

Edwin Lasonder

List of Publications by Year in descending order

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59
papers

4,643
citations

126708

33
h-index

133063

59
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61
all docs

61
docs citations

61
times ranked

5950
citing authors

#	ARTICLE	IF	CITATIONS
1	cAMP-Dependent Signaling Pathways as Potential Targets for Inhibition of Plasmodium falciparum Blood Stages. <i>Frontiers in Microbiology</i> , 2021, 12, 684005.	1.5	3
2	Plasmodium berghei LAPs form an extended protein complex that facilitates crystalloid targeting and biogenesis. <i>Journal of Proteomics</i> , 2020, 227, 103925.	1.2	13
3	Ubiquitin activation is essential for schizont maturation in Plasmodium falciparum blood-stage development. <i>PLoS Pathogens</i> , 2020, 16, e1008640.	2.1	24
4	<sc>NAD</sc> (P) transhydrogenase has vital non-mitochondrial functions in malaria parasite transmission. <i>EMBO Reports</i> , 2020, 21, e47832.	2.0	13
5	Vesiculation of Red Blood Cells in the Blood Bank: A Multi-Omics Approach towards Identification of Causes and Consequences. <i>Proteomes</i> , 2020, 8, 6.	1.7	12
6	Proteomic analysis discovers the differential expression of novel proteins and phosphoproteins in meningioma including NEK9, HK2 and SET and deregulation of RNA metabolism. <i>EBioMedicine</i> , 2019, 40, 77-91.	2.7	54
7	Unravelling the immune signature of Plasmodium falciparum transmission-reducing immunity. <i>Nature Communications</i> , 2018, 9, 558.	5.8	83
8	Global Proteome and Phospho-proteome Analysis of Merlin-deficient Meningioma and Schwannoma Identifies PDLIM2 as a Novel Therapeutic Target. <i>EBioMedicine</i> , 2017, 16, 76-86.	2.7	22
9	LCCL protein complex formation in Plasmodium is critically dependent on LAP1. <i>Molecular and Biochemical Parasitology</i> , 2017, 214, 87-90.	0.5	11
10	Clinical Proteomics: From Biological Sample to Clinical Exploitation. <i>Proteomes</i> , 2017, 5, 10.	1.7	5
11	Plasmodium falciparum infection induces dynamic changes in the erythrocyte phospho-proteome. <i>Blood Cells, Molecules, and Diseases</i> , 2016, 58, 35-44.	0.6	16
12	The TRPM7 interactome defines a cytoskeletal complex linked to neuroblastoma progression. <i>European Journal of Cell Biology</i> , 2016, 95, 465-474.	1.6	23
13	Proteomics of Human Dendritic Cell Subsets Reveals Subset-Specific Surface Markers and Differential Inflammasome Function. <i>Cell Reports</i> , 2016, 16, 2953-2966.	2.9	72
14	Comparative Proteomics and Functional Analysis Reveal a Role of Plasmodium falciparum Osmiophilic Bodies in Malaria Parasite Transmission. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3243-3255.	2.5	40
15	Integrated transcriptomic and proteomic analyses of <i>P. falciparum</i> gametocytes: molecular insight into sex-specific processes and translational repression. <i>Nucleic Acids Research</i> , 2016, 44, 6087-6101.	6.5	216
16	The scaffold protein KSR1, a novel therapeutic target for the treatment of Merlin-deficient tumors. <i>Oncogene</i> , 2016, 35, 3443-3453.	2.6	13
17	Proteome Based Construction of the Lymphocyte Function-Associated Antigen 1 (LFA-1) Interactome in Human Dendritic Cells. <i>PLoS ONE</i> , 2016, 11, e0149637.	1.1	2
18	Extensive differential protein phosphorylation as intraerythrocytic <i>Plasmodium falciparum</i> schizonts develop into extracellular invasive merozoites. <i>Proteomics</i> , 2015, 15, 2716-2729.	1.3	61

