Marcus Bantscheff

List of Publications by Year
in descending order

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114 papers	18,981 citations	23544 58 h-index	21521 114 g-index

128 all docs	128 docs citations	128 times ranked	27187 citing authors

#	Article	IF	Citations
1	The emerging role of mass spectrometry-based proteomics in drug discovery. Nature Reviews Drug Discovery, 2022, 21, 637-654.	21.5	110
2	Patient-derived gene and protein expression signatures of NGLY1 deficiency. Journal of Biochemistry, 2022, 171, 187-199.	0.9	9
3	Interval-Based Secretomics Unravels Acute-Phase Response in Hepatocyte Model Systems. Molecular and Cellular Proteomics, 2022, 21, 100241.	2.5	2
4	Affinity Enrichment for Target Deconvolution and. Methods in Molecular Biology, 2021, 2228, 237-252.	0.4	3
5	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. Nature Methods, 2021, 18, 84-91.	9.0	49
6	Improved Proteomics-Based Drug Mechanism-of-Action Studies Using 16-Plex Isobaric Mass Tags. Journal of Proteome Research, 2021, 20, 1792-1801.	1.8	29
7	Ca ²⁺ signals critical for egress and gametogenesis in malaria parasites depend on a multipass membrane protein that interacts with PKG. Science Advances, 2021, 7, .	4.7	34
8	SARS-CoV-2 drives JAK1/2-dependent local complement hyperactivation. Science Immunology, 2021, 6, .	5.6	144
9	BRD4 methylation by the methyltransferase SETD6 regulates selective transcription to control mRNA translation. Science Advances, 2021, 7, .	4.7	23
10	A Bayesian semi-parametric model for thermal proteome profiling. Communications Biology, 2021, 4, 810.	2.0	6
11	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. Nature Cancer, 2021, 2, 1002-1017.	5.7	99
12	Discovery and Characterisation of Highly Cooperative FAKâ€Đegrading PROTACs. Angewandte Chemie - International Edition, 2021, 60, 23327-23334.	7.2	58
13	Discovery and Characterisation of Highly Cooperative FAKâ€Đegrading PROTACs. Angewandte Chemie, 2021, 133, 23515-23522.	1.6	4
14	The multi-target aspect of an MmpL3 inhibitor: The BM212 series of compounds bind EthR2, a transcriptional regulator of ethionamide activation. Cell Surface, 2021, 7, 100068.	1.5	3
15	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. Nature Cancer, 2021, 2, 1002-1017.	5.7	23
16	Optimization of Orally Bioavailable PI3KÎ´ Inhibitors and Identification of Vps34 as a Key Selectivity Target. Journal of Medicinal Chemistry, 2020, 63, 638-655.	2.9	15
17	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. Nature Communications, 2020, 11, 5783.	5.8	34
18	CDK12 inhibition reduces abnormalities in cells from patients with myotonic dystrophy and in a mouse model. Science Translational Medicine, 2020, 12, .	5.8	12

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19	Mass-spectrometry-based draft of the Arabidopsis proteome. Nature, 2020, 579, 409-414.	13.7	328
20	Selective targeting of BD1 and BD2 of the BET proteins in cancer and immunoinflammation. Science, 2020, 368, 387-394.	6.0	274
21	Extended pharmacodynamic responses observed upon PROTAC-mediated degradation of RIPK2. Communications Biology, 2020, 3, 140.	2.0	125
22	Identifying drug targets in tissues and whole blood with thermal-shift profiling. Nature Biotechnology, 2020, 38, 303-308.	9.4	111
23	Meltome atlasâ€"thermal proteome stability across the tree of life. Nature Methods, 2020, 17, 495-503.	9.0	152
24	Loss of N-Glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines. G3: Genes, Genomes, Genetics, 2020, 10, 1585-1597.	0.8	14
25	Biological plasticity rescues target activity in CRISPR knock outs. Nature Methods, 2019, 16, 1087-1093.	9.0	159
26	Chemical proteomics reveals target selectivity of clinical Jak inhibitors in human primary cells. Scientific Reports, 2019, 9, 14159.	1.6	39
27	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. Molecular and Cellular Proteomics, 2019, 18, 2506-2515.	2.5	75
28	Discovery of GSK8612, a Highly Selective and Potent TBK1 Inhibitor. ACS Medicinal Chemistry Letters, 2019, 10, 780-785.	1.3	48
29	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. Nature Communications, 2019, 10, 1155.	5.8	181
30	Advanced proteomics approaches to unravel protein homeostasis. Drug Discovery Today: Technologies, 2019, 31, 99-108.	4.0	17
31	PROTAC-Mediated Degradation of Brutonâ€™s Tyrosine Kinase Is Inhibited by Covalent Binding. ACS Chemical Biology, 2019, 14, 342-347.	1.6	122
32	Systematic analysis of protein turnover in primary cells. Nature Communications, 2018, 9, 689.	5.8	280
33	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. Cell, 2018, 173, 260-274.e25.	13.5	186
34	Selectively Targeting the Kinome-Conserved Lysine of PI3KÎ´ as a General Approach to Covalent Kinase Inhibition. Journal of the American Chemical Society, 2018, 140, 932-939.	6.6	73
35	Design of amidobenzimidazole STING receptor agonists with systemic activity. Nature, 2018, 564, 439-443.	13.7	505
36	Tau interactome mappingÂbased identification of Otub1 as Tau deubiquitinase involved in accumulation of pathological Tau forms in vitro and in vivo. Acta Neuropathologica, 2017, 133, 731-749.	3.9	74

