

Oliver Kohlbacher

List of Publications by Year in descending order

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Version: 2024-02-01

259
papers

17,937
citations

19657
61
h-index

18647
119
g-index

299
all docs

299
docs citations

299
times ranked

28247
citing authors

#	ARTICLE	IF	CITATIONS
1	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013, 500, 477-481.	27.8	1,168
2	Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020, 17, 905-908.	19.0	650
3	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	16.8	623
4	OptiType: precision HLA typing from next-generation sequencing data. <i>Bioinformatics</i> , 2014, 30, 3310-3316.	4.1	566
5	NRPSpredictor2—a web server for predicting NRPS adenylation domain specificity. <i>Nucleic Acids Research</i> , 2011, 39, W362-W367.	14.5	559
6	OpenMS – An open-source software framework for mass spectrometry. <i>BMC Bioinformatics</i> , 2008, 9, 163.	2.6	556
7	Visualization of omics data for systems biology. <i>Nature Methods</i> , 2010, 7, S56-S68.	19.0	548
8	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
9	SARS-CoV-2-derived peptides define heterologous and COVID-19-induced T cell recognition. <i>Nature Immunology</i> , 2021, 22, 74-85.	14.5	490
10	Sequence co-evolution gives 3D contacts and structures of protein complexes. <i>ELife</i> , 2014, 3, .	6.0	452
11	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	28.9	419
12	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). <i>Nucleic Acids Research</i> , 2005, 33, 5799-5808.	14.5	388
13	MultiLoc: prediction of protein subcellular localization using N-terminal targeting sequences, sequence motifs and amino acid composition. <i>Bioinformatics</i> , 2006, 22, 1158-1165.	4.1	290
14	From hype to reality: data science enabling personalized medicine. <i>BMC Medicine</i> , 2018, 16, 150.	5.5	278
15	MultiLoc2: integrating phylogeny and Gene Ontology terms improves subcellular protein localization prediction. <i>BMC Bioinformatics</i> , 2009, 10, 274.	2.6	264
16	YLoc—an interpretable web server for predicting subcellular localization. <i>Nucleic Acids Research</i> , 2010, 38, W497-W502.	14.5	263
17	TOPP—the OpenMS proteomics pipeline. <i>Bioinformatics</i> , 2007, 23, e191-e197.	4.1	249
18	Photo-cross-linking and high-resolution mass spectrometry for assignment of RNA-binding sites in RNA-binding proteins. <i>Nature Methods</i> , 2014, 11, 1064-1070.	19.0	218

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19	Simultaneous alignment of short reads against multiple genomes. <i>Genome Biology</i> , 2009, 10, R98.	9.6	215
20	WIPI proteins: essential PtdIns3P effectors at the nascent autophagosome. <i>Journal of Cell Science</i> , 2015, 128, 207-17.	2.0	214
21	Tools for Label-free Peptide Quantification. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 549-556.	3.8	198
22	Reentrant Condensation of Proteins in Solution Induced by Multivalent Counterions. <i>Physical Review Letters</i> , 2008, 101, 148101.	7.8	184
23	Immunoinformatics and epitope prediction in the age of genomic medicine. <i>Genome Medicine</i> , 2015, 7, 119.	8.2	178
24	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014381-1-M111.014381-10.	3.8	175
25	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	27.8	172
26	Elucidating the evolutionary conserved DNA-binding specificities of WRKY transcription factors by molecular dynamics and in vitro binding assays. <i>Nucleic Acids Research</i> , 2013, 41, 9764-9778.	14.5	161
27	The immunopeptidomic landscape of ovarian carcinomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9942-E9951.	7.1	152
28	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016, 13, 651-656.	19.0	147
29	An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 1628-1644.	3.7	146
30	Going from where to why—interpretable prediction of protein subcellular localization. <i>Bioinformatics</i> , 2010, 26, 1232-1238.	4.1	133
31	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	3.8	130
32	HLA Ligand Atlas: a benign reference of HLA-presented peptides to improve T-cell-based cancer immunotherapy. , 2021, 9, e002071.		126
33	SherLoc2: A High-Accuracy Hybrid Method for Predicting Subcellular Localization of Proteins. <i>Journal of Proteome Research</i> , 2009, 8, 5363-5366.	3.7	122
34	SherLoc: high-accuracy prediction of protein subcellular localization by integrating text and protein sequence data. <i>Bioinformatics</i> , 2007, 23, 1410-1417.	4.1	113
35	Multi-omics discovery of exome-derived neoantigens in hepatocellular carcinoma. <i>Genome Medicine</i> , 2019, 11, 28.	8.2	107
36	Universality of protein reentrant condensation in solution induced by multivalent metal ions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3450-3457.	2.6	106