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19	Malaria Parasites Co-opt Human Factor H to Prevent Complement-Mediated Lysis in the Mosquito Midgut. <i>Cell Host and Microbe</i> , 2013, 13, 29-41.	5.1	86
20	Protein tyrosine phosphatase SHP2/PTPN11 mistargeting as a consequence of SH2-domain point mutations associated with Noonan Syndrome and leukemia. <i>Journal of Proteomics</i> , 2013, 84, 132-147.	1.2	18
21	P190BCR-ABL1 Signaling Modulates The Function Of Tumor Suppressor Protein IKZF1. <i>Blood</i> , 2013, 122, 3809-3809.	0.6	0
22	Iterative orthology prediction uncovers new mitochondrial proteins and identifies C12orf62 as the human ortholog of COX14, a protein involved in the assembly of cytochrome c oxidase. <i>Genome Biology</i> , 2012, 13, R12.	13.9	100
23	The proteome of erythrocyte-derived microparticles from plasma: new clues for erythrocyte aging and vesiculation. <i>Journal of Proteomics</i> , 2012, 76, 203-210.	1.2	97
24	Insights into the Plasmodium falciparum schizont phospho-proteome. <i>Microbes and Infection</i> , 2012, 14, 811-819.	1.0	49
25	The <i>Plasmodium falciparum</i> Schizont Phosphoproteome Reveals Extensive Phosphatidylinositol and cAMP-Protein Kinase A Signaling. <i>Journal of Proteome Research</i> , 2012, 11, 5323-5337.	1.8	128
26	Impaired ubiquitin-proteasome-mediated PGC protein turnover and induced mitochondrial biogenesis secondary to complex I deficiency. <i>Proteomics</i> , 2012, 12, 1349-1362.	1.3	8
27	Unraveling the human dendritic cell phagosome proteome by organellar enrichment ranking. <i>Journal of Proteomics</i> , 2012, 75, 1547-1562.	1.2	27
28	Erythrocyte membrane changes of chorea-acanthocytosis are the result of altered Lyn kinase activity. <i>Blood</i> , 2011, 118, 5652-5663.	0.6	73
29	Experimentally controlled downregulation of the histone chaperone FACT in <i>Plasmodium berghei</i> reveals that it is critical to male gamete fertility. <i>Cellular Microbiology</i> , 2011, 13, 1956-1974.	1.1	43
30	Protein Export Marks the Early Phase of Gametocytogenesis of the Human Malaria Parasite Plasmodium falciparum. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1437-1448.	2.5	228
31	An alternatively spliced CXCL16 isoform expressed by dendritic cells is a secreted chemoattractant for CXCR6+ cells. <i>Journal of Leukocyte Biology</i> , 2010, 87, 1029-1039.	1.5	29
32	Universal Features of Post-Transcriptional Gene Regulation Are Critical for Plasmodium Zygote Development. <i>PLoS Pathogens</i> , 2010, 6, e1000767.	2.1	237
33	Dominant Processes during Human Dendritic Cell Maturation Revealed by Integration of Proteome and Transcriptome at the Pathway Level. <i>Journal of Proteome Research</i> , 2010, 9, 1727-1737.	1.8	45
34	The proteome of red cell membranes and vesicles during storage in blood bank conditions. <i>Transfusion</i> , 2008, 48, 827-835.	0.8	64
35	The kinases TRPM6 and TRPM7, but not eEF2 kinase, phosphorylate the assembly domain of myosin IIA, IIB and IIC. <i>FEBS Letters</i> , 2008, 582, 2993-2997.	1.3	74
36	RACK1 Inhibits TRPM6 Activity via Phosphorylation of the Fused Kinase Domain. <i>Current Biology</i> , 2008, 18, 168-176.	1.8	67

