

Marcus Bantscheff

List of Publications by Year in descending order

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114
papers

18,981
citations

23567

58
h-index

21540

114
g-index

128
all docs

128
docs citations

128
times ranked

27187
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.	27.8	1,697
2	Quantitative mass spectrometry in proteomics: a critical review. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 1017-1031.	3.7	1,448
3	Inhibition of BET recruitment to chromatin as an effective treatment for MLL-fusion leukaemia. <i>Nature</i> , 2011, 478, 529-533.	27.8	1,354
4	Quantitative chemical proteomics reveals mechanisms of action of clinical ABL kinase inhibitors. <i>Nature Biotechnology</i> , 2007, 25, 1035-1044.	17.5	979
5	Catalytic in vivo protein knockdown by small-molecule PROTACs. <i>Nature Chemical Biology</i> , 2015, 11, 611-617.	8.0	879
6	A selective jumonji H3K27 demethylase inhibitor modulates the proinflammatory macrophage response. <i>Nature</i> , 2012, 488, 404-408.	27.8	822
7	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , 2014, 346, 1255-784.	12.6	812
8	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 939-965.	3.7	695
9	Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. <i>Nature Biotechnology</i> , 2011, 29, 255-265.	17.5	597
10	Design of amidobenzimidazole STING receptor agonists with systemic activity. <i>Nature</i> , 2018, 564, 439-443.	27.8	505
11	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. <i>Nature Protocols</i> , 2015, 10, 1567-1593.	12.0	481
12	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2394-2404.	3.8	350
13	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.	27.8	328
14	Increased expression of BIN1 mediates Alzheimer genetic risk by modulating tau pathology. <i>Molecular Psychiatry</i> , 2013, 18, 1225-1234.	7.9	321
15	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018, 9, 689.	12.8	280
16	Selective targeting of BD1 and BD2 of the BET proteins in cancer and immunoinflammation. <i>Science</i> , 2020, 368, 387-394.	12.6	274
17	Confident Phosphorylation Site Localization Using the Mascot Delta Score. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S12.	3.8	247
18	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , 2015, 12, 1129-1131.	19.0	244

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19	Measuring and Managing Ratio Compression for Accurate iTRAQ/TMT Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 3586-3598.	3.7	238
20	Ion Coalescence of Neutron Encoded TMT 10-Plex Reporter Ions. <i>Analytical Chemistry</i> , 2014, 86, 3594-3601.	6.5	235
21	Robust and Sensitive iTRAQ Quantification on an LTQ Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1702-1713.	3.8	219
22	Antimalarial efficacy of MMV390048, an inhibitor of <i>Plasmodium</i> phosphatidylinositol 4-kinase. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	204
23	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. <i>Nature Chemical Biology</i> , 2016, 12, 908-910.	8.0	189
24	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. <i>Cell</i> , 2018, 173, 260-274.e25.	28.9	186
25	High-Resolution Enabled TMT 8-plexing. <i>Analytical Chemistry</i> , 2012, 84, 7188-7194.	6.5	181
26	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , 2019, 10, 1155.	12.8	181
27	Class III Phosphatidylinositol 4-Kinase Alpha and Beta Are Novel Host Factor Regulators of Hepatitis C Virus Replication. <i>Journal of Virology</i> , 2009, 83, 10058-10074.	3.4	179
28	Mass spectrometric proteome analyses of synovial fluids and plasmas from patients suffering from rheumatoid arthritis and comparison to reactive arthritis or osteoarthritis. <i>Electrophoresis</i> , 2002, 23, 3445-3456.	2.4	174
29	Potent and selective chemical probe of hypoxic signalling downstream of HIF-1 α hydroxylation via VHL inhibition. <i>Nature Communications</i> , 2016, 7, 13312.	12.8	167
30	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019, 16, 1087-1093.	19.0	159
31	Mass Spectrometry-Based Proteomics in Preclinical Drug Discovery. <i>Chemistry and Biology</i> , 2012, 19, 72-84.	6.0	156
32	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
33	Meltome atlas thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	19.0	152
34	New IDH1 mutant inhibitors for treatment of acute myeloid leukemia. <i>Nature Chemical Biology</i> , 2015, 11, 878-886.	8.0	151
35	SARS-CoV-2 drives JAK1/2-dependent local complement hyperactivation. <i>Science Immunology</i> , 2021, 6, .	11.9	144
36	A selective inhibitor reveals PI3K β dependence of TH17 cell differentiation. <i>Nature Chemical Biology</i> , 2012, 8, 576-582.	8.0	136

