# Sven Degroeve

List of Publications by Year
in descending order

| 46 | 6,653 | 236925 | 233421 |
|----|-------|--------|--------|
| papers | citations | 25 | 45 |
| | | h-index | g-index |

| 55 | 55 | 55 | 9400 |
|----|----|----|------|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Orthogonal proteomics methods to unravel the HOTAIR interactome. Scientific Reports, 2022, 12, 1513. | 3.3 | 3 |
| 2 | Interpretation of the DOME Recommendations for Machine Learning in Proteomics and Metabolomics. Journal of Proteome Research, 2022, 21, 1204-1207. | 3.7 | 7 |
| 3 | MS2Rescore: Data-Driven Rescoring Dramatically Boosts Immunopeptide Identification Rates. Molecular and Cellular Proteomics, 2022, 21, 100266. | 3.8 | 34 |
| 4 | Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection. Journal of Proteome Research, 2021, 20, 3353-3364. | 3.7 | 10 |
| 5 | Cov-MS: A Community-Based Template Assay for Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients. Jacs Au, 2021, 1, 750-765. | 7.9 | 29 |
| 6 | Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. Molecular and Cellular Proteomics, 2021, 20, 100076. | 3.8 | 31 |
| 7 | DeepLC can predict retention times for peptides that carry as-yet unseen modifications. Nature Methods, 2021, 18, 1363-1369. | 19.0 | 95 |
| 8 | Massively parallel interrogation of protein fragment secretability using SECRiFY reveals features influencing secretory system transit. Nature Communications, 2021, 12, 6414. | 12.8 | 5 |
| 9 | Removing the Hidden Data Dependency of DIA with Predicted Spectral Libraries. Proteomics, 2020, 20, e1900306. | 2.2 | 38 |
| 10 | The Age of Data‐Driven Proteomics: How Machine Learning Enables Novel Workflows. Proteomics, 2020, 20, e1900351. | 2.2 | 34 |
| 11 | Generalized Calibration Across Liquid Chromatography Setups for Generic Prediction of Small-Molecule Retention Times. Analytical Chemistry, 2020, 92, 6571-6578. | 6.5 | 26 |
| 12 | Comprehensive and Empirical Evaluation of Machine Learning Algorithms for Small Molecule LC Retention Time Prediction. Analytical Chemistry, 2019, 91, 3694-3703. | 6.5 | 64 |
| 13 | Updated MS²PIP web server delivers fast and accurate MS² peak intensity prediction for multiple fragmentation methods, instruments and labeling techniques. Nucleic Acids Research, 2019, 47, W295-W299. | 14.5 | 77 |
| 14 | Accurate peptide fragmentation predictions allow data driven approaches to replace and improve upon proteomics search engine scoring functions. Bioinformatics, 2019, 35, 5243-5248. | 4.1 | 52 |
| 15 | Data-Driven Rescoring of Metabolite Annotations Significantly Improves Sensitivity. Analytical Chemistry, 2018, 90, 11636-11642. | 6.5 | 8 |
| 16 | MAPPI-DAT: data management and analysis for protein†"protein interaction data from the high-throughput MAPPIT cell microarray platform. Bioinformatics, 2017, 33, 1424-1425. | 4.1 | 2 |
| 17 | Identification of Quantitative Proteomic Differences between Mycobacterium tuberculosis Lineages with Altered Virulence. Frontiers in Microbiology, 2016, 7, 813. | 3.5 | 34 |
| 18 | Designing biomedical proteomics experiments: state-of-the-art and future perspectives. Expert Review of Proteomics, 2016, 13, 495-511. | 3.0 | 13 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------| 
| 19 | A Pipeline for Differential Proteomics in Unsequenced Species. Journal of Proteome Research, 2016, 15, 1963-1970. | 3.7 | 10 |
| 20 | MS$^2$PIP prediction server: compute and visualize MS$^2$peak intensity predictions for CID and HCD fragmentation. Nucleic Acids Research, 2015, 43, W326-W330. | 14.5 | 63 |
| 21 | A Decoy-Free Approach to the Identification of Peptides. Journal of Proteome Research, 2015, 14, 1792-1798. | 3.7 | 35 |