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37	Genetic variation in human drug-related genes. <i>Genome Medicine</i> , 2017, 9, 117.	8.2	104
38	The antigenic landscape of multiple myeloma: mass spectrometry (re)defines targets for T-cellâ€‘based immunotherapy. <i>Blood</i> , 2015, 126, 1203-1213.	1.4	103
39	Interplay of pH and Binding of Multivalent Metal Ions: Charge Inversion and Reentrant Condensation in Protein Solutions. <i>Journal of Physical Chemistry B</i> , 2013, 117, 5777-5787.	2.6	97
40	SANDPUMA: ensemble predictions of nonribosomal peptide chemistry reveal biosynthetic diversity across <i>Actinobacteria</i> . <i>Bioinformatics</i> , 2017, 33, 3202-3210.	4.1	89
41	Plants Release Precursors of Histone Deacetylase Inhibitors to Suppress Growth of Competitors. <i>Plant Cell</i> , 2015, 27, 3175-3189.	6.6	86
42	OpenMS â€‘ A platform for reproducible analysis of mass spectrometry data. <i>Journal of Biotechnology</i> , 2017, 261, 142-148.	3.8	85
43	Novel Formulation of Nonlocal Electrostatics. <i>Physical Review Letters</i> , 2004, 93, 108104.	7.8	83
44	Time-resolved characterization of cAMP/PKA-dependent signaling reveals that platelet inhibition is a concerted process involving multiple signaling pathways. <i>Blood</i> , 2014, 123, e1-e10.	1.4	80
45	Retention Time Prediction Improves Identification in Nontargeted Lipidomics Approaches. <i>Analytical Chemistry</i> , 2015, 87, 7698-7704.	6.5	80
46	SVMHC: a server for prediction of MHC-binding peptides. <i>Nucleic Acids Research</i> , 2006, 34, W194-W197.	14.5	79
47	POPIK: T-cell reactivity prediction using support vector machines and string kernels. <i>BMC Bioinformatics</i> , 2011, 12, 446.	2.6	79
48	Induction of neoantigen-reactive T cells from healthy donors. <i>Nature Protocols</i> , 2019, 14, 1926-1943.	12.0	78
49	Absolute Myoglobin Quantitation in Serum by Combining Two-Dimensional Liquid Chromatographyâ€‘Electrospray Ionization Mass Spectrometry and Novel Data Analysis Algorithms. <i>Journal of Proteome Research</i> , 2006, 5, 414-421.	3.7	77
50	Integrated modeling of the major events in the MHC class I antigen processing pathway. <i>Protein Science</i> , 2005, 14, 2132-2140.	7.6	76
51	Personalized peptide vaccine-induced immune response associated with long-term survival of a metastatic cholangiocarcinoma patient. <i>Journal of Hepatology</i> , 2016, 65, 849-855.	3.7	75
52	TOPPView: An Open-Source Viewer for Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2009, 8, 3760-3763.	3.7	74
53	Automated Label-free Quantification of Metabolites from Liquid Chromatographyâ€‘Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 348-359.	3.8	74
54	Prediction of dual protein targeting to plant organelles. <i>New Phytologist</i> , 2009, 183, 224-236.	7.3	73