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37	Activation of the Amino Acid Response Pathway Blunts the Effects of Cardiac Stress. Journal of the American Heart Association, 2017, 6, .	1.6	26
38	Antimalarial efficacy of MMV390048, an inhibitor of Plasmodium phosphatidylinositol 4-kinase. Science Translational Medicine, 2017, 9, .	5.8	204
39	Discovery of a Highly Selective Tankyrase Inhibitor Displaying Growth Inhibition Effects against a Diverse Range of Tumor Derived Cell Lines. Journal of Medicinal Chemistry, 2017, 60, 5455-5471.	2.9	24
40	Monitoring Cell-surface N-Glycoproteome Dynamics by Quantitative Proteomics Reveals Mechanistic Insights into Macrophage Differentiation. Molecular and Cellular Proteomics, 2017, 16, 770-785.	2.5	41
41	Monitoring Dynamic Changes of the Cell Surface Glycoproteome by Quantitative Proteomics. Methods in Molecular Biology, 2017, 1647, 47-59.	0.4	0
42	Differential Kinobeads Profiling for Target Identification of Irreversible Kinase Inhibitors. ACS Chemical Biology, 2017, 12, 2515-2521.	1.6	26
43	Wilhelm et al. reply. Nature, 2017, 547, E23-E23.	13.7	7
44	Drug-perturbation-based stratification of blood cancer. Journal of Clinical Investigation, 2017, 128, 427-445.	3.9	124
45	A Modular Probe Strategy for Drug Localization, Target Identification and Target Occupancy Measurement on Single Cell Level. ACS Chemical Biology, 2016, 11, 2541-2550.	1.6	70
46	Interrogating the Druggability of the 2-Oxoglutarate-Dependent Dioxygenase Target Class by Chemical Proteomics. ACS Chemical Biology, 2016, 11, 2002-2010.	1.6	36
47	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. Nature Chemical Biology, 2016, 12, 908-910.	3.9	189
48	THPP target assignment reveals EchA6 as an essential fatty acid shuttle in mycobacteria. Nature Microbiology, 2016, 1, 15006.	5.9	57
49	Potent and selective chemical probe of hypoxic signalling downstream of HIF-Î± hydroxylation via VHL inhibition. Nature Communications, 2016, 7, 13312.	5.8	167
50	Identification of KasA as the cellular target of an anti-tubercular scaffold. Nature Communications, 2016, 7, 12581.	5.8	72
51	Mutational Analysis of Glycogen Synthase Kinase 3Î² Protein Kinase Together with Kinome-Wide Binding and Stability Studies Suggests Context-Dependent Recognition of Kinases by the Chaperone Heat Shock Protein 90. Molecular and Cellular Biology, 2016, 36, 1007-1018.	1.1	9
52	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. ACS Chemical Biology, 2016, 11, 1245-1254.	1.6	82
53	Discovery of Novel Small Molecules that Activate Satellite Cell Proliferation and Enhance Repair of Damaged Muscle. ACS Chemical Biology, 2016, 11, 518-529.	1.6	16
54	Discovery and Characterization of GSK2801, a Selective Chemical Probe for the Bromodomains BAZ2A and BAZ2B. Journal of Medicinal Chemistry, 2016, 59, 1410-1424.	2.9	133

