

Hans Jct Wessels

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

3,542
citations

304743

22
h-index

315739

38
g-index

40
all docs

40
docs citations

40
times ranked

5303
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of cerebrospinal fluid biomarkers for parkinsonism using a proteomics approach. <i>Npj Parkinson's Disease</i> , 2021, 7, 107.	5.3	11
2	Affimers as an alternative to antibodies for protein biomarker enrichment. <i>Protein Expression and Purification</i> , 2020, 174, 105677.	1.3	13
3	Proteomic profiling of striatal tissue of a rat model of Parkinson's disease after implantation of collagen-encapsulated human umbilical cord mesenchymal stem cells. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2020, 14, 1077-1086.	2.7	4
4	Complexome analysis of the nitrite-dependent methanotroph <i>Methylomirabilis lanthanidiphila</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2019, 1860, 734-744.	1.0	18
5	O-glycosylation disorders pave the road for understanding the complex human O-glycosylation machinery. <i>Current Opinion in Structural Biology</i> , 2019, 56, 107-118.	5.7	22
6	The future of protein biomarker research in type 2 diabetes mellitus. <i>Expert Review of Proteomics</i> , 2019, 16, 105-115.	3.0	6
7	Chemically triggered drug release from an antibody-drug conjugate leads to potent antitumour activity in mice. <i>Nature Communications</i> , 2018, 9, 1484.	12.8	175
8	Towards a routine application of Top-Down approaches for label-free discovery workflows. <i>Journal of Proteomics</i> , 2018, 175, 12-26.	2.4	17
9	Integrated Chemometrics and Statistics to Drive Successful Proteomics Biomarker Discovery. <i>Proteomes</i> , 2018, 6, 20.	3.5	19
10	The Assembly Pathway of Mitochondrial Respiratory Chain Complex I. <i>Cell Metabolism</i> , 2017, 25, 128-139.	16.2	325
11	Proteomic Analysis of the Hydrogen and Carbon Monoxide Metabolism of <i>Methanothermobacter marburgensis</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1049.	3.5	27
12	Membrane-bound electron transport systems of an anammox bacterium: A complexome analysis. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1694-1704.	1.0	89
13	Proteomics of Human Dendritic Cell Subsets Reveals Subset-Specific Surface Markers and Differential Inflammasome Function. <i>Cell Reports</i> , 2016, 16, 2953-2966.	6.4	72
14	Bacterial Electron Transfer Chains Primed by Proteomics. <i>Advances in Microbial Physiology</i> , 2016, 68, 219-352.	2.4	5
15	XoxF-Type Methanol Dehydrogenase from the Anaerobic Methanotroph <i>Candidatus Methylomirabilis oxyfera</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1442-1451.	3.1	75
16	Whole Cell Formaldehyde Cross-Linking Simplifies Purification of Mitochondrial Nucleoids and Associated Proteins Involved in Mitochondrial Gene Expression. <i>PLoS ONE</i> , 2015, 10, e0116726.	2.5	38
17	Proteomics-Identified Bvg-Activated Autotransporters Protect against <i>Bordetella pertussis</i> in a Mouse Model. <i>PLoS ONE</i> , 2014, 9, e105011.	2.5	50
18	The vaccine potential of <i>Bordetella pertussis</i> biofilm-derived membrane proteins. <i>Emerging Microbes and Infections</i> , 2014, 3, 1-9.	6.5	46

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19	Isolation and characterization of a prokaryotic cell organelle from the anammox bacterium <i>Kuenenia stuttgartiensis</i> . <i>Molecular Microbiology</i> , 2014, 94, 794-802.	2.5	72
20	Peptide microarrays to probe for competition for binding sites in a protein interaction network. <i>Journal of Proteomics</i> , 2013, 89, 71-80.	2.4	5
21	Analysis of 953 Human Proteins from a Mitochondrial HEK293 Fraction by Complexome Profiling. <i>PLoS ONE</i> , 2013, 8, e68340.	2.5	51
22	Effects of Nitrogen Dioxide and Anoxia on Global Gene and Protein Expression in Long-Term Continuous Cultures of <i>Nitrosomonas eutropha</i> C91. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4788-4794.	3.1	15
23	A comprehensive full factorial LC-MS/MS proteomics benchmark data set. <i>Proteomics</i> , 2012, 12, 2276-2281.	2.2	12
24	Impaired ubiquitin-proteasome-mediated PGC protein turnover and induced mitochondrial biogenesis secondary to complex I deficiency. <i>Proteomics</i> , 2012, 12, 1349-1362.	2.2	8
25	Evolution of a new enzyme for carbon disulphide conversion by an acidothermophilic archaeon. <i>Nature</i> , 2011, 478, 412-416.	27.8	91
26	Pinpointing Biomarkers in Proteomic LC/MS Data by Moving-Window Discriminant Analysis. <i>Analytical Chemistry</i> , 2011, 83, 5197-5206.	6.5	4
27	A predicted physicochemically distinct sub-proteome associated with the intracellular organelle of the anammox bacterium <i>Kuenenia stuttgartiensis</i> . <i>BMC Genomics</i> , 2010, 11, 299.	2.8	26
28	Improved parametric time warping for proteomics. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010, 104, 65-74.	3.5	65
29	A functional peptidyl-tRNA hydrolase, ICT1, has been recruited into the human mitochondrial ribosome. <i>EMBO Journal</i> , 2010, 29, 1116-1125.	7.8	167
30	Nitrite-driven anaerobic methane oxidation by oxygenic bacteria. <i>Nature</i> , 2010, 464, 543-548.	27.8	1,521
31	LC-MS/MS as an alternative for SDS-PAGE in blue native analysis of protein complexes. <i>Proteomics</i> , 2009, 9, 4221-4228.	2.2	80
32	Automated measurement of permethylated serum N-glycans by MALDI-linear ion trap mass spectrometry. <i>Carbohydrate Research</i> , 2009, 344, 1550-1557.	2.3	33
33	Mutations in NDUFAF3 (C3ORF60), Encoding an NDUFAF4 (C6ORF66)-Interacting Complex I Assembly Protein, Cause Fatal Neonatal Mitochondrial Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 718-727.	6.2	155
34	The human mitochondrial ribosome recycling factor is essential for cell viability. <i>Nucleic Acids Research</i> , 2008, 36, 5787-5799.	14.5	102
35	Proteomic profiling and identification in peritoneal fluid of children treated by peritoneal dialysis. <i>Nephrology Dialysis Transplantation</i> , 2008, 23, 2402-2405.	0.7	32
36	Protein Complexes in the Archaeon <i>Methanothermobacter thermoautotrophicus</i> Analyzed by Blue Native/SDS-PAGE and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1653-1663.	3.8	79

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37	Serial Isoelectric Focusing as an Effective and Economic Way to Obtain Maximal Resolution and High-Throughput in 2D-Based Comparative Proteomics of Scarce Samples:Â Proof-of-Principle. Journal of Proteome Research, 2005, 4, 2364-2368.	3.7	3