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55	Data Integration for Future Medicine (DIFUTURE). <i>Methods of Information in Medicine</i> , 2018, 57, e57-e65.	1.2	73
56	Reduced Rate of Inpatient Hospital Admissions in 18 German University Hospitals During the COVID-19 Lockdown. <i>Frontiers in Public Health</i> , 2020, 8, 594117.	2.7	73
57	Statistical learning of peptide retention behavior in chromatographic separations: a new kernel-based approach for computational proteomics. <i>BMC Bioinformatics</i> , 2007, 8, 468.	2.6	70
58	GeneTrailExpress: a web-based pipeline for the statistical evaluation of microarray experiments. <i>BMC Bioinformatics</i> , 2008, 9, 552.	2.6	69
59	Activation of lymphoma-associated MyD88 mutations via allosterically-induced TIR-domain oligomerization. <i>Blood</i> , 2014, 124, 3896-3904.	1.4	69
60	PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. <i>Journal of Proteome Research</i> , 2015, 14, 2988-2997.	3.7	69
61	MetaRoute: fast search for relevant metabolic routes for interactive network navigation and visualization. <i>Bioinformatics</i> , 2008, 24, 2108-2109.	4.1	68
62	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. <i>Methods in Molecular Biology</i> , 2011, 696, 353-367.	0.9	68
63	Large-scale discovery of protein interactions at residue resolution using co-evolution calculated from genomic sequences. <i>Nature Communications</i> , 2021, 12, 1396.	12.8	68
64	The mzQuantML Data Standard for Mass Spectrometry-based Quantitative Studies in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2332-2340.	3.8	66
65	Structural and Functional Characterization of the Bacterial Type III Secretion Export Apparatus. <i>PLoS Pathogens</i> , 2016, 12, e1006071.	4.7	66
66	Copper oxide nanoparticle toxicity profiling using untargeted metabolomics. <i>Particle and Fibre Toxicology</i> , 2015, 13, 49.	6.2	65
67	MetaProSIP: Automated Inference of Stable Isotope Incorporation Rates in Proteins for Functional Metaproteomics. <i>Journal of Proteome Research</i> , 2015, 14, 619-627.	3.7	64
68	BALL - biochemical algorithms library 1.3. <i>BMC Bioinformatics</i> , 2010, 11, 531.	2.6	62
69	Distributed Analytics on Sensitive Medical Data: The Personal Health Train. <i>Data Intelligence</i> , 2020, 2, 96-107.	1.5	62
70	Food monitoring: Screening of the geographical origin of white asparagus using FT-NIR and machine learning. <i>Food Control</i> , 2019, 104, 318-325.	5.5	61
71	Modeling metabolic networks in <i>C. glutamicum</i> : a comparison of rate laws in combination with various parameter optimization strategies. <i>BMC Systems Biology</i> , 2009, 3, 5.	3.0	59
72	The MoSGrid Science Gateway – A Complete Solution for Molecular Simulations. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 2232-2245.	5.3	58

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73	The HLA ligandome landscape of chronic myeloid leukemia delineates novel T-cell epitopes for immunotherapy. <i>Blood</i> , 2019, 133, 550-565.	1.4	57
74	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017, 150, 170-182.	2.4	56
75	Mapping the HLA Ligandome of Colorectal Cancer Reveals an Imprint of Malignant Cell Transformation. <i>Cancer Research</i> , 2018, 78, 4627-4641.	0.9	56
76	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	3.8	55
77	A Combinatorial Approach to Protein Docking with Flexible Side Chains. <i>Journal of Computational Biology</i> , 2002, 9, 597-612.	1.6	54
78	A computational platform for high-throughput analysis of RNA sequences and modifications by mass spectrometry. <i>Nature Communications</i> , 2020, 11, 926.	12.8	54
79	BALLView: a tool for research and education in molecular modeling. <i>Bioinformatics</i> , 2006, 22, 365-366.	4.1	53
80	<i>De novo</i> peptide sequencing by tandem MS using complementary CID and electron transfer dissociation. <i>Electrophoresis</i> , 2009, 30, 3736-3747.	2.4	53
81	Machine learning competition in immunology – Prediction of HLA class I binding peptides. <i>Journal of Immunological Methods</i> , 2011, 374, 1-4.	1.4	53
82	BALLDock/SLICK: A New Method for Protein-Carbohydrate Docking. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1616-1625.	5.4	52
83	A novel algorithm for detecting differentially regulated paths based on gene set enrichment analysis. <i>Bioinformatics</i> , 2009, 25, 2787-2794.	4.1	51
84	TOPPAS: A Graphical Workflow Editor for the Analysis of High-Throughput Proteomics Data. <i>Journal of Proteome Research</i> , 2012, 11, 3914-3920.	3.7	50
85	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	7.7	49
86	Implications for selectivity of 3,4-diarylquinolinones as p38 β -MAP kinase inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008, 18, 1431-1435.	2.2	48
87	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , 2016, 12, e1004920.	3.2	47
88	A Fully Computational Model for Predicting Percutaneous Drug Absorption. <i>Journal of Chemical Information and Modeling</i> , 2006, 46, 424-429.	5.4	46
89	Automated scaffold selection for enzyme design. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 74-83.	2.6	45
90	Probabilistic Consensus Scoring Improves Tandem Mass Spectrometry Peptide Identification. <i>Journal of Proteome Research</i> , 2011, 10, 3332-3343.	3.7	45