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55	Catalytic in vivo protein knockdown by small-molecule PROTACs. Nature Chemical Biology, 2015, 11, 611-617.	3.9	879
56	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. Molecular and Cellular Proteomics, 2015, 14, 2394-2404.	2.5	350
57	New IDH1 mutant inhibitors for treatment of acute myeloid leukemia. Nature Chemical Biology, 2015, 11, 878-886.	3.9	151
58	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. Nature Methods, 2015, 12, 1129-1131.	9.0	244
59	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. Nature Protocols, 2015, 10, 1567-1593.	5.5	481
60	New Allosteric Inhibitors of Mutant IDH1 in Acute Myeloid Leukemia. Blood, 2015, 126, 787-787.	0.6	1
61	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. Molecular and Cellular Proteomics, 2014, 13, 3709-3715.	2.5	98
62	Mass-spectrometry-based draft of the human proteome. Nature, 2014, 509, 582-587.	13.7	1,697
63	Kruidenier et al. reply. Nature, 2014, 514, E2-E2.	13.7	18
64	The Commonly Used PI3-Kinase Probe LY294002 Is an Inhibitor of BET Bromodomains. ACS Chemical Biology, 2014, 9, 495-502.	1.6	97
65	Ion Coalescence of Neutron Encoded TMT 10-Plex Reporter Ions. Analytical Chemistry, 2014, 86, 3594-3601.	3.2	235
66	Chemoproteomics Reveals Time-Dependent Binding of Histone Deacetylase Inhibitors to Endogenous Repressor Complexes. ACS Chemical Biology, 2014, 9, 1736-1746.	1.6	52
67	Tracking cancer drugs in living cells by thermal profiling of the proteome. Science, 2014, 346, 1255784.	6.0	812
68	The structure based design of dual HDAC/BET inhibitors as novel epigenetic probes. MedChemComm, 2014, 5, 342-351.	3.5	66
69	Mapping Protein Complexes Using Covalently Linked Antibodies and Isobaric Mass Tags. Methods in Molecular Biology, 2014, 1156, 279-291.	0.4	4
70	Quantifying Small Molecule-Induced Changes in Cellular Protein Expression and Posttranslational Modifications Using Isobaric Mass Tags. Methods in Molecular Biology, 2014, 1156, 431-443.	0.4	1
71	Increased expression of BIN1 mediates Alzheimer genetic risk by modulating tau pathology. Molecular Psychiatry, 2013, 18, 1225-1234.	4.1	321
72	Affinity Profiling of the Cellular Kinome for the Nucleotide Cofactors ATP, ADP, and GTP. ACS Chemical Biology, 2013, 8, 599-607.	1.6	73

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73	Measuring and Managing Ratio Compression for Accurate iTRAQ/TMT Quantification. Journal of Proteome Research, 2013, 12, 3586-3598.	1.8	238
74	Mass Spectrometry-Based Chemoproteomic Approaches. Methods in Molecular Biology, 2012, 803, 3-13.	0.4	8
75	Mass spectrometry approaches to monitor proteinâ€“drug interactions. Methods, 2012, 57, 430-440.	1.9	22
76	Chemical Proteomic Analysis Reveals the Drugability of the Kinome of Trypanosoma brucei. ACS Chemical Biology, 2012, 7, 1858-1865.	1.6	53
77	A selective jumonji H3K27 demethylase inhibitor modulates the proinflammatory macrophage response. Nature, 2012, 488, 404-408.	13.7	822
78	Hsp90 inhibition differentially destabilises MAP kinase and TGF-beta signalling components in cancer cells revealed by kinase-targeted chemoproteomics. BMC Cancer, 2012, 12, 38.	1.1	41
79	Affinity Purification of Proteins Binding to Kinase Inhibitors Immobilized on Self-Assembling Monolayers. Methods in Molecular Biology, 2012, 795, 149-160.	0.4	0
80	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. Analytical and Bioanalytical Chemistry, 2012, 404, 939-965.	1.9	695
81	High-Resolution Enabled TMT 8-plexing. Analytical Chemistry, 2012, 84, 7188-7194.	3.2	181
82	Quantitative mass spectrometry in proteomics. Analytical and Bioanalytical Chemistry, 2012, 404, 937-938.	1.9	27
83	A selective inhibitor reveals PI3KÎ³ dependence of TH17 cell differentiation. Nature Chemical Biology, 2012, 8, 576-582.	3.9	136
84	Mass Spectrometry-Based Proteomics in Preclinical Drug Discovery. Chemistry and Biology, 2012, 19, 72-84.	6.2	156
85	Chemoproteomic approaches to drug target identification and drug profiling. Bioorganic and Medicinal Chemistry, 2012, 20, 1973-1978.	1.4	88
86	Determination of Kinase Inhibitor Potencies in Cell Extracts by Competition Binding Assays and Isobaric Mass Tags. Methods in Molecular Biology, 2012, 803, 141-155.	0.4	2
87	Inhibition of BET recruitment to chromatin as an effective treatment for MLL-fusion leukaemia. Nature, 2011, 478, 529-533.	13.7	1,354
88	Chemoproteomics-Based Design of Potent LRRK2-Selective Lead Compounds That Attenuate Parkinsonâ€™s Disease-Related Toxicity in Human Neurons. ACS Chemical Biology, 2011, 6, 1021-1028.	1.6	131
89	Delayed Fragmentation and Optimized Isolation Width Settings for Improvement of Protein Identification and Accuracy of Isobaric Mass Tag Quantification on Orbitrap-Type Mass Spectrometers. Analytical Chemistry, 2011, 83, 8959-8967.	3.2	102
90	Chemoproteomics-based kinome profiling and target deconvolution of clinical multi-kinase inhibitors in primary chronic lymphocytic leukemia cells. Leukemia, 2011, 25, 89-100.	3.3	74

