

Ulrich Omasits

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

3,322
citations

304743

22
h-index

501196

28
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30
all docs

30
docs citations

30
times ranked

6069
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell-surface SLC nucleoside transporters and purine levels modulate BRD4-dependent chromatin states. <i>Nature Metabolism</i> , 2021, 3, 651-664.	11.9	7
2	Epistasis-driven identification of SLC25A51 as a regulator of human mitochondrial NAD import. <i>Nature Communications</i> , 2020, 11, 6145.	12.8	78
3	TASL is the SLC15A4-associated adaptor for IRF5 activation by TLR7. <i>Nature</i> , 2020, 581, 316-322.	27.8	117
4	The RESOLUTE consortium: unlocking SLC transporters for drug discovery. <i>Nature Reviews Drug Discovery</i> , 2020, 19, 429-430.	46.4	53
5	A substrate-based ontology for human solute carriers. <i>Molecular Systems Biology</i> , 2020, 16, e9652.	7.2	31
6	Proteotype profiling unmasks a viral signalling network essential for poxvirus assembly and transcriptional competence. <i>Nature Microbiology</i> , 2018, 3, 588-599.	13.3	10
7	The in silico human surfaceome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10988-E10997.	7.1	250
8	The Bicarbonate Transporter SLC4A7 Plays a Key Role in Macrophage Phagosome Acidification. <i>Cell Host and Microbe</i> , 2018, 23, 766-774.e5.	11.0	65
9	Explosive cell lysis as a mechanism for the biogenesis of bacterial membrane vesicles and biofilms. <i>Nature Communications</i> , 2016, 7, 11220.	12.8	487
10	A Peptidomimetic Antibiotic Targets Outer Membrane Proteins and Disrupts Selectively the Outer Membrane in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 1921-1932.	3.4	97
11	54-Dependent Response to Nitrogen Limitation and Virulence in <i>Burkholderia cenocepacia</i> Strain H111. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4077-4089.	3.1	44
12	A Mass Spectrometric-Derived Cell Surface Protein Atlas. <i>PLoS ONE</i> , 2015, 10, e0121314.	2.5	356
13	Protter: interactive protein feature visualization and integration with experimental proteomic data. <i>Bioinformatics</i> , 2014, 30, 884-886.	4.1	1,090
14	A Link between Arabinose Utilization and Oxalotrophy in <i>Bradyrhizobium japonicum</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 2094-2101.	3.1	28
15	Proteome-wide identification of predominant subcellular protein localizations in a bacterial model organism. <i>Journal of Proteomics</i> , 2014, 99, 123-137.	2.4	55
16	Combine and Conquer: Surfactants, Solvents, and Chaotropes for Robust Mass Spectrometry Based Analyses of Membrane Proteins. <i>Analytical Chemistry</i> , 2014, 86, 1551-1559.	6.5	57
17	Improved prediction of peptide detectability for targeted proteomics using a rank-based algorithm and organism-specific data. <i>Journal of Proteomics</i> , 2014, 108, 269-283.	2.4	43
18	Proteomics Analysis of <i>Psychotria</i> Leaf Nodule Symbiosis: Improved Genome Annotation and Metabolic Predictions. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1325-1333.	2.6	27

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19	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. <i>Genome Research</i> , 2013, 23, 1916-1927.	5.5	91
20	The Hemolymph Proteome of Fed and Starved <i>Drosophila</i> Larvae. <i>PLoS ONE</i> , 2013, 8, e67208.	2.5	55
21	The AHL- and BDSF-Dependent Quorum Sensing Systems Control Specific and Overlapping Sets of Genes in <i>Burkholderia cenocepacia</i> H111. <i>PLoS ONE</i> , 2012, 7, e49966.	2.5	70
22	Proteomic Analysis Reveals Drug Accessible Cell Surface N-Glycoproteins of Primary and Established Glioblastoma Cell Lines. <i>Journal of Proteome Research</i> , 2012, 11, 4885-4893.	3.7	20
23	A Comparative Approach Linking Molecular Dynamics of Altered Peptide Ligands and MHC with In Vivo Immune Responses. <i>PLoS ONE</i> , 2010, 5, e11653.	2.5	31
24	A critical cross-validation of high throughput structural binding prediction methods for pMHC. <i>Journal of Computer-Aided Molecular Design</i> , 2009, 23, 301-307.	2.9	35
25	3-Layer-based analysis of peptide-MHC interaction: In silico prediction, peptide binding affinity and T cell activation in a relevant allergen-specific model. <i>Molecular Immunology</i> , 2009, 46, 1839-1844.	2.2	43
26	jSimMacs for GROMACS: A Java Application for Advanced Molecular Dynamics Simulations with Remote Access Capability. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2412-2417.	5.4	15
27	Side chain substitution benchmark for peptide/MHC interaction. <i>Protein Science</i> , 2008, 17, 977-982.	7.6	26
28	Analysis of key parameters for molecular dynamics of pMHC molecules. <i>Molecular Simulation</i> , 2008, 34, 781-793.	2.0	37