-index
43 all docs	43 docs citations	43 times ranked	9446 citing authors

#	Article	IF	Citations
1	ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Research, 2003, 31, 3784-3788.	6.5	4,128
2	The mouse SWISS-2D PAGE database: a tool for proteomics study of diabetes and obesity. Proteomics, 2001, 1, 136-163.	1.3	155
3	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. Electrophoresis, 1999, 20, 3535-3550.	1.3	140
4	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. Analytical Chemistry, 1999, 71, 4981-4988.	3.2	127
5	SWISS-2DPAGE, ten years later. Proteomics, 2004, 4, 2352-2356.	1.3	104
6	Combining low- and high-energy tandem mass spectra for optimized peptide quantification with isobaric tags. Journal of Proteomics, 2010, 73, 769-777.	1.2	99
7	'98Escherichia coli SWISS-2DPAGE database update. Electrophoresis, 1998, 19, 1960-1971.	1.3	90
8	Guidelines for reporting the use of gel electrophoresis in proteomics. Nature Biotechnology, 2008, 26, 863-864.	9.4	61
9	Correlation of proteomic and transcriptomic profiles of Staphylococcus aureus during the post-exponential phase of growth. Journal of Microbiological Methods, 2005, 60, 247-257.	0.7	59
10	EasyProt â€" An easy-to-use graphical platform for proteomics data analysis. Journal of Proteomics, 2013, 79, 146-160.	1.2	57
11	Two-dimensional electrophoresis resources available from ExPASy. Electrophoresis, 1999, 20, 3568-3571.	1.3	47
12	The World-2DPAGE Constellation to promote and publish gel-based proteomics data through the ExPASy server. Journal of Proteomics, 2008, 71, 245-248.	1.2	47
13	Chromosomal Distribution of Transposable Elements in <i>Drosophila melanogaster</i> Test of the Ectopic Recombination Model for Maintenance of Insertion Site Number. Genetics, 1996, 144, 197-204.	1.2	46
14	The establishment of a human liver nuclei two-dimensional electrophoresis reference map. Electrophoresis, 2000, 21, 3483-3487.	1.3	40
15	Quantitative Analysis of Human Cerebrospinal Fluid Proteins Using a Combination of Cysteine Tagging and Amine-Reactive Isobaric Labeling. Journal of Proteome Research, 2011, 10, 249-258.	1.8	37
16	Proteomic Analysis of Rhizoctonia solani Identifies Infection-specific, Redox Associated Proteins and Insight into Adaptation to Different Plant Hosts. Molecular and Cellular Proteomics, 2016, 15, 1188-1203.	2.5	37
17	The Make 2D-DB II package: Conversion of federated two-dimensional gel electrophoresis databases into a relational format and interconnection of distributed databases. Proteomics, 2003, 3, 1441-1444.	1.3	34
18	Title is missing!. Genetica, 1997, 100, 161-166.	0.5	31

#	ARTICLE	IF	CITATIONS
19	The molecular scanner: concept and developments. Current Opinion in Biotechnology, 2004, 15, 17-23.	3.3	28
20	Management and dissemination of MS proteomic data with PROTICdb: Example of a quantitative comparison between methods of protein extraction. Proteomics, 2013, 13, 1457-1466.	1.3	25
21	Make2ddb: A simple package to set up a two-dimensional electrophoresis database for the World Wide Web. Electrophoresis, 1997, 18, 2755-2758.	1.3	24
22	Current status of the SWISS-2DPAGE database. Nucleic Acids Research, 1998, 26, 332-333.	6.5	23
23	Guidelines for reporting the use of gel image informatics in proteomics. Nature Biotechnology, 2010, 28, 655-656.	9.4	22
24	MIAPEGelDB, a web-based submission tool and public repository for MIAPE gel electrophoresis documents. Journal of Proteomics, 2008, 71, 249-251.	1.2	19
25	The Gel Electrophoresis Markup Language (GelML) from the Proteomics Standards Initiative. Proteomics, 2010, 10, 3073-3081.	1.3	19
26	The SWISS-2DPAGE database: what has changed during the last year. Nucleic Acids Research, 1999, 27, 289-291.	6.5	18
27	Hydrogen/deuterium exchange for higher specificity of protein identification by peptide mass fingerprinting. Rapid Communications in Mass Spectrometry, 2002, 16, 616-626.	0.7	18
28	Integration of Two In-depth Quantitative Proteomics Approaches Determines the Kallikrein-related Peptidase 7 (KLK7) Degradome in Ovarian Cancer Cell Secretome. Molecular and Cellular Proteomics, 2019, 18, 818a-836.	2.5	16
29	Human Hemolysate Glycated Proteome. Analytical Chemistry, 2011, 83, 5673-5680.	3.2	15
30	Constructing a 2-D Database for the World Wide Web. , 1999, 112, 411-416.		6
31	Site-specific glycosylation of the Newcastle disease virus haemagglutinin-neuraminidase. Glycoconjugate Journal, 2017, 34, 181-197.	1.4	6
32	Mass-spectrometry data for Rhizoctonia solani proteins produced during infection of wheat and vegetative growth. Data in Brief, 2016, 8, 267-271.	0.5	5
33	A suite of tools to analyse and publish 2â€ÐE data. Proteomics, 2008, 8, 4907-4909.	1.3	3
34	Using bioinformatic resources in the proteomic analysis of biological fluids. Proteomics - Clinical Applications, 2007, 1, 900-915.	0.8	2
35	Maintenance of transposable element copy number in natural populations of Drosophila melanogaster and D. simulans. Contemporary Issues in Genetics and Evolution, 1997, , 161-166.	0.9	1
36	2D PAGE Databases for Proteins in Human Body Fluids. , 2007, , 137-146.		1

#	Article	IF	Citations
37	Chromosomal distribution and population dynamics of the 412 retrotransposon in a natural population of Drosophila melanogaster. Chromosoma, 1995, 103, 693-699.	1.0	1
38	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
39	SPS' Digest: The Swiss Proteomics Society selection of proteomics articles. Proteomics, 2005, 5, 3045-3047.	1.3	0