

# Conrad Bessant

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

3,457  
citations

159585

30  
h-index

144013

57  
g-index

67  
all docs

67  
docs citations

67  
times ranked

5762  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of mental and physical disorders associated with COVID-19 in online health forums: a natural language processing study. <i>BMJ Open</i> , 2021, 11, e056601.	1.9	8
2	Blood pro-resolving mediators are linked with synovial pathology and are predictive of DMARD responsiveness in rheumatoid arthritis. <i>Nature Communications</i> , 2020, 11, 5420.	12.8	51
3	Characterization of four subtypes in morphologically normal tissue excised proximal and distal to breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 38.	5.2	12
4	Reconstructing kinase network topologies from phosphoproteomics data reveals cancer-associated rewiring. <i>Nature Biotechnology</i> , 2020, 38, 493-502.	17.5	72
5	Investigating Comorbidity of Mental and Physical Disorders in Online Health Forums. , 2020, , .		2
6	High throughput discovery of protein variants using proteomics informed by transcriptomics. <i>Nucleic Acids Research</i> , 2018, 46, 4893-4902.	14.5	5
7	Deconstruction of a Metastatic Tumor Microenvironment Reveals a Common Matrix Response in Human Cancers. <i>Cancer Discovery</i> , 2018, 8, 304-319.	9.4	255
8	PITDB: a database of translated genomic elements. <i>Nucleic Acids Research</i> , 2018, 46, D1223-D1228.	14.5	2
9	Proteomics informed by transcriptomics for characterising active transposable elements and genome annotation in <i>Aedes aegypti</i> . <i>BMC Genomics</i> , 2017, 18, 101.	2.8	49
10	Ensemble-based support vector machine classifiers as an efficient tool for quality assessment of beef fillets from electronic nose data. <i>Analytical Methods</i> , 2016, 8, 3711-3721.	2.7	43
11	Novel application of heuristic optimisation enables the creation and thorough evaluation of robust support vector machine ensembles for machine learning applications. <i>Metabolomics</i> , 2016, 12, 16.	3.0	14
12	The mzqLibrary – An open source Java library supporting the HUPO-PSI quantitative proteomics standard. <i>Proteomics</i> , 2015, 15, 3152-3162.	2.2	5
13	Galaxy Integrated Omics: Web-based Standards-Compliant Workflows for Proteomics Informed by Transcriptomics*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3087-3093.	3.8	30
14	Application of gas chromatography mass spectrometry (GC-MS) in conjunction with multivariate classification for the diagnosis of gastrointestinal diseases. <i>Metabolomics</i> , 2014, 10, 1113-1120.	3.0	21
15	A tutorial for software development in quantitative proteomics using PSI standard formats. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 88-97.	2.3	4
16	Current trends in machine-learning methods applied to spectroscopic cancer diagnosis. <i>TrAC - Trends in Analytical Chemistry</i> , 2014, 59, 17-25.	11.4	27
17	Computational Approaches to Selected Reaction Monitoring Assay Design. <i>Methods in Molecular Biology</i> , 2013, 1007, 219-235.	0.9	2
18	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

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19	Analysis of Volatile Organic Compounds of Bacterial Origin in Chronic Gastrointestinal Diseases. Inflammatory Bowel Diseases, 2013, 19, 2069-2078.	1.9	88
20	MRMaid: The SRM Assay Design Tool for Arabidopsis and Other Species. Frontiers in Plant Science, 2012, 3, 164.	3.6	30
21	MRMaid 2.0: Mining PRIDE for Evidence-Based SRM Transitions. OMICS A Journal of Integrative Biology, 2012, 16, 483-488.	2.0	15
22	De novo derivation of proteomes from transcriptomes for transcript and protein identification. Nature Methods, 2012, 9, 1207-1211.	19.0	167
23	A Critical Appraisal of Techniques, Software Packages, and Standards for Quantitative Proteomic Analysis. OMICS A Journal of Integrative Biology, 2012, 16, 431-442.	2.0	50
24	Evaluation of a gas sensor array and pattern recognition for the identification of bladder cancer from urine headspace. Analyst, The, 2011, 136, 359-364.	3.5	63
25	Current Perspectives and Recommendations for the Development of Mass Spectrometry Methods for the Determination of Allergens in Foods. Journal of AOAC INTERNATIONAL, 2011, 94, 1026-1033.	1.5	103
26	The quantification of pollutants in drinking water by use of artificial neural networks. Natural Computing, 2011, 10, 77-90.	3.0	9
27	Assessment of robustness and transferability of classification models built for cancer diagnostics using Raman spectroscopy. Journal of Raman Spectroscopy, 2011, 42, 897-903.	2.5	12
28	Support vector machine ensembles for breast cancer type prediction from mid-FTIR micro-calcification spectra. Chemometrics and Intelligent Laboratory Systems, 2011, 107, 363-370.	3.5	44
29	Application of multiple response optimization design to quantum dot-encoded microsphere bioconjugates hybridization assay. Analytical Biochemistry, 2011, 414, 23-30.	2.4	6
30	Current perspectives and recommendations for the development of mass spectrometry methods for the determination of allergens in foods. Journal of AOAC INTERNATIONAL, 2011, 94, 1026-33.	1.5	26
31	Tissular model/sensor seamless system for qualified analysis and its characterization. Biochemical Engineering Journal, 2010, 52, 110-115.	3.6	2
32	Free computational resources for designing selected reaction monitoring transitions. Proteomics, 2010, 10, 1106-1126.	2.2	57
33	Electronic-Nose Technology Using Sputum Samples in Diagnosis of Patients with Tuberculosis. Journal of Clinical Microbiology, 2010, 48, 4235-4238.	3.9	69
34	MRMaid-DB: A Repository of Published SRM Transitions. Journal of Proteome Research, 2010, 9, 620-625.	3.7	19
35	Mining Proteomic MS/MS Data for MRM Transitions. Methods in Molecular Biology, 2010, 604, 187-199.	0.9	6
36	Investigation of support vector machines and Raman spectroscopy for lymph node diagnostics. Analyst, The, 2010, 135, 895.	3.5	97