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37	Revealing promiscuous drug-target interactions by chemical proteomics. <i>Drug Discovery Today</i> , 2009, 14, 1021-1029.	6.4	134
38	Discovery and Characterization of GSK2801, a Selective Chemical Probe for the Bromodomains BAZ2A and BAZ2B. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 1410-1424.	6.4	133
39	Chemoproteomics-Based Design of Potent LRRK2-Selective Lead Compounds That Attenuate Parkinson's Disease-Related Toxicity in Human Neurons. <i>ACS Chemical Biology</i> , 2011, 6, 1021-1028.	3.4	131
40	Extended pharmacodynamic responses observed upon PROTAC-mediated degradation of RIPK2. <i>Communications Biology</i> , 2020, 3, 140.	4.4	125
41	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	8.2	124
42	PROTAC-Mediated Degradation of Bruton's Tyrosine Kinase Is Inhibited by Covalent Binding. <i>ACS Chemical Biology</i> , 2019, 14, 342-347.	3.4	122
43	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , 2020, 38, 303-308.	17.5	111
44	The emerging role of mass spectrometry-based proteomics in drug discovery. <i>Nature Reviews Drug Discovery</i> , 2022, 21, 637-654.	46.4	110
45	Delayed Fragmentation and Optimized Isolation Width Settings for Improvement of Protein Identification and Accuracy of Isobaric Mass Tag Quantification on Orbitrap-Type Mass Spectrometers. <i>Analytical Chemistry</i> , 2011, 83, 8959-8967.	6.5	102
46	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. <i>Nature Cancer</i> , 2021, 2, 1002-1017.	13.2	99
47	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.	3.8	98
48	The Commonly Used PI3-Kinase Probe LY294002 Is an Inhibitor of BET Bromodomains. <i>ACS Chemical Biology</i> , 2014, 9, 495-502.	3.4	97
49	Chemoproteomic approaches to drug target identification and drug profiling. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 1973-1978.	3.0	88
50	Targeted data acquisition for improved reproducibility and robustness of proteomic mass spectrometry assays. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1668-1679.	2.8	83
51	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2016, 11, 1245-1254.	3.4	82
52	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2506-2515.	3.8	75
53	Chemoproteomics-based kinome profiling and target deconvolution of clinical multi-kinase inhibitors in primary chronic lymphocytic leukemia cells. <i>Leukemia</i> , 2011, 25, 89-100.	7.2	74
54	Tau interactome mapping-based identification of Otub1 as Tau deubiquitinase involved in accumulation of pathological Tau forms in vitro and in vivo. <i>Acta Neuropathologica</i> , 2017, 133, 731-749.	7.7	74