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37	TRPM7 Regulates Myosin IIA Filament Stability and Protein Localization by Heavy Chain Phosphorylation. <i>Journal of Molecular Biology</i> , 2008, 378, 790-803.	2.0	125
38	Proteomic Profiling of Plasmodium Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. <i>PLoS Pathogens</i> , 2008, 4, e1000195.	2.1	191
39	The regulation of SIRT2 function by cyclin-dependent kinases affects cell motility. <i>Journal of Cell Biology</i> , 2008, 180, 915-929.	2.3	198
40	The proteome of red cell membranes and vesicles during storage in blood bank conditions. <i>Transfusion</i> , 2008, 48, 827-835.	0.8	99
41	Massive Autophosphorylation of the Ser/Thr-Rich Domain Controls Protein Kinase Activity of TRPM6 and TRPM7. <i>PLoS ONE</i> , 2008, 3, e1876.	1.1	88
42	Epitope Analysis of the Malaria Surface Antigen Pfs48/45 Identifies a Subdomain That Elicits Transmission Blocking Antibodies. <i>Journal of Biological Chemistry</i> , 2007, 282, 17148-17156.	1.6	70
43	Shotgun immunoproteomics to identify disease-associated bacterial antigens: Application to human colon cancer. <i>Proteomics - Clinical Applications</i> , 2007, 1, 429-434.	0.8	15
44	Profiling the humoral immune response in colon cancer patients: Diagnostic antigens from <i>Streptococcus bovis</i> . <i>International Journal of Cancer</i> , 2006, 119, 2127-2135.	2.3	91
45	A Feed-Forward Repression Mechanism Anchors the Sin3/Histone Deacetylase and N-CoR/SMRT Corepressors on Chromatin. <i>Molecular and Cellular Biology</i> , 2006, 26, 5226-5236.	1.1	26
46	MBD2/NuRD and MBD3/NuRD, Two Distinct Complexes with Different Biochemical and Functional Properties. <i>Molecular and Cellular Biology</i> , 2006, 26, 843-851.	1.1	290
47	Characterization of Lysine 56 of Histone H3 as an Acetylation Site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25949-25952.	1.6	105
48	Proteome Analysis of Separated Male and Female Gametocytes Reveals Novel Sex-Specific Plasmodium Biology. <i>Cell</i> , 2005, 121, 675-687.	13.5	336
49	In Vitro Targeting Reveals Intrinsic Histone Tail Specificity of the Sin3/Histone Deacetylase and N-CoR/SMRT Corepressor Complexes. <i>Molecular and Cellular Biology</i> , 2004, 24, 2364-2372.	1.1	43
50	The solution structure and DNA-binding properties of the cold-shock domain of the human Y-box protein YB-1. <i>Journal of Molecular Biology</i> , 2002, 316, 317-326.	2.0	121
51	Analysis of the Plasmodium falciparum proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	13.7	596
52	Sequence-specific assignment of the PAH2 domain of Sin3B free and bound to Mad1. <i>Journal of Biomolecular NMR</i> , 2001, 19, 377-378.	1.6	4
53	Kinetic Analysis of Synthetic Analogues of Linear-Epitope Peptides of Glycoprotein D of Herpes Simplex Virus Type 1 by Surface Plasmon Resonance. <i>FEBS Journal</i> , 1996, 240, 209-214.	0.2	14
54	Measurement of affinity in serum samples of antigen-free, germ-free and conventional mice after hyperimmunization with 2,4-dinitrophenyl keyhole limpet hemocyanin, using surface plasmon resonance. <i>European Journal of Immunology</i> , 1995, 25, 1680-1686.	1.6	20

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55	Identification of the core residues of the epitope of a monoclonal antibody raised against glycoprotein D of herpes simplex virus type 1 by screening of a random peptide library. <i>European Journal of Immunology</i> , 1994, 24, 3188-3193.	1.6	38
56	Characterization of a synthetic 37-residue fragment of a monoclonal antibody against herpes virus by capillary electrophoresis/electrospray (ionspray) mass spectrometry and ^{252}Cf plasma desorption mass spectrometry. <i>Biological Mass Spectrometry</i> , 1994, 23, 346-352.	0.5	9
57	Interaction of lysozyme with synthetic anti-lysozyme D1.3 antibody fragments studied by affinity chromatography and surface plasmon resonance. <i>Journal of Chromatography A</i> , 1994, 676, 91-98.	1.8	17
58	A fast and sensitive method for the evaluation of binding of phage clones selected from a surface displayed library. <i>Nucleic Acids Research</i> , 1994, 22, 545-546.	6.5	22
59	An NMR and DSC study of the interaction of phospholipid vesicles with some anti-inflammatory agents. <i>Journal of Colloid and Interface Science</i> , 1990, 139, 469-478.	5.0	55