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91	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	12.8	45
92	Computational modeling of the sugarâ€ˆlectin interaction. <i>Advanced Drug Delivery Reviews</i> , 2004, 56, 437-457.	13.7	43
93	LC-MSsim â€ˆ a simulation software for liquid chromatography mass spectrometry data. <i>BMC Bioinformatics</i> , 2008, 9, 423.	2.6	42
94	The role of phosphorylatable serine residues in the DNA-binding domain of Arabidopsis bZIP transcription factors. <i>European Journal of Cell Biology</i> , 2010, 89, 175-183.	3.6	42
95	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	3.8	42
96	HLA ligandome analysis of primary chronic lymphocytic leukemia (CLL) cells under lenalidomide treatment confirms the suitability of lenalidomide for combination with T-cell-based immunotherapy. <i>Oncolmmunology</i> , 2018, 7, e1316438.	4.6	42
97	Electrostatic potentials of proteins in water: a structured continuum approach. <i>Bioinformatics</i> , 2007, 23, e99-e103.	4.1	41
98	Using Atom Mapping Rules for an Improved Detection of Relevant Routes in Weighted Metabolic Networks. <i>Journal of Computational Biology</i> , 2008, 15, 565-576.	1.6	41
99	Designing string-of-beads vaccines with optimal spacers. <i>Genome Medicine</i> , 2016, 8, 9.	8.2	41
100	FLASHDeconv: Ultrafast, High-Quality Feature Deconvolution for Top-Down Proteomics. <i>Cell Systems</i> , 2020, 10, 213-218.e6.	6.2	41
101	BALLView: An object-oriented molecular visualization and modeling framework. <i>Journal of Computer-Aided Molecular Design</i> , 2005, 19, 791-800.	2.9	40
102	SLICK â€™ Scoring and Energy Functions for Proteinâ€™Carbohydrate Interactions. <i>Journal of Chemical Information and Modeling</i> , 2006, 46, 1635-1642.	5.4	40
103	Optimal de novo Design of MRM Experiments for Rapid Assay Development in Targeted Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 2696-2704.	3.7	40
104	Virtual screening and experimental validation reveal novel small-molecule inhibitors of 14-3-3 proteinâ€™protein interactions. <i>Chemical Communications</i> , 2013, 49, 8468.	4.1	40
105	A Single Sign-On Infrastructure for Science Gateways on a Use Case for Structural Bioinformatics. <i>Journal of Grid Computing</i> , 2012, 10, 769-790.	3.9	39
106	Binding Pocket Optimization by Computational Protein Design. <i>PLoS ONE</i> , 2012, 7, e52505.	2.5	39
107	Comparative immunopeptidomics of humans and their pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13268-13272.	7.1	38
108	Development of a fluorescence-based assay for screening of modulators of human Organic Anion Transporter 1B3 (OATP1B3). <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2006, 62, 39-43.	4.3	38

