Nils Kurzawa

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6150273/publications.pdf

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23	1,765	471509 17	642732 23
papers	citations	h-index	g-index

30	30	30	2123
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Drug Target Identification in Tissues by Thermal Proteome Profiling. Annual Review of Pharmacology and Toxicology, 2022, 62, 465-482.	9.4	31
2	Rtpca: an R package for differential thermal proximity coaggregation analysis. Bioinformatics, 2021, 37, 431-433.	4.1	14
3	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. Nature Methods, 2021, 18, 84-91.	19.0	49
4	SARSâ€CoVâ€2 infection remodels the host protein thermal stability landscape. Molecular Systems Biology, 2021, 17, e10188.	7.2	17
5	Impact of phosphorylation on thermal stability of proteins. Nature Methods, 2021, 18, 757-759.	19.0	58
6	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. MSystems, 2021, 6, e0081321.	3.8	9
7	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. Nature Communications, 2020, 11, 3583.	12.8	38
8	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. Nature Communications, 2020, 11, 5783.	12.8	34
9	The functional proteome landscape of Escherichia coli. Nature, 2020, 588, 473-478.	27.8	58
10	Identifying drug targets in tissues and whole blood with thermal-shift profiling. Nature Biotechnology, 2020, 38, 303-308.	17.5	111
11	Thermal proteome profiling for interrogating protein interactions. Molecular Systems Biology, 2020, 16, e9232.	7.2	150
12	Meltome atlasâ€”thermal proteome stability across the tree of life. Nature Methods, 2020, 17, 495-503.	19.0	152
13	Aggregation and disaggregation features of the human proteome. Molecular Systems Biology, 2020, 16, e9500.	7.2	25
14	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. Biology Methods and Protocols, 2020, 5, bpaa022.	2.2	11
15	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. Molecular and Cellular Proteomics, 2019, 18, 2506-2515.	3.8	75
16	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. Nature Communications, 2019, 10, 1155.	12.8	181
17	Systematic analysis of protein turnover in primary cells. Nature Communications, 2018, 9, 689.	12.8	280
18	Pervasive Protein Thermal Stability Variation during the Cell Cycle. Cell, 2018, 173, 1495-1507.e18.	28.9	183

#	Article	IF	Citations
19	Thermal proteome profiling in bacteria: probing protein state inÂvivo. Molecular Systems Biology, 2018, 14, e8242.	7.2	130
20	Neural Circuits Trained with Standard Reinforcement Learning Can Accumulate Probabilistic Information during Decision Making. Neural Computation, 2017, 29, 368-393.	2.2	2
21	A comprehensive comparison of tools for differential ChIP-seq analysis. Briefings in Bioinformatics, 2016, 17, bbv110.	6.5	89
22	MapMyFlu: visualizing spatio-temporal relationships between related influenza sequences. Nucleic Acids Research, 2015, 43, W547-W551.	14.5	5
23	Creating functional engineered variants of the single-module non-ribosomal peptide synthetase IndC by T domain exchange. Molecular BioSystems, 2014, 10, 1709-1718.	2.9	35