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91	Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. Nature Biotechnology, 2011, 29, 255-265.	9.4	597
92	Confident Phosphorylation Site Localization Using the Mascot Delta Score. Molecular and Cellular Proteomics, 2011, 10, S1-S12.	2.5	247
93	Inhibition of BET Recruitment to Chromatin As An Effective Treatment for MLL-Fusion Leukaemia. Blood, 2011, 118, 55-55.	0.6	5
94	Targeted data acquisition for improved reproducibility and robustness of proteomic mass spectrometry assays. Journal of the American Society for Mass Spectrometry, 2010, 21, 1668-1679.	1.2	83
95	H-Score, a Mass Accuracy Driven Rescoring Approach for Improved Peptide Identification in Modification Rich Samples. Journal of Proteome Research, 2010, 9, 5511-5516.	1.8	34
96	Evaluation of Data Analysis Strategies for Improved Mass Spectrometry-Based Phosphoproteomics. Analytical Chemistry, 2010, 82, 9843-9849.	3.2	8
97	Class III Phosphatidylinositol 4-Kinase Alpha and Beta Are Novel Host Factor Regulators of Hepatitis C Virus Replication. Journal of Virology, 2009, 83, 10058-10074.	1.5	179
98	Revealing promiscuous drugâ€“target interactions by chemical proteomics. Drug Discovery Today, 2009, 14, 1021-1029.	3.2	134
99	Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167.	9.4	155
100	Chemical and Pathway Proteomics. Molecular and Cellular Proteomics, 2008, 7, 1887-1901.	2.5	43
101	Robust and Sensitive iTRAQ Quantification on an LTQ Orbitrap Mass Spectrometer. Molecular and Cellular Proteomics, 2008, 7, 1702-1713.	2.5	219
102	Pathway Proteomics and Chemical Proteomics Team Up in Drug Discovery. Neurodegenerative Diseases, 2007, 4, 270-280.	0.8	19
103	Quantitative chemical proteomics reveals mechanisms of action of clinical ABL kinase inhibitors. Nature Biotechnology, 2007, 25, 1035-1044.	9.4	979
104	Quantitative mass spectrometry in proteomics: a critical review. Analytical and Bioanalytical Chemistry, 2007, 389, 1017-1031.	1.9	1,448
105	Differential proteome analysis and mass spectrometric characterization of germ line development-related proteins ofCaenorhabditis elegans. Proteomics, 2004, 4, 2283-2295.	1.3	32
106	Femtomol sensitivity post-digest18O labeling for relative quantification of differential protein complex composition. Rapid Communications in Mass Spectrometry, 2004, 18, 869-876.	0.7	55
107	Proteome Analysis of Diseased Joints from Mice Suffering from Collagen-Induced Arthritis. Clinical Chemistry and Laboratory Medicine, 2003, 41, 1622-32.	1.4	24
108	Mass spectrometric proteome analyses of synovial fluids and plasmas from patients suffering from rheumatoid arthritis and comparison to reactive arthritis or osteoarthritis. Electrophoresis, 2002, 23, 3445-3456.	1.3	174

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109	An improved two-step calibration method for matrix-assisted laser desorption/ionization time-of-flight mass spectra for proteomics. Rapid Communications in Mass Spectrometry, 2002, 16, 1892-1895.	0.7	14
110	Rational design and molecular characterization of a chimaeric response regulator protein. Journal of Molecular Biology, 2001, 310, 283-290.	2.0	10
111	Dimerization of signalling modules of the EvgAS and BvgAS phosphorelay systems. BBA - Proteins and Proteomics, 2000, 1478, 341-354.	2.1	25
112	Structure-function relationships in the Bvg and Evg two-component phosphorelay systems. International Journal of Medical Microbiology, 2000, 290, 317-323.	1.5	8
113	Identification of Linker Regions and Domain Borders of the Transcription Activator Protein NtrC fromEscherichia coliby Limited Proteolysis,In-GelDigestion, and Mass Spectrometryâ€. Biochemistry, 1999, 38, 11012-11020.	1.2	36
114	Probing the tertiary structure of multidomain proteins by limited proteolysis and mass spectrometry. European Journal of Mass Spectrometry, 1998, 4, 279.	0.7	11