Frederique Lisacek

List of Publications by Year
in descending order

137 papers	12,877 citations	116194 36 h-index	31191 106 g-index
154 all docs	154 docs citations	154 times ranked	28225 citing authors

#	Article	IF	Citations
1	An Interactive View of Glycosylation. Methods in Molecular Biology, 2022, 2370, 41-65.	0.4	0
2	LectinOracle: A Generalizable Deep Learning Model for Lectinâ€"Glycan Binding Prediction. Advanced Science, 2022, 9, e2103807.	5.6	18
3	Bioinformatics Resources for the Study of Glycan-Mediated Protein Interactions. Journal of Visualized Experiments, 2022, , .	0.2	0
4	Dealing with the Ambiguity of Glycan Substructure Search. Molecules, 2022, 27, 65.	1.7	6
5	In silico analysis of the human milk oligosaccharide glycome reveals key enzymes of their biosynthesis. Scientific Reports, 2022, 12, .	1.6	7
6	Adduct annotation in liquid chromatography/high-resolution mass spectrometry to enhance compound identification. Analytical and Bioanalytical Chemistry, 2021, 413, 503-517.	1.9	17
7	Glycoinformatics Resources Integrated Through the GlySpace Alliance. , 2021, , 507-521.		2
8	Glycan Compositions with GlyConnect Compozitorâto Enhance Glycopeptide Identification. Methods in Molecular Biology, 2021, 2361, 109-127.	0.4	5
9	The glycoconjugate ontology (GlycoCoO) for standardizing the annotation of glycoconjugate data and its application. Glycobiology, 2021, 31, 741-750.	1.3	7
10	Expasy, the Swiss Bioinformatics Resource Portal, as designed by its users. Nucleic Acids Research, 2021, 49, W216-W227.	6.5	333
11	Proteome-wide prediction of bacterial carbohydrate-binding proteins as a tool for understanding commensal and pathogen colonisation of the vaginal microbiome. Npj Biofilms and Microbiomes, 2021, 7, 49.	2.9	11
12	A Comprehensive Phylogenetic and Bioinformatics Survey of Lectins in the Fungal Kingdom. Journal of Fungi (Basel, Switzerland), 2021, 7, 453.	1.5	19
13	LectomeXplore, an update of UniLectin for the discovery of carbohydrate-binding proteins based on a new lectin classification. Nucleic Acids Research, 2021, 49, D1548-D1554.	6.5	31
14	GlycoBioinformatics. Beilstein Journal of Organic Chemistry, 2021, 17, 2726-2728.	1.3	2
15	UniLectin, A Oneâ€Stopâ€Shop to Explore andÂStudyÂCarbohydrateâ€BindingÂProteins. Current Protocols, 2021, 1, e305.	1.3	4
16	Bioinformatics in Immunoglobulin Glycosylation Analysis. Experientia Supplementum (2012), 2021, 112, 205-233.	0.5	0
17	The GlySpace Alliance: toward a collaborative global glycoinformatics community. Glycobiology, 2020, 30, 70-71.	1.3	28
18	Structure and engineering of tandem repeat lectins. Current Opinion in Structural Biology, 2020, 62, 39-47.	2.6	29

