

Sven Degroeve

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

6,653
citations

236925

25
h-index

233421

45
g-index

55
all docs

55
docs citations

55
times ranked

9400
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	12.6	3,945
2	Genome analysis of the smallest free-living eukaryote <i>Ostreococcus tauri</i> unveils many unique features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11647-11652.	7.1	809
3	Random forests as a tool for ecohydrological distribution modelling. <i>Ecological Modelling</i> , 2007, 207, 304-318.	2.5	293
4	MS2PIP: a tool for MS/MS peak intensity prediction. <i>Bioinformatics</i> , 2013, 29, 3199-3203.	4.1	108
5	Large-scale structural analysis of the core promoter in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2005, 33, 4255-4264.	14.5	103
6	DeepLC can predict retention times for peptides that carry as-yet unseen modifications. <i>Nature Methods</i> , 2021, 18, 1363-1369.	19.0	95
7	Feature subset selection for splice site prediction. <i>Bioinformatics</i> , 2002, 18, S75-S83.	4.1	93
8	SpliceMachine: predicting splice sites from high-dimensional local context representations. <i>Bioinformatics</i> , 2005, 21, 1332-1338.	4.1	92
9	Updated MS ² PIP web server delivers fast and accurate MS ² peak intensity prediction for multiple fragmentation methods, instruments and labeling techniques. <i>Nucleic Acids Research</i> , 2019, 47, W295-W299.	14.5	77
10	Comprehensive and Empirical Evaluation of Machine Learning Algorithms for Small Molecule LC Retention Time Prediction. <i>Analytical Chemistry</i> , 2019, 91, 3694-3703.	6.5	64
11	MS ² PIP prediction server: compute and visualize MS ² peak intensity predictions for CID and HCD fragmentation. <i>Nucleic Acids Research</i> , 2015, 43, W326-W330.	14.5	63
12	Analysis of the Resolution Limitations of Peptide Identification Algorithms. <i>Journal of Proteome Research</i> , 2011, 10, 5555-5561.	3.7	60
13	Bioinformatics Analysis of a <i>Saccharomyces cerevisiae</i> N-Terminal Proteome Provides Evidence of Alternative Translation Initiation and Post-Translational N-Terminal Acetylation. <i>Journal of Proteome Research</i> , 2011, 10, 3578-3589.	3.7	53
14	Machine learning applications in proteomics research: How the past can boost the future. <i>Proteomics</i> , 2014, 14, 353-366.	2.2	52
15	Accurate peptide fragmentation predictions allow data driven approaches to replace and improve upon proteomics search engine scoring functions. <i>Bioinformatics</i> , 2019, 35, 5243-5248.	4.1	52
16	Fast feature selection using a simple estimation of distribution algorithm: a case study on splice site prediction. <i>Bioinformatics</i> , 2003, 19, ii179-ii188.	4.1	51
17	Feature selection for splice site prediction: a new method using EDA-based feature ranking. <i>BMC Bioinformatics</i> , 2004, 5, 64.	2.6	49
18	Translation initiation site prediction on a genomic scale: beauty in simplicity. <i>Bioinformatics</i> , 2007, 23, i418-i423.	4.1	48

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19	Predicting Tryptic Cleavage from Proteomics Data Using Decision Tree Ensembles. <i>Journal of Proteome Research</i> , 2013, 12, 2253-2259.	3.7	48
20	Proteome-derived Peptide Libraries to Study the Substrate Specificity Profiles of Carboxypeptidases. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2096-2110.	3.8	40
21	Removing the Hidden Data Dependency of DIA with Predicted Spectral Libraries. <i>Proteomics</i> , 2020, 20, e1900306.	2.2	38
22	A Decoy-Free Approach to the Identification of Peptides. <i>Journal of Proteome Research</i> , 2015, 14, 1792-1798.	3.7	35
23	Identification of Quantitative Proteomic Differences between <i>Mycobacterium tuberculosis</i> Lineages with Altered Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 813.	3.5	34
24	The Age of Data-Driven Proteomics: How Machine Learning Enables Novel Workflows. <i>Proteomics</i> , 2020, 20, e1900351.	2.2	34
25	MS2Rescore: Data-Driven Rescoring Dramatically Boosts Immunopeptide Identification Rates. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100266.	3.8	34
26	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100076.	3.8	31
27	A posteriori quality control for the curation and reuse of public proteomics data. <i>Proteomics</i> , 2011, 11, 2182-2194.	2.2	29
28	Cov-MS: A Community-Based Template Assay for Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients. <i>Jacs Au</i> , 2021, 1, 750-765.	7.9	29
29	Generalized Calibration Across Liquid Chromatography Setups for Generic Prediction of Small-Molecule Retention Times. <i>Analytical Chemistry</i> , 2020, 92, 6571-6578.	6.5	26
30	Combining quantitative proteomics data processing workflows for greater sensitivity. <i>Nature Methods</i> , 2011, 8, 481-483.	19.0	18
31	Asn ₃ , a Reliable, Robust, and Universal Lock Mass for Improved Accuracy in LC-MS and LC-MS/MS. <i>Analytical Chemistry</i> , 2013, 85, 11054-11060.	6.5	13
32	Designing biomedical proteomics experiments: state-of-the-art and future perspectives. <i>Expert Review of Proteomics</i> , 2016, 13, 495-511.	3.0	13
33	Towards a human proteomics atlas. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1069-1077.	3.7	12
34	Digging into Acceptor Splice Site Prediction: An Iterative Feature Selection Approach. <i>Lecture Notes in Computer Science</i> , 2004, , 386-397.	1.3	11
35	A Pipeline for Differential Proteomics in Unsequenced Species. <i>Journal of Proteome Research</i> , 2016, 15, 1963-1970.	3.7	10
36	Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection. <i>Journal of Proteome Research</i> , 2021, 20, 3353-3364.	3.7	10

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37	Data-Driven Rescoring of Metabolite Annotations Significantly Improves Sensitivity. <i>Analytical Chemistry</i> , 2018, 90, 11636-11642.	6.5	8
38	A reproducibility-based evaluation procedure for quantifying the differences between MS/MS peak intensity normalization methods. <i>Proteomics</i> , 2011, 11, 1172-1180.	2.2	7
39	Interpretation of the DOME Recommendations for Machine Learning in Proteomics and Metabolomics. <i>Journal of Proteome Research</i> , 2022, 21, 1204-1207.	3.7	7
40	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
41	The Effect of Peptide Identification Search Algorithms on MS2-Based Label-Free Protein Quantification. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 443-448.	2.0	3
42	Orthogonal proteomics methods to unravel the HOTAIR interactome. <i>Scientific Reports</i> , 2022, 12, 1513.	3.3	3
43	MAPPI-DAT: data management and analysis for protein-protein interaction data from the high-throughput MAPPIT cell microarray platform. <i>Bioinformatics</i> , 2017, 33, 1424-1425.	4.1	2
44	Feature Ranking Using an EDA-based Wrapper Approach. <i>Studies in Fuzziness and Soft Computing</i> , 2006, , 243-257.	0.8	2
45	Support Vector Machines for Bass and Snare Drum Recognition. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2005, , 616-623.	0.2	2
46	Feature Ranking Using an EDA-based Wrapper Approach. , 2006, , 243-257.		0