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109	BNDDB – The Biochemical Network Database. BMC Bioinformatics, 2007, 8, 367.	2.6	36
110	Improving Peptide Identification in Proteome Analysis by a Two-Dimensional Retention Time Filtering Approach. Journal of Proteome Research, 2009, 8, 4109-4115.	3.7	36
111	Combining Structure and Sequence Information Allows Automated Prediction of Substrate Specificities within Enzyme Families. PLoS Computational Biology, 2010, 6, e1000636.	3.2	36
112	Universal peptide vaccines – Optimal peptide vaccine design based on viral sequence conservation. Vaccine, 2011, 29, 8745-8753.	3.8	35
113	Competing Salt Effects on Phase Behavior of Protein Solutions: Tailoring of Protein Interaction by the Binding of Multivalent Ions and Charge Screening. Journal of Physical Chemistry B, 2014, 118, 11365-11374.	2.6	35
114	MHCquant: Automated and Reproducible Data Analysis for Immunopectidomics. Journal of Proteome Research, 2019, 18, 3876-3884.	3.7	35
115	Testing and Validation of Computational Methods for Mass Spectrometry. Journal of Proteome Research, 2016, 15, 809-814.	3.7	34
116	HIGH-ACCURACY PEAK PICKING OF PROTEOMICS DATA USING WAVELET TECHNIQUES. , 2005, , .		33
117	A Mathematical Framework for the Selection of an Optimal Set of Peptides for Epitope-Based Vaccines. PLoS Computational Biology, 2008, 4, e1000246.	3.2	32
118	OptiTope—a web server for the selection of an optimal set of peptides for epitope-based vaccines. Nucleic Acids Research, 2009, 37, W617-W622.	14.5	32
119	Workflows for automated downstream data analysis and visualization in large-scale computational mass spectrometry. Proteomics, 2015, 15, 1443-1447.	2.2	32
120	EpiToolKit—a web-based workbench for vaccine design. Bioinformatics, 2015, 31, 2211-2213.	4.1	32
121	FRED 2: an immunoinformatics framework for Python. Bioinformatics, 2016, 32, 2044-2046.	4.1	32
122	Identification of Ppar γ -modulated miRNA hubs that target the fibrotic tumor microenvironment. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 454-463.	7.1	32
123	BiNA: A Visual Analytics Tool for Biological Network Data. PLoS ONE, 2014, 9, e87397.	2.5	31
124	Food Authentication: Small-Molecule Profiling as a Tool for the Geographic Discrimination of German White Asparagus. Journal of Agricultural and Food Chemistry, 2018, 66, 13328-13339.	5.2	31
125	Peak intensity prediction in MALDI-TOF mass spectrometry: A machine learning study to support quantitative proteomics. BMC Bioinformatics, 2008, 9, 443.	2.6	30
126	Novel Machine Learning Methods for MHC Class I Binding Prediction. Lecture Notes in Computer Science, 2010, , 98-109.	1.3	30

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127	Profile and Molecular Modeling of 3-(Indole-3-yl)-4-(3,4,5-trimethoxyphenyl)-1H-pyrrole-2,5dione (1) as a Highly Selective VEGF-R2/3 Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 7549-7553.	6.4	29
128	LFQProfiler and RNPxl: Open-Source Tools for Label-Free Quantification and Proteinâ€“RNA Cross-Linking Integrated into Proteome Discoverer. <i>Journal of Proteome Research</i> , 2016, 15, 3441-3448.	3.7	29
129	Analysis of Genomic DNA from Medieval Plague Victims Suggests Long-Term Effect of <i>Yersinia pestis</i> on Human Immunity Genes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4059-4076.	8.9	29
130	In melanoma, <i>Hippo</i> signaling is affected by copy number alterations and <i>YAP</i> 1 overexpression impairs patient survival. <i>Pigment Cell and Melanoma Research</i> , 2014, 27, 671-673.	3.3	28
131	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. <i>Methods in Molecular Biology</i> , 2010, 604, 201-211.	0.9	27
132	Lectin-sugar interaction. <i>FEBS Journal</i> , 2002, 269, 1518-1524.	0.2	26
133	SNEP: SNP-derived Epitope Prediction program for minor H antigens. <i>Immunogenetics</i> , 2005, 57, 816-820.	2.4	26
134	Comparison of different sample preparation techniques for NIR screening and their influence on the geographical origin determination of almonds (<i>Prunus dulcis</i> MILL.). <i>Food Control</i> , 2020, 115, 107302.	5.5	26
135	Analysis of proteinâ€“RNA interactions in CRISPR proteins and effector complexes by UV-induced cross-linking and mass spectrometry. <i>Methods</i> , 2015, 89, 138-148.	3.8	25
136	Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100071.	3.8	25
137	A statistical learning approach to the modeling of chromatographic retention of oligonucleotides incorporating sequence and secondary structure data. <i>Nucleic Acids Research</i> , 2007, 35, 4195-4202.	14.5	23
138	DNA-binding proteins from marine bacteria expand the known sequence diversity of TALE-like repeats. <i>Nucleic Acids Research</i> , 2015, 43, gkv1053.	14.5	23
139	Scaling home automation to public buildings: A distributed multiuser setup for OpenHAB 2., 2017, , .		23
140	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. <i>Analytical Chemistry</i> , 2020, 92, 15968-15974.	6.5	23
141	Application of displacement chromatography for the proteome analysis of a human plasma protein fraction. <i>Journal of Chromatography A</i> , 2010, 1217, 3321-3329.	3.7	22
142	An unusually high substitution rate in transplant-associated BK polyomavirus in vivo is further concentrated in HLA-C-bound viral peptides. <i>PLoS Pathogens</i> , 2018, 14, e1007368.	4.7	22
143	Challenges of big data integration in the life sciences. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 6791-6800.	3.7	22
144	Multiple Layers of Phospho-Regulation Coordinate Metabolism and the Cell Cycle in Budding Yeast. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 338.	3.7	22

