

Nils Kurzawa

List of Publications by Year in descending order

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

Version: 2024-02-01

23
papers

1,765
citations

471509

17
h-index

642732

23
g-index

30
all docs

30
docs citations

30
times ranked

2123
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic analysis of protein turnover in primary cells. Nature Communications, 2018, 9, 689.	12.8	280
2	Pervasive Protein Thermal Stability Variation during the Cell Cycle. Cell, 2018, 173, 1495-1507.e18.	28.9	183
3	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. Nature Communications, 2019, 10, 1155.	12.8	181
4	Meltome atlas—thermal proteome stability across the tree of life. Nature Methods, 2020, 17, 495-503.	19.0	152
5	Thermal proteome profiling for interrogating protein interactions. Molecular Systems Biology, 2020, 16, e9232.	7.2	150
6	Thermal proteome profiling in bacteria: probing protein state <i>in vivo</i> . Molecular Systems Biology, 2018, 14, e8242.	7.2	130
7	Identifying drug targets in tissues and whole blood with thermal-shift profiling. Nature Biotechnology, 2020, 38, 303-308.	17.5	111
8	A comprehensive comparison of tools for differential ChIP-seq analysis. Briefings in Bioinformatics, 2016, 17, bbv110.	6.5	89
9	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. Molecular and Cellular Proteomics, 2019, 18, 2506-2515.	3.8	75
10	The functional proteome landscape of Escherichia coli. Nature, 2020, 588, 473-478.	27.8	58
11	Impact of phosphorylation on thermal stability of proteins. Nature Methods, 2021, 18, 757-759.	19.0	58
12	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. Nature Methods, 2021, 18, 84-91.	19.0	49
13	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PPI and PP2A. Nature Communications, 2020, 11, 3583.	12.8	38
14	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
15	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. Nature Communications, 2020, 11, 5783.	12.8	34
16	Drug Target Identification in Tissues by Thermal Proteome Profiling. Annual Review of Pharmacology and Toxicology, 2022, 62, 465-482.	9.4	31
17	Aggregation and disaggregation features of the human proteome. Molecular Systems Biology, 2020, 16, e9500.	7.2	25
18	SARS-CoV-2 infection remodels the host protein thermal stability landscape. Molecular Systems Biology, 2021, 17, e10188.	7.2	17

#	ARTICLE	IF	CITATIONS
19	Rtpca: an R package for differential thermal proximity coaggregation analysis. <i>Bioinformatics</i> , 2021, 37, 431-433.	4.1	14
20	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. <i>Biology Methods and Protocols</i> , 2020, 5, bpa022.	2.2	11
21	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. <i>MSystems</i> , 2021, 6, e0081321.	3.8	9
22	MapMyFlu: visualizing spatio-temporal relationships between related influenza sequences. <i>Nucleic Acids Research</i> , 2015, 43, W547-W551.	14.5	5
23	Neural Circuits Trained with Standard Reinforcement Learning Can Accumulate Probabilistic Information during Decision Making. <i>Neural Computation</i> , 2017, 29, 368-393.	2.2	2