| 22 | Machine learning applications in proteomics research: How the past can boost the future. Proteomics, 2014, 14, 353-366. | 2.2 | 52 |
| 23 | Asn$_3$, a Reliable, Robust, and Universal Lock Mass for Improved Accuracy in LC–MS and LC–MS/MS. Analytical Chemistry, 2013, 85, 11054-11060. | 6.5 | 13 |
| 24 | MS2PIP: a tool for MS/MS peak intensity prediction. Bioinformatics, 2013, 29, 3199-3203. | 4.1 | 108 |
| 25 | Predicting Tryptic Cleavage from Proteomics Data Using Decision Tree Ensembles. Journal of Proteome Research, 2013, 12, 2253-2259. | 3.7 | 48 |
| 26 | Proteome-derived Peptide Libraries to Study the Substrate Specificity Profiles of Carboxypeptidases. Molecular and Cellular Proteomics, 2013, 12, 2096-2110. | 3.8 | 40 |
| 27 | The Effect of Peptide Identification Search Algorithms on MS2-Based Label-Free Protein Quantification. OMICS A Journal of Integrative Biology, 2012, 16, 443-448. | 2.0 | 3 |
| 28 | Towards a human proteomics atlas. Analytical and Bioanalytical Chemistry, 2012, 404, 1069-1077. | 3.7 | 12 |
| 29 | Analysis of the Resolution Limitations of Peptide Identification Algorithms. Journal of Proteome Research, 2011, 10, 5555-5561. | 3.7 | 60 |
| 30 | Bioinformatics Analysis of a *Saccharomyces cerevisiae* N-Terminal Proteome Provides Evidence of Alternative Translation Initiation and Post-Translational N-Terminal Acetylation. Journal of Proteome Research, 2011, 10, 3578-3589. | 3.7 | 53 |
| 31 | Combining quantitative proteomics data processing workflows for greater sensitivity. Nature Methods, 2011, 8, 481-483. | 19.0 | 18 |
| 32 | A posteriori quality control for the curation and reuse of public proteomics data. Proteomics, 2011, 11, 2182-2194. | 2.2 | 29 |
| 33 | A reproducibility–based evaluation procedure for quantifying the differences between MS/MS peak intensity normalization methods. Proteomics, 2011, 11, 1172-1180. | 2.2 | 7 |
| 34 | Translation initiation site prediction on a genomic scale: beauty in simplicity. Bioinformatics, 2007, 23, i418-i423. | 4.1 | 48 |
| 35 | Random forests as a tool for ecohydrological distribution modelling. Ecological Modelling, 2007, 207, 304-318. | 2.5 | 293 |
| 36 | Genome analysis of the smallest free-living eukaryote Ostreococcus tauri unveils many unique features. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11647-11652. | 7.1 | 809 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 37 | The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. &amp; Gray). Science, 2006, 313, 1596-1604. | 12.6 | 3,945 |
| 38 | Feature Ranking Using an EDA-based Wrapper Approach. Studies in Fuzziness and Soft Computing, 2006, , 243-257. | 0.8 | 2 |
| 39 | Feature Ranking Using an EDA-based Wrapper Approach. , 2006, , 243-257. | | 0 |
| 40 | SpliceMachine: predicting splice sites from high-dimensional local context representations. Bioinformatics, 2005, 21, 1332-1338. | 4.1 | 92 |
| 41 | Large-scale structural analysis of the core promoter in mammalian and plant genomes. Nucleic Acids Research, 2005, 33, 4255-4264. | 14.5 | 103 |
| 42 | Support Vector Machines for Bass and Snare Drum Recognition. Studies in Classification, Data Analysis, and Knowledge Organization, 2005, , 616-623. | 0.2 | 2 |
| 43 | Feature selection for splice site prediction: a new method using EDA-based feature ranking. BMC Bioinformatics, 2004, 5, 64. | 2.6 | 49 |
| 44 | Digging into Acceptor Splice Site Prediction: An Iterative Feature Selection Approach. Lecture Notes in Computer Science, 2004, , 386-397. | 1.3 | 11 |
| 45 | Fast feature selection using a simple estimation of distribution algorithm: a case study on splice site prediction. Bioinformatics, 2003, 19, ii179-ii188. | 4.1 | 51 |
| 46 | Feature subset selection for splice site prediction. Bioinformatics, 2002, 18, S75-S83. | 4.1 | 93 |