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145	Analysis of protein-DNA interactions in chromatin by UV induced cross-linking and mass spectrometry. Nature Communications, 2020, 11, 5250.	12.8	22
146	High-accuracy peak picking of proteomics data using wavelet techniques. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 243-54.	0.7	22
147	From sequence to structure and back again: approaches for predicting protein-DNA binding. Proteome Science, 2004, 2, 3.	1.7	21
148	Structure-Activity Relationships in Chromatography: Retention Prediction of Oligonucleotides with Support Vector Regression. Angewandte Chemie - International Edition, 2006, 45, 7009-7012.	13.8	21
149	EpiToolKit—a web server for computational immunomics. Nucleic Acids Research, 2008, 36, W519-W522.	14.5	21
150	KIRMES: kernel-based identification of regulatory modules in euchromatic sequences. Bioinformatics, 2009, 25, 2126-2133.	4.1	21
151	Protein (multi-)location prediction: utilizing interdependencies via a generative model. Bioinformatics, 2015, 31, i365-i374.	4.1	21
152	Food authentication: Determination of the geographical origin of almonds (<i>Prunus dulcis</i> Mill.) via near-infrared spectroscopy. Microchemical Journal, 2021, 160, 105702.	4.5	21
153	FRED—a framework for T-cell epitope detection. Bioinformatics, 2009, 25, 2758-2759.	4.1	20
154	Carfilzomib alters the HLA-presented peptidome of myeloma cells and impairs presentation of peptides with aromatic C-termini. Blood Cancer Journal, 2016, 6, e411-e411.	6.2	20
155	Untargeted Metabolomics Reveals Molecular Effects of Ketogenic Diet on Healthy and Tumor Xenograft Mouse Models. International Journal of Molecular Sciences, 2019, 20, 3873.	4.1	20
156	EPIFANY: A Method for Efficient High-Confidence Protein Inference. Journal of Proteome Research, 2020, 19, 1060-1072.	3.7	20
157	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. Communications Biology, 2021, 4, 113.	4.4	20
158	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. Journal of Proteomics, 2013, 87, 134-138.	2.4	19
159	Mass-Spectrometry-Based Proteomics Reveals Organ-Specific Expression Patterns To Be Used as Forensic Evidence. Journal of Proteome Research, 2016, 15, 182-192.	3.7	19
160	Determination of the Geographical Origin of <i>Asparagus officinalis</i> L. by ¹ H NMR Spectroscopy. Journal of Agricultural and Food Chemistry, 2020, 68, 14353-14363.	5.2	19
161	Multiple Instance Learning Allows MHC Class II Epitope Predictions Across Alleles. Lecture Notes in Computer Science, 2008, , 210-221.	1.3	19
162	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	1.6	19

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163	Towards <i>in silico</i> design of epitope-based vaccines. Expert Opinion on Drug Discovery, 2009, 4, 1047-1060.	5.0	18
164	Covalent attachment of pyridoxal-phosphate derivatives to 14-3-3 proteins. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1051-3; author reply E1054.	7.1	18
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