PÃ¤r Nordlund

List of Publications by Year
in descending order

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41 papers	7,626 citations	257450 24 h-index	302126 39 g-index
45 all docs	45 docs citations	45 times ranked	11324 citing authors

#	Article	IF	Citations
1	Monitoring Drug Target Engagement in Cells and Tissues Using the Cellular Thermal Shift Assay. Science, 2013, 341, 84-87.	12.6	1,444
2	Ribonucleotide Reductases. Annual Review of Biochemistry, 2006, 75, 681-706.	11.1	978
3	The cellular thermal shift assay for evaluating drug target interactions in cells. Nature Protocols, 2014, 9, 2100-2122.	12.0	900
4	Tracking cancer drugs in living cells by thermal profiling of the proteome. Science, 2014, 346, 1255784.	12.6	812
5	Thermofluor-based high-throughput stability optimization of proteins for structural studies. Analytical Biochemistry, 2006, 357, 289-298.	2.4	733
6	Chemical screening methods to identify ligands that promote protein stability, protein crystallization, and structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15835-15840.	7.1	526
7	Understanding transport by the major facilitator superfamily (MFS): structures pave the way. Nature Reviews Molecular Cell Biology, 2016, 17, 123-132.	37.0	376
8	The Cellular Thermal Shift Assay: A Novel Biophysical Assay for In Situ Drug Target Engagement and Mechanistic Biomarker Studies. Annual Review of Pharmacology and Toxicology, 2016, 56, 141-161.	9.4	213
9	A saposin-lipoprotein nanoparticle system for membrane proteins. Nature Methods, 2016, 13, 345-351.	19.0	209
10	Thermal proximity coaggregation for system-wide profiling of protein complex dynamics in cells. Science, 2018, 359, 1170-1177.	12.6	161
11	Identifying purine nucleoside phosphorylase as the target of quinine using cellular thermal shift assay. Science Translational Medicine, 2019, 11, .	12.4	153
12	CETSA screening identifies known and novel thymidylate synthase inhibitors and slow intracellular activation of 5-fluorouracil. Nature Communications, 2016, 7, 11040.	12.8	126
13	Modulation of Protein-Interaction States through the Cell Cycle. Cell, 2018, 173, 1481-1494.e13.	28.9	116
14	Selectivity mechanism of a bacterial homolog of the human drug-peptide transporters PepT1 and PepT2. Nature Structural and Molecular Biology, 2014, 21, 728-731.	8.2	93
15	Horizontal Cell Biology: Monitoring Global Changes of Protein Interaction States with the Proteome-Wide Cellular Thermal Shift Assay (CETSA). Annual Review of Biochemistry, 2019, 88, 383-408.	11.1	83
16	Cellular thermal shift assay for the identification of drugâ€“target interactions in the Plasmodium falciparum proteome. Nature Protocols, 2020, 15, 1881-1921.	12.0	79
17	Engineering protein thermostability using a generic activity-independent biophysical screen inside the cell. Nature Communications, 2013, 4, 2901.	12.8	74
18	Dual blockade of the lipid kinase PIP4Ks and mitotic pathways leads to cancer-selective lethality. Nature Communications, 2017, 8, 2200.	12.8	63

#	ARTICLE	IF	CITATIONS
19	Structural Basis for Phosphoinositide Substrate Recognition, Catalysis, and Membrane Interactions in Human Inositol Polyphosphate 5-Phosphatases. Structure, 2014, 22, 744-755.	3.3	46
20	An efficient proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions. PLoS ONE, 2018, 13, e0208273.	2.5	41
21	CETSA in integrated proteomics studies of cellular processes. Current Opinion in Chemical Biology, 2020, 54, 54-62.	6.1	40
22	New ideas for non-animal approaches to predict repeated-dose systemic toxicity: Report from an EPAA Blue Sky Workshop. Regulatory Toxicology and Pharmacology, 2020, 114, 104668.	2.7	33
23	Monitoring structural modulation of redox-sensitive proteins in cells with MS-CETSA. Redox Biology, 2019, 24, 101168.	9.0	31
24	VP22 core domain from Herpes simplex virus 1 reveals a surprising structural conservation in both the Alpha- and Gammaherpesvirinae subfamilies. Journal of General Virology, 2015, 96, 1436-1445.	2.9	26
25	Molecular insights into substrate recognition and catalytic mechanism of the chaperone and FKBP peptidyl-prolyl isomerase SlyD. BMC Biology, 2016, 14, 82.	3.8	26
26	Target identification and validation of natural products with label-free methodology: A critical review from 2005 to 2020. , 2020, 216, 107690.		25
27	Structural and dynamic insights into substrate binding and catalysis of human lipocalin prostaglandin D synthase. Journal of Lipid Research, 2013, 54, 1630-1643.	4.2	24
28	Structural Basis for the Specificity of Human NUDT16 and Its Regulation by Inosine Monophosphate. PLoS ONE, 2015, 10, e0131507.	2.5	22
29	CETSA-based target engagement of taxanes as biomarkers for efficacy and resistance. Scientific Reports, 2019, 9, 19384.	3.3	22
30	Understanding specificity in metabolic pathwaysâ€"Structural biology of human nucleotide metabolism. Biochemical and Biophysical Research Communications, 2010, 396, 157-163.	2.1	21
31	CETSA interaction proteomics define specific RNA-modification pathways as key components of fluorouracil-based cancer drug cytotoxicity. Cell Chemical Biology, 2022, 29, 572-585.e8.	5.2	18
32	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. PLoS ONE, 2015, 10, e0143947.	2.5	16
33	Structure of the C-Terminal Domain of the Multifunctional ICP27 Protein from Herpes Simplex Virus 1. Journal of Virology, 2015, 89, 8828-8839.	3.4	16
34	Structural and Biochemical Characterization of Human PR70 in Isolation and in Complex with the Scaffolding Subunit of Protein Phosphatase 2A. PLoS ONE, 2014, 9, e101846.	2.5	14
35	The structure and catalytic mechanism of human sphingomyelin phosphodiesterase like 3a â€“ an acid sphingomyelinase homologue with a novel nucleotide hydrolase activity. FEBS Journal, 2016, 283, 1107-1123.	4.7	13
36	Recent advances in proteomeâ€wide labelâ€free target deconvolution for bioactive small molecules. Medicinal Research Reviews, 2021, 41, 2893-2926.	10.5	13

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37	Interaction between human BAP31 and respiratory syncytial virus small hydrophobic (SH) protein. Virology, 2015, 482, 105-110.	2.4	12
38	Mutant p53-reactivating compound APR-246 synergizes with asparaginase in inducing growth suppression in acute lymphoblastic leukemia cells. Cell Death and Disease, 2021, 12, 709.	6.3	11
39	Quantitation of ERK1/2 inhibitor cellular target occupancies with a reversible slow off-rate probe. Chemical Science, 2018, 9, 8608-8618.	7.4	9
40	Structure of the Open Reading Frame 49 Protein Encoded by Kaposi's Sarcoma-Associated Herpesvirus. Journal of Virology, 2017, 91, .	3.4	3
41	New prepacked 96â€well filter plates, His MultiTrap FF and His MultiTrap HP for reproducible purification screening of histidineâ€tagged proteins. FASEB Journal, 2006, 20, A103.	0.5	0