Ulrich Omasits

List of Publications by Year
in descending order

28 papers	3,322 citations	304743 22 h-index	501196 28 g-index
30 all docs	30 docs citations	30 times ranked	6069 citing authors

#	Article	IF	Citations
1	Protter: interactive protein feature visualization and integration with experimental proteomic data. Bioinformatics, 2014, 30, 884-886.	4.1	1,090
2	Explosive cell lysis as a mechanism for the biogenesis of bacterial membrane vesicles and biofilms. Nature Communications, 2016, 7, 11220.	12.8	487
3	A Mass Spectrometric-Derived Cell Surface Protein Atlas. PLoS ONE, 2015, 10, e0121314.	2.5	356
4	The in silico human surfaceome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10988-E10997.	7.1	250
5	TASL is the SLC15A4-associated adaptor for IRF5 activation by TLR7–9. Nature, 2020, 581, 316-322.	27.8	117
6	A Peptidomimetic Antibiotic Targets Outer Membrane Proteins and Disrupts Selectively the Outer Membrane in Escherichia coli. Journal of Biological Chemistry, 2016, 291, 1921-1932.	3.4	97
7	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. Genome Research, 2013, 23, 1916-1927.	5.5	91
8	Epistasis-driven identification of SLC25A51 as a regulator of human mitochondrial NAD import. Nature Communications, 2020, 11, 6145.	12.8	78
9	The AHL- and BDSF-Dependent Quorum Sensing Systems Control Specific and Overlapping Sets of Genes in Burkholderia cenocepacia H111. PLoS ONE, 2012, 7, e49966.	2.5	70
10	The Bicarbonate Transporter SLC4A7 Plays a Key Role in Macrophage Phagosome Acidification. Cell Host and Microbe, 2018, 23, 766-774.e5.	11.0	65
11	Combine and Conquer: Surfactants, Solvents, and Chaotropes for Robust Mass Spectrometry Based Analyses of Membrane Proteins. Analytical Chemistry, 2014, 86, 1551-1559.	6.5	57
12	The Hemolymph Proteome of Fed and Starved Drosophila Larvae. PLoS ONE, 2013, 8, e67208.	2.5	55
13	Proteome-wide identification of predominant subcellular protein localizations in a bacterial model organism. Journal of Proteomics, 2014, 99, 123-137.	2.4	55
14	The RESOLUTE consortium: unlocking SLC transporters for drug discovery. Nature Reviews Drug Discovery, 2020, 19, 429-430.	46.4	53
15	σ54-Dependent Response to Nitrogen Limitation and Virulence in Burkholderia cenocepacia Strain H111. Applied and Environmental Microbiology, 2015, 81, 4077-4089.	3.1	44
16	3-Layer-based analysis of peptide–MHC interaction: In silico prediction, peptide binding affinity and T cell activation in a relevant allergen-specific model. Molecular Immunology, 2009, 46, 1839-1844.	2.2	43
17	Improved prediction of peptide detectability for targeted proteomics using a rank-based algorithm and organism-specific data. Journal of Proteomics, 2014, 108, 269-283.	2.4	43
18	Analysis of key parameters for molecular dynamics of pMHC molecules. Molecular Simulation, 2008, 34, 781-793.	2.0	37

#	Article	IF	Citations
19	A critical cross-validation of high throughput structural binding prediction methods for pMHC. Journal of Computer-Aided Molecular Design, 2009, 23, 301-307.	2.9	35
20	A Comparative Approach Linking Molecular Dynamics of Altered Peptide Ligands and MHC with In Vivo Immune Responses. PLoS ONE, 2010, 5, e11653.	2.5	31
21	A substrate€based ontology for human solute carriers. Molecular Systems Biology, 2020, 16, e9652.	7.2	31
22	A Link between Arabinose Utilization and Oxalotrophy in Bradyrhizobium japonicum. Applied and Environmental Microbiology, 2014, 80, 2094-2101.	3.1	28
23	Proteomics Analysis of <i>Psychotria</i> Leaf Nodule Symbiosis: Improved Genome Annotation and Metabolic Predictions. Molecular Plant-Microbe Interactions, 2013, 26, 1325-1333.	2.6	27
24	Side chain substitution benchmark for peptide/MHC interaction. Protein Science, 2008, 17, 977-982.	7.6	26
25	Proteomic Analysis Reveals Drug Accessible Cell Surface N-Glycoproteins of Primary and Established Glioblastoma Cell Lines. Journal of Proteome Research, 2012, 11, 4885-4893.	3.7	20
26	jSimMacs for GROMACS: A Java Application for Advanced Molecular Dynamics Simulations with Remote Access Capability. Journal of Chemical Information and Modeling, 2009, 49, 2412-2417.	5.4	15
27	Proteotype profiling unmasks a viral signalling network essential for poxvirus assembly and transcriptional competence. Nature Microbiology, 2018, 3, 588-599.	13.3	10
28	Cell-surface SLC nucleoside transporters and purine levels modulate BRD4-dependent chromatin states. Nature Metabolism, 2021, 3, 651-664.	11.9	7