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19	Automatic Annotation and Dereplication of Tandem Mass Spectra of Peptidic Natural Products. Analytical Chemistry, 2020, 92, 15862-15871.	3.2	18
20	GAG-DB, the New Interface of the Three-Dimensional Landscape of Glycosaminoglycans. Biomolecules, 2020, 10, 1660.	1.8	16
21	Examining and Fine-tuning the Selection of Glycan Compositions with GlyConnect Compozitor. Molecular and Cellular Proteomics, 2020, 19, 1602-1618.	2.5	17
22	Structural Database for Lectins and the UniLectin Web Platform. Methods in Molecular Biology, 2020, 2132, 1-14.	0.4	10
23	OUP accepted manuscript. Nucleic Acids Research, 2020, 48, D465-D469.	6.5	51
24	Proteome Informatics. , 2019, , 60-75.		0
25	Towards a standardized bioinformatics infrastructure for N- and O-glycomics. Nature Communications, 2019, 10, 3275.	5.8	70
26	Kendrick Mass Defect Approach Combined to NORINE Database for Molecular Formula Assignment of Nonribosomal Peptides. Journal of the American Society for Mass Spectrometry, 2019, 30, 2608-2616.	1.2	3
27	A targeted proteomics approach reveals a serum protein signature as diagnostic biomarker for resectable gastric cancer. EBioMedicine, 2019, 44, 322-333.	2.7	52
28	Updates to the Symbol Nomenclature for Glycans guidelines. Glycobiology, 2019, 29, 620-624.	1.3	292
29	A Bioinformatics View of Glycan–Virus Interactions. Viruses, 2019, 11, 374.	1.5	4
30	Architecture and Evolution of Blade Assembly in Î²-propeller Lectins. Structure, 2019, 27, 764-775.e3.	1.6	27
31	Sweet and Sour Ehrlichia: Glycoproteomics and Phosphoproteomics Reveal New Players in Ehrlichia ruminantium Physiology and Pathogenesis. Frontiers in Microbiology, 2019, 10, 450.	1.5	8
32	rBAN: retro-biosynthetic analysis of nonribosomal peptides. Journal of Cheminformatics, 2019, 11, 13.	2.8	16
33	A pipeline to translate glycosaminoglycan sequences into 3D models. Application to the exploration of glycosaminoglycan conformational space. Glycobiology, 2019, 29, 36-44.	1.3	28
34	GlyConnect: Glycoproteomics Goes Visual, Interactive, and Analytical. Journal of Proteome Research, 2019, 18, 664-677.	1.8	95
35	UniLectin3D, a database of carbohydrate binding proteins with curated information on 3D structures and interacting ligands. Nucleic Acids Research, 2019, 47, D1236-D1244.	6.5	82
36	Understanding the glycome: an interactive view of glycosylation from glycocompositions to glycoepitopes. Glycobiology, 2018, 28, 349-362.	1.3	21

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37	Bioinformatics Support for Farm Animal Proteomics. , 2018, , 361-386.		0
38	PepSweetener: A Web‑Based Tool to Support Manual Annotation of Intact Glycopeptide MS Spectra. Proteomics - Clinical Applications, 2018, 12, e1700069.	0.8	7
39	SugarSketcher: Quick and Intuitive Online Glycan Drawing. Molecules, 2018, 23, 3206.	1.7	14
40	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. Journal of Proteome Research, 2018, 17, 4160-4170.	1.8	21
41	Glycomics@ExPASy: Bridging the Gap. Molecular and Cellular Proteomics, 2018, 17, 2164-2176.	2.5	48
42	Optimization by infusion of multiple reaction monitoring transitions for sensitive quantification of peptides by liquid chromatography/mass spectrometry. Rapid Communications in Mass Spectrometry, 2017, 31, 753-761.	0.7	8
43	Glycosaminoglycanomics: where we are. Glycoconjugate Journal, 2017, 34, 339-349.	1.4	40
44	Glycoforest 1.0. Analytical Chemistry, 2017, 89, 10932-10940.	3.2	24
45	GlyTouCan: an accessible glycan structure repository. Glycobiology, 2017, 27, 915-919.	1.3	123
46	Databases and Associated Tools for Glycomics and Glycoproteomics. Methods in Molecular Biology, 2017, 1503, 235-264.	0.4	44
47	Peptidomic and transcriptomic profiling of four distinct spider venoms. PLoS ONE, 2017, 12, e0172966.	1.1	25
48	Navigating the Glycome Space and Connecting the Glycoproteome. Methods in Molecular Biology, 2017, 1558, 139-158.	0.4	4
49	Exploring the UniCarbKB Database. , 2017, , 197-214.		2
50	SugarBindDB. , 2017, , 247-260.		2
51	GlycoSiteAlign: Glycosite Alignment Based on Glycan Structure. Journal of Proteome Research, 2016, 15, 3916-3928.	1.8	7
52	Dedicated Software Enhancing Data-independent Acquisition Methods in Mass Spectrometry. Chimia, 2016, 70, 293.	0.3	3
53	Mining Large Scale Tandem Mass Spectrometry Data for Protein Modifications Using Spectral Libraries. Journal of Proteome Research, 2016, 15, 721-731.	1.8	26
54	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64

