

PÃr Nordlund

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

7,626
citations

257450

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302126

39
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docs citations

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times ranked

11324
citing authors

#	ARTICLE	IF	CITATIONS
1	CETSA interaction proteomics define specific RNA-modification pathways as key components of fluorouracil-based cancer drug cytotoxicity. <i>Cell Chemical Biology</i> , 2022, 29, 572-585.e8.	5.2	18
2	Recent advances in proteome-wide label-free target deconvolution for bioactive small molecules. <i>Medicinal Research Reviews</i> , 2021, 41, 2893-2926.	10.5	13
3	Mutant p53-reactivating compound APR-246 synergizes with asparaginase in inducing growth suppression in acute lymphoblastic leukemia cells. <i>Cell Death and Disease</i> , 2021, 12, 709.	6.3	11
4	CETSA in integrated proteomics studies of cellular processes. <i>Current Opinion in Chemical Biology</i> , 2020, 54, 54-62.	6.1	40
5	New ideas for non-animal approaches to predict repeated-dose systemic toxicity: Report from an EPAA Blue Sky Workshop. <i>Regulatory Toxicology and Pharmacology</i> , 2020, 114, 104668.	2.7	33
6	Cellular thermal shift assay for the identification of drug-target interactions in the Plasmodium falciparum proteome. <i>Nature Protocols</i> , 2020, 15, 1881-1921.	12.0	79
7	Target identification and validation of natural products with label-free methodology: A critical review from 2005 to 2020. , 2020, 216, 107690.		25
8	Monitoring structural modulation of redox-sensitive proteins in cells with MS-CETSA. <i>Redox Biology</i> , 2019, 24, 101168.	9.0	31
9	Horizontal Cell Biology: Monitoring Global Changes of Protein Interaction States with the Proteome-Wide Cellular Thermal Shift Assay (CETSA). <i>Annual Review of Biochemistry</i> , 2019, 88, 383-408.	11.1	83
10	CETSA-based target engagement of taxanes as biomarkers for efficacy and resistance. <i>Scientific Reports</i> , 2019, 9, 19384.	3.3	22
11	Identifying purine nucleoside phosphorylase as the target of quinine using cellular thermal shift assay. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	153
12	Modulation of Protein-Interaction States through the Cell Cycle. <i>Cell</i> , 2018, 173, 1481-1494.e13.	28.9	116
13	Thermal proximity coaggregation for system-wide profiling of protein complex dynamics in cells. <i>Science</i> , 2018, 359, 1170-1177.	12.6	161
14	An efficient proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions. <i>PLoS ONE</i> , 2018, 13, e0208273.	2.5	41
15	Quantitation of ERK1/2 inhibitor cellular target occupancies with a reversible slow off-rate probe. <i>Chemical Science</i> , 2018, 9, 8608-8618.	7.4	9
16	Structure of the Open Reading Frame 49 Protein Encoded by Kaposi's Sarcoma-Associated Herpesvirus. <i>Journal of Virology</i> , 2017, 91, .	3.4	3
17	Dual blockade of the lipid kinase PIP4Ks and mitotic pathways leads to cancer-selective lethality. <i>Nature Communications</i> , 2017, 8, 2200.	12.8	63
18	Molecular insights into substrate recognition and catalytic mechanism of the chaperone and FKBP peptidyl-prolyl isomerase SlyD. <i>BMC Biology</i> , 2016, 14, 82.	3.8	26

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19	CETSA screening identifies known and novel thymidylate synthase inhibitors and slow intracellular activation of 5-fluorouracil. <i>Nature Communications</i> , 2016, 7, 11040.	12.8	126
20	The structure and catalytic mechanism of human sphingomyelin phosphodiesterase like 3a " an acid sphingomyelinase homologue with a novel nucleotide hydrolase activity. <i>FEBS Journal</i> , 2016, 283, 1107-1123.	4.7	13
21	Understanding transport by the major facilitator superfamily (MFS): structures pave the way. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 123-132.	37.0	376
22	The Cellular Thermal Shift Assay: A Novel Biophysical Assay for In Situ Drug Target Engagement and Mechanistic Biomarker Studies. <i>Annual Review of Pharmacology and Toxicology</i> , 2016, 56, 141-161.	9.4	213
23	A saposin-lipoprotein nanoparticle system for membrane proteins. <i>Nature Methods</i> , 2016, 13, 345-351.	19.0	209
24	Structural Basis for the Specificity of Human NUDT16 and Its Regulation by Inosine Monophosphate. <i>PLoS ONE</i> , 2015, 10, e0131507.	2.5	22
25	Structure of the Varicella Zoster Virus Thymidylate Synthase Establishes Functional and Structural Similarities as the Human Enzyme and Potentiates Itself as a Target of Brivudine. <i>PLoS ONE</i> , 2015, 10, e0143947.	2.5	16
26	Interaction between human BAP31 and respiratory syncytial virus small hydrophobic (SH) protein. <i>Virology</i> , 2015, 482, 105-110.	2.4	12
27	VP22 core domain from Herpes simplex virus 1 reveals a surprising structural conservation in both the Alpha- and Gammaherpesvirinae subfamilies. <i>Journal of General Virology</i> , 2015, 96, 1436-1445.	2.9	26
28	Structure of the C-Terminal Domain of the Multifunctional ICP27 Protein from Herpes Simplex Virus 1. <i>Journal of Virology</i> , 2015, 89, 8828-8839.	3.4	16
29	Selectivity mechanism of a bacterial homolog of the human drug-peptide transporters PepT1 and PepT2. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 728-731.	8.2	93
30	The cellular thermal shift assay for evaluating drug target interactions in cells. <i>Nature Protocols</i> , 2014, 9, 2100-2122.	12.0	900
31	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , 2014, 346, 1255784.	12.6	812
32	Structural Basis for Phosphoinositide Substrate Recognition, Catalysis, and Membrane Interactions in Human Inositol Polyphosphate 5-Phosphatases. <i>Structure</i> , 2014, 22, 744-755.	3.3	46
33	Structural and Biochemical Characterization of Human PR70 in Isolation and in Complex with the Scaffolding Subunit of Protein Phosphatase 2A. <i>PLoS ONE</i> , 2014, 9, e101846.	2.5	14
34	Engineering protein thermostability using a generic activity-independent biophysical screen inside the cell. <i>Nature Communications</i> , 2013, 4, 2901.	12.8	74
35	Monitoring Drug Target Engagement in Cells and Tissues Using the Cellular Thermal Shift Assay. <i>Science</i> , 2013, 341, 84-87.	12.6	1,444
36	Structural and dynamic insights into substrate binding and catalysis of human lipocalin prostaglandin D synthase. <i>Journal of Lipid Research</i> , 2013, 54, 1630-1643.	4.2	24

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37	Understanding specificity in metabolic pathwaysâ€”Structural biology of human nucleotide metabolism. <i>Biochemical and Biophysical Research Communications</i> , 2010, 396, 157-163.	2.1	21
38	Chemical screening methods to identify ligands that promote protein stability, protein crystallization, and structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15835-15840.	7.1	526
39	Thermofluor-based high-throughput stability optimization of proteins for structural studies. <i>Analytical Biochemistry</i> , 2006, 357, 289-298.	2.4	733
40	Ribonucleotide Reductases. <i>Annual Review of Biochemistry</i> , 2006, 75, 681-706.	11.1	978
41	New prepacked 96â€well filter plates, His MultiTrap FF and His MultiTrap HP for reproducible purification screening of histidineâ€tagged proteins. <i>FASEB Journal</i> , 2006, 20, A103.	0.5	0