

Isabelle Becher

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1038575/publications.pdf>

Version: 2024-02-01

22
papers

3,026
citations

361296

20
h-index

677027

22
g-index

27
all docs

27
docs citations

27
times ranked

4932
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. <i>Nature Biotechnology</i> , 2011, 29, 255-265.	9.4	597
2	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018, 9, 689.	5.8	280
3	Measuring and Managing Ratio Compression for Accurate iTRAQ/TMT Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 3586-3598.	1.8	238
4	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. <i>Nature Chemical Biology</i> , 2016, 12, 908-910.	3.9	189
5	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. <i>Cell</i> , 2018, 173, 260-274.e25.	13.5	186
6	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , 2018, 173, 1495-1507.e18.	13.5	183
7	High-Resolution Enabled TMT 8-plexing. <i>Analytical Chemistry</i> , 2012, 84, 7188-7194.	3.2	181
8	Discovery of I-BRD9, a Selective Cell Active Chemical Probe for Bromodomain Containing Protein 9 Inhibition. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 1425-1439.	2.9	177
9	Meltome atlas thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	9.0	152
10	Thermal proteome profiling for interrogating protein interactions. <i>Molecular Systems Biology</i> , 2020, 16, e9232.	3.2	150
11	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , 2020, 38, 303-308.	9.4	111
12	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.	2.5	98
13	Functional interdependence of BRD4 and DOT1L in MLL leukemia. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 673-681.	3.6	92
14	Affinity Profiling of the Cellular Kinome for the Nucleotide Cofactors ATP, ADP, and GTP. <i>ACS Chemical Biology</i> , 2013, 8, 599-607.	1.6	73
15	Impact of phosphorylation on thermal stability of proteins. <i>Nature Methods</i> , 2021, 18, 757-759.	9.0	58
16	GSK6853, a Chemical Probe for Inhibition of the BRPF1 Bromodomain. <i>ACS Medicinal Chemistry Letters</i> , 2016, 7, 552-557.	1.3	54
17	Chemoproteomics Reveals Time-Dependent Binding of Histone Deacetylase Inhibitors to Endogenous Repressor Complexes. <i>ACS Chemical Biology</i> , 2014, 9, 1736-1746.	1.6	52
18	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. <i>Nature Methods</i> , 2021, 18, 84-91.	9.0	49

#	ARTICLE	IF	CITATIONS
19	H-Score, a Mass Accuracy Driven Rescoring Approach for Improved Peptide Identification in Modification Rich Samples. <i>Journal of Proteome Research</i> , 2010, 9, 5511-5516.	1.8	34
20	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020, 11, 5783.	5.8	34
21	Isocotoin suppresses hepatitis E virus replication through inhibition of heat shock protein 90. <i>Antiviral Research</i> , 2021, 185, 104997.	1.9	15
22	Quantifying Small Molecule-Induced Changes in Cellular Protein Expression and Posttranslational Modifications Using Isobaric Mass Tags. <i>Methods in Molecular Biology</i> , 2014, 1156, 431-443.	0.4	1