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55	SugarBindDB, a resource of glycan-mediated host–pathogen interactions. Nucleic Acids Research, 2016, 44, D1243-D1250.	6.5	40
56	Unrestricted modification search reveals lysine methylation as major modification induced by tissue formalin fixation and paraffin embedding. Proteomics, 2015, 15, 2568-2579.	1.3	40
57	Property Graph vs RDF Triple Store: A Comparison on Glycan Substructure Search. PLoS ONE, 2015, 10, e0144578.	1.1	37
58	Processing strategies and software solutions for data–independent acquisition in mass spectrometry. Proteomics, 2015, 15, 964-980.	1.3	143
59	Uncovering Intense Protein Diversification in a Cone Snail Venom Gland Using an Integrative Venomics Approach. Journal of Proteome Research, 2015, 14, 628-638.	1.8	15
60	MzJava: An open source library for mass spectrometry data processing. Journal of Proteomics, 2015, 129, 63-70.	1.2	25
61	Optimization of human dendritic cell sample preparation for mass spectrometry-based proteomic studies. Analytical Biochemistry, 2015, 484, 40-50.	1.1	16
62	Ranking Fragment Ions Based on Outlier Detection for Improved Label-Free Quantification in Data-Independent Acquisition LC–MS/MS. Journal of Proteome Research, 2015, 14, 4581-4593.	1.8	19
63	The Use of Variable Q1 Isolation Windows Improves Selectivity in LC–SWATH–MS Acquisition. Journal of Proteome Research, 2015, 14, 4359-4371.	1.8	151
64	UniCarbKB: Emergent Knowledgebase for Glycomics. , 2015, , 215-222.		1
65	Comparative Proteomic Profiling of Ehrlichia ruminantium Pathogenic Strain and Its High-Passaged Attenuated Strain Reveals Virulence and Attenuation-Associated Proteins. PLoS ONE, 2015, 10, e0145328.	1.1	28
66	SugarBindDB SugarBindDB : Resource of Pathogen Pathogen Lectin-Glycan Interactions Lectin-glycan interactions. , 2015, , 275-282.		0
67	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	6.5	13
68	Pathway analysis and transcriptomics improve protein identification by shotgun proteomics from samples comprising small number of cells - a benchmarking study. BMC Genomics, 2014, 15, S1.	1.2	22
69	Toolboxes for a standardised and systematic study of glycans. BMC Bioinformatics, 2014, 15, S9.	1.2	58
70	Integrated Bio-Search: challenges and trends for the integration, search and comprehensive processing of biological information. BMC Bioinformatics, 2014, 15, S2.	1.2	11
71	GlycoDigest: a tool for the targeted use of exoglycosidase digestions in glycan structure determination. Bioinformatics, 2014, 30, 3131-3133.	1.8	29
72	UniCarbKB: building a knowledge platform for glycoproteomics. Nucleic Acids Research, 2014, 42, D215-D221.	6.5	147