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37	MRMaid, the Web-based Tool for Designing Multiple Reaction Monitoring (MRM) Transitions. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 696-705.	3.8	95
38	Recent developments in public proteomic MS repositories and pipelines. <i>Proteomics</i> , 2009, 9, 861-881.	2.2	42
39	Comparison of Novel Decoy Database Designs for Optimizing Protein Identification Searches Using ABRF sPRG2006 Standard MS/MS Data Sets. <i>Journal of Proteome Research</i> , 2009, 8, 1782-1791.	3.7	34
40	Fourier transform infrared spectroscopic studies of T-cell lymphoma, B-cell lymphoid and myeloid leukaemia cell lines. <i>Analyst, The</i> , 2009, 134, 763-768.	3.5	24
41	Dyes Assay for Measuring Physicochemical Parameters. <i>Analytical Chemistry</i> , 2009, 81, 2311-2316.	6.5	24
42	Evaluation of a combination of SIFT-MS and multivariate data analysis for the diagnosis of <i>Mycobacterium bovis</i> in wild badgers. <i>Analyst, The</i> , 2009, 134, 1922.	3.5	25
43	Protein-folding location can regulate manganese-binding versus copper- or zinc-binding. <i>Nature</i> , 2008, 455, 1138-1142.	27.8	281
44	Public proteomic MS repositories and pipelines: available tools and biological applications. <i>Proteomics</i> , 2007, 7, 2769-2786.	2.2	34
45	Genome annotating proteomics pipelines: available tools. <i>Expert Review of Proteomics</i> , 2006, 3, 621-629.	3.0	5
46	GAPP: A Fully Automated Software for the Confident Identification of Human Peptides from Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2006, 5, 2849-2852.	3.7	41
47	Mapping the Arabidopsis organelle proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6518-6523.	7.1	518
48	Quantitative proteomic approach to study subcellular localization of membrane proteins. <i>Nature Protocols</i> , 2006, 1, 1778-1789.	12.0	96
49	Prospects for Clinical Application of Electronic-Nose Technology to Early Detection of <i>Mycobacterium tuberculosis</i> in Culture and Sputum. <i>Journal of Clinical Microbiology</i> , 2006, 44, 2039-2045.	3.9	141
50	i-Tracker: For quantitative proteomics using iTRAQ. <i>BMC Genomics</i> , 2005, 6, 145.	2.8	275
51	Determination of partial amino acid composition from tandem mass spectra for use in peptide identification strategies. <i>Proteomics</i> , 2005, 5, 1787-1796.	2.2	4
52	Protein and peptide identification algorithms using MS for use in high-throughput, automated pipelines. <i>Proteomics</i> , 2005, 5, 4082-4095.	2.2	59
53	Confident protein identification using the average peptide score method coupled with search-specific, ab initio thresholds. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 3363-3368.	1.5	29
54	Monitoring haemodialysis using electronic nose and chemometrics. <i>Biosensors and Bioelectronics</i> , 2004, 19, 1581-1590.	10.1	42

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55	Simultaneous quantification of analytes in quaternary mixtures using dual pulse staircase voltammetry and genetically optimised neural networks. <i>Analyst, The</i> , 2004, 129, 355.	3.5	16
56	A liquid handling system for the automated acquisition of data for training, validating and testing calibration models. <i>Sensors and Actuators B: Chemical</i> , 2003, 88, 149-154.	7.8	11
57	Identification of Oil Contaminants on Polymer Coated Beverage Cans Using Fluorescence Spectroscopy. <i>Applied Spectroscopy</i> , 2003, 57, 1042-1048.	2.2	3
58	Identification of oil contaminants on polymer coated beverage cans using Raman spectroscopy. <i>Analyst, The</i> , 2002, 127, 297-303.	3.5	2
59	Principal components analysis for the visualisation of multidimensional chemical data acquired by scanning Raman microspectroscopy. <i>Analyst, The</i> , 2002, 127, 1261-1266.	3.5	10
60	Chemometric Evaluation of Synchronous Scan Fluorescence Spectroscopy for the Determination of Regulatory Conformance and Usage History of Insulation Oils. <i>Applied Spectroscopy</i> , 2001, 55, 840-846.	2.2	13
61	A chemometric analysis of dual pulse staircase voltammograms obtained in mixtures of ethanol, fructose and glucose. <i>Journal of Electroanalytical Chemistry</i> , 2000, 489, 76-83.	3.8	37
62	A ten channel fibre-optic device for distributed sensing of underground hydrocarbon leakage. <i>Journal of Environmental Monitoring</i> , 2000, 2, 670-673.	2.1	6
63	Integrated processing of triply coupled diode array liquid chromatography electrospray mass spectrometric signals by chemometric methods. <i>Analyst, The</i> , 1999, 124, 1733-1744.	3.5	5
64	Simultaneous Determination of Ethanol, Fructose, and Glucose at an Unmodified Platinum Electrode Using Artificial Neural Networks. <i>Analytical Chemistry</i> , 1999, 71, 2806-2813.	6.5	47
65	An object oriented approach to electroanalytical technique implementation. <i>Electroanalysis</i> , 1997, 9, 926-931.	2.9	7