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73	Proteomics Pioneer Award 2013: Professor Amos Bairoch, University of Geneva, Switzerland*. EuPA Open Proteomics, 2014, 2, 34.	2.5	0
74	SugarBindDB, a Resource of Pathogen Lectin-Glycan Interactions. , 2014, , 1-7.		1
75	UniCarbKB: An Emergent Knowledge Base for Glycomics. , 2014, , 1-7.		0
76	SugarBindDB, a Resource of Pathogen Lectin-Glycan Interactions. , 2014, , 1-6.		1
77	SugarBind database (SugarBindDB): a resource of pathogen lectins and corresponding glycan targets. Journal of Molecular Recognition, 2013, 26, 426-431.	1.1	21
78	PanelomiX: A threshold-based algorithm to create panels of biomarkers. Translational Proteomics, 2013, 1, 57-64.	1.2	29
79	Comparative analysis of Leishmania exoproteomes: Implication for host–pathogen interactions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2653-2662.	1.1	8
80	EasyProt â€" An easy-to-use graphical platform for proteomics data analysis. Journal of Proteomics, 2013, 79, 146-160.	1.2	57
81	Clustering and Filtering Tandem Mass Spectra Acquired in Data-Independent Mode. Journal of the American Society for Mass Spectrometry, 2013, 24, 1862-1871.	1.2	15
82	Position-specific scoring matrix and hidden Markov model complement each other for the prediction of conopeptide superfamilies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 717-724.	1.1	12
83	Absolute quantification of transcription factors during cellular differentiation using multiplexed targeted proteomics. Nature Methods, 2013, 10, 570-576.	9.0	82
84	ConoDictor: a tool for prediction of conopeptide superfamilies. Nucleic Acids Research, 2012, 40, W238-W241.	6.5	28
85	Identification and classification of conopeptides using profile Hidden Markov Models. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 488-492.	1.1	18
86	Glycans, the forgotten biomolecular actors of the big picture. EMBnet Journal, 2012, 18, 87.	0.2	1
87	Human Hemolysate Glycated Proteome. Analytical Chemistry, 2011, 83, 5673-5680.	3.2	15
88	Addressing Trypsin Bias in Large Scale (Phospho)proteome Analysis by Size Exclusion Chromatography and Secondary Digestion of Large Post-Trypsin Peptides. Journal of Proteome Research, 2011, 10, 800-811.	1.8	35
89	QuickMod: A Tool for Open Modification Spectrum Library Searches. Journal of Proteome Research, 2011, 10, 2913-2921.	1.8	58
90	pROC: an open-source package for R and S+ to analyze and compare ROC curves. BMC Bioinformatics, 2011, 12, 77.	1.2	8,498

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91	An improved method for the construction of decoy peptide MS/MS spectra suitable for the accurate estimation of false discovery rates. Proteomics, 2011, 11, 4085-4095.	1.3	25
92	UniCarbKB: Putting the pieces together for glycomics research. Proteomics, 2011, 11, 4117-4121.	1.3	55
93	UniCarb-DB: a database resource for glycomic discovery. Bioinformatics, 2011, 27, 1343-1344.	1.8	128
94	LC/MS Data Processing for Label-Free Quantitative Analysis. Methods in Molecular Biology, 2011, 696, 369-377.	0.4	1
95	A multiparameter panel method for outcome prediction following aneurysmal subarachnoid hemorrhage. Intensive Care Medicine, 2010, 36, 107-115.	3.9	75
96	Early activation of the fatty acid metabolism pathway by chronic high glucose exposure in rat insulin secretory β‐cells. Proteomics, 2010, 10, 59-71.	1.3	14
97	Unrestricted identification of modified proteins using MS/MS. Proteomics, 2010, 10, 671-686.	1.3	86
98	Image analysis tools and emerging algorithms for expression proteomics. Proteomics, 2010, 10, 4226-4257.	1.3	46
99	Glycation Isotopic Labeling with 13C-Reducing Sugars for Quantitative Analysis of Glycated Proteins in Human Plasma. Molecular and Cellular Proteomics, 2010, 9, 579-592.	2.5	70
100	SwissPIT: An workflow‐based platform for analyzing tandem‐MS spectra using the Grid. Proteomics, 2009, 9, 2648-2655.	1.3	15
101	A simple workflow to increase MS2 identification rate by subsequent spectral library search. Proteomics, 2009, 9, 1731-1736.	1.3	32
102	Getting a grip on proteomics data â€" Proteomics Data Collection (ProDaC). Proteomics, 2009, 9, 3928-3933.	1.3	15
103	Bioinformatics for protein biomarker panel classification: what is needed to bring biomarker panels into<i>in vitro</i>diagnostics?. Expert Review of Proteomics, 2009, 6, 675-689.	1.3	51
104	X-Rank: A Robust Algorithm for Small Molecule Identification Using Tandem Mass Spectrometry. Analytical Chemistry, 2009, 81, 7604-7610.	3.2	72
105	Database Interrogation Algorithms for Identification of Proteins in Proteomic Separations. Methods in Molecular Biology, 2009, 519, 515-531.	0.4	2
106	A Combined CXCL10, CXCL8 and H-FABP Panel for the Staging of Human African Trypanosomiasis Patients. PLoS Neglected Tropical Diseases, 2009, 3, e459.	1.3	62
107	High-Throughput Data Analysis of Proteomic Mass Spectra on the SwissBioGrid. , 2009, , 228-244.		0
108	Analytical Bioinformatics for Proteomics. , 2009, , 169-196.		0

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109	A suite of tools to analyse and publish 2â€ĐE data. Proteomics, 2008, 8, 4907-4909.	1.3	3
110	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
111	MIAPEGelDB, a web-based submission tool and public repository for MIAPE gel electrophoresis documents. Journal of Proteomics, 2008, 71, 249-251.	1.2	19
112	pICarver: A Software Tool and Strategy for Peptides Isoelectric Focusing. Journal of Proteome Research, 2008, 7, 4336-4345.	1.8	11
113	swissPIT: a novel approach for pipelined analysis of mass spectrometry data. Bioinformatics, 2008, 24, 1416-1417.	1.8	7
114	Functional specifications of an integrated proteomics information management and analysis platform. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 6065-9.	0.5	0
115	Using bioinformatic resources in the proteomic analysis of biological fluids. Proteomics - Clinical Applications, 2007, 1, 900-915.	0.8	2
116	Assignment of protein function and discovery of novel nucleolar proteins based on automatic analysis of MEDLINE. Proteomics, 2007, 7, 921-931.	1.3	16
117	Systems Biology. Proteomics, 2007, 7, 825-827.	1.3	3
118	Proteome informatics II: Bioinformatics for comparative proteomics. Proteomics, 2006, 6, 5445-5466.	1.3	34
119	Using argumentation to retrieve articles with similar citations: An inquiry into improving related articles search in the MEDLINE digital library. International Journal of Medical Informatics, 2006, 75, 488-495.	1.6	36
120	Deciphering the human nucleolar proteome. Mass Spectrometry Reviews, 2006, 25, 215-234.	2.8	92
121	Web-based MS/MS Data Analysis. Proteomics, 2006, 6, 22-32.	1.3	6
122	Extracting key sentences with latent argumentative structuring. Studies in Health Technology and Informatics, 2005, 116, 835-40.	0.2	0
123	Fine-tuning the prediction of sequences cleaved by signal peptidase II: A curated set of proven and predicted lipoproteins ofEscherichia coli K-12. Proteomics, 2004, 4, 1597-1613.	1.3	36
124	Shaping Biological Knowledge: Applications in Proteomics. Comparative and Functional Genomics, 2004, 5, 190-195.	2.0	5
125	Methods of Computational Genomics. , 2004, , 279-342.		0
126	Using protein motif combinations to update KEGG pathway maps and orthologue tables. Genome Informatics, 2004, 15, 266-75.	0.4	6

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127	Investigating protein domain combinations in complete proteomes. Computational Biology and Chemistry, 2003, 27, 481-495.	1.1	4
128	Consistency checks for characterizing protein forms. Computational Biology and Chemistry, 2003, 27, 29-35.	1.1	8
129	Shaping biological knowledge. Pharmacogenomics, 2003, 4, 5-8.	0.6	4
130	Computer-Aided Strategies for Characterizing Protein Isoforms. , 2003, , 259-268.		0
131	Probabilistic alignment of motifs with sequences. Bioinformatics, 2002, 18, 1091-1101.	1.8	26
132	A multi-agent system simulating human splice site recognition. Computers & Chemistry, 1999, 23, 219-231.	1.2	7
133	Global analysis of genomic texts: The distribution of AGCT tetranucleotides in theEscherichia coli andBacillus subtilis genomes predicts translational frameshifting and ribosomal hopping in several genes. Electrophoresis, 1998, 19, 515-527.	1.3	14
134	Codon usage and gene function are related in sequences of Arabidopsis thaliana. Gene, 1998, 209, GC1-GC38.	1.0	154
135	Exon prediction in eucaryotic genomes. Biochimie, 1996, 78, 327-334.	1.3	10
136	Very Fast Identification of RNA Motifs in Genomic DNA. Application to tRNA Search in the Yeast Genome. Journal of Molecular Biology, 1996, 264, 46-55.	2.0	42
137	Automatic Identification of Group I Intron Cores in Genomic DNA Sequences. Journal of Molecular Biology, 1994, 235, 1206-1217.	2.0	54