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55	Affinity Profiling of the Cellular Kinome for the Nucleotide Cofactors ATP, ADP, and GTP. <i>ACS Chemical Biology</i> , 2013, 8, 599-607.	3.4	73
56	Selectively Targeting the Kinome-Conserved Lysine of PI3K β as a General Approach to Covalent Kinase Inhibition. <i>Journal of the American Chemical Society</i> , 2018, 140, 932-939.	13.7	73
57	Identification of KasA as the cellular target of an anti-tubercular scaffold. <i>Nature Communications</i> , 2016, 7, 12581.	12.8	72
58	A Modular Probe Strategy for Drug Localization, Target Identification and Target Occupancy Measurement on Single Cell Level. <i>ACS Chemical Biology</i> , 2016, 11, 2541-2550.	3.4	70
59	The structure based design of dual HDAC/BET inhibitors as novel epigenetic probes. <i>MedChemComm</i> , 2014, 5, 342-351.	3.4	66
60	Discovery and Characterisation of Highly Cooperative FAK β -Degrading PROTACs. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 23327-23334.	13.8	58
61	THPP target assignment reveals EchA6 as an essential fatty acid shuttle in mycobacteria. <i>Nature Microbiology</i> , 2016, 1, 15006.	13.3	57
62	Femtomol sensitivity post-digest ¹⁸ O labeling for relative quantification of differential protein complex composition. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 869-876.	1.5	55
63	Chemical Proteomic Analysis Reveals the Drugability of the Kinome of <i>Trypanosoma brucei</i> . <i>ACS Chemical Biology</i> , 2012, 7, 1858-1865.	3.4	53
64	Chemoproteomics Reveals Time-Dependent Binding of Histone Deacetylase Inhibitors to Endogenous Repressor Complexes. <i>ACS Chemical Biology</i> , 2014, 9, 1736-1746.	3.4	52
65	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. <i>Nature Methods</i> , 2021, 18, 84-91.	19.0	49
66	Discovery of GSK8612, a Highly Selective and Potent TBK1 Inhibitor. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 780-785.	2.8	48
67	Chemical and Pathway Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1887-1901.	3.8	43
68	Hsp90 inhibition differentially destabilises MAP kinase and TGF-beta signalling components in cancer cells revealed by kinase-targeted chemoproteomics. <i>BMC Cancer</i> , 2012, 12, 38.	2.6	41
69	Monitoring Cell-surface N-Glycoproteome Dynamics by Quantitative Proteomics Reveals Mechanistic Insights into Macrophage Differentiation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 770-785.	3.8	41
70	Chemical proteomics reveals target selectivity of clinical Jak inhibitors in human primary cells. <i>Scientific Reports</i> , 2019, 9, 14159.	3.3	39
71	Identification of Linker Regions and Domain Borders of the Transcription Activator Protein NtrC from <i>Escherichia coli</i> by Limited Proteolysis, In-Gel Digestion, and Mass Spectrometry. <i>Biochemistry</i> , 1999, 38, 11012-11020.	2.5	36
72	Interrogating the Druggability of the 2-Oxoglutarate-Dependent Dioxygenase Target Class by Chemical Proteomics. <i>ACS Chemical Biology</i> , 2016, 11, 2002-2010.	3.4	36

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73	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.	3.7	34
74	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020, 11, 5783.	12.8	34
75	Ca ²⁺ signals critical for egress and gametogenesis in malaria parasites depend on a multipass membrane protein that interacts with PKG. <i>Science Advances</i> , 2021, 7, .	10.3	34
76	Differential proteome analysis and mass spectrometric characterization of germ line development-related proteins of <i>Caenorhabditis elegans</i> . <i>Proteomics</i> , 2004, 4, 2283-2295.	2.2	32
77	Improved Proteomics-Based Drug Mechanism-of-Action Studies Using 16-Plex Isobaric Mass Tags. <i>Journal of Proteome Research</i> , 2021, 20, 1792-1801.	3.7	29
78	Quantitative mass spectrometry in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 937-938.	3.7	27
79	Activation of the Amino Acid Response Pathway Blunts the Effects of Cardiac Stress. <i>Journal of the American Heart Association</i> , 2017, 6, .	3.7	26
80	Differential Kinobeads Profiling for Target Identification of Irreversible Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2017, 12, 2515-2521.	3.4	26
81	Dimerization of signalling modules of the EvgAS and BvgAS phosphorelay systems. <i>BBA - Proteins and Proteomics</i> , 2000, 1478, 341-354.	2.1	25
82	Proteome Analysis of Diseased Joints from Mice Suffering from Collagen-Induced Arthritis. <i>Clinical Chemistry and Laboratory Medicine</i> , 2003, 41, 1622-32.	2.3	24
83	Discovery of a Highly Selective Tankyrase Inhibitor Displaying Growth Inhibition Effects against a Diverse Range of Tumor Derived Cell Lines. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5455-5471.	6.4	24
84	BRD4 methylation by the methyltransferase SETD6 regulates selective transcription to control mRNA translation. <i>Science Advances</i> , 2021, 7, .	10.3	23
85	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. <i>Nature Cancer</i> , 2021, 2, 1002-1017.	13.2	23
86	Mass spectrometry approaches to monitor protein-drug interactions. <i>Methods</i> , 2012, 57, 430-440.	3.8	22
87	Pathway Proteomics and Chemical Proteomics Team Up in Drug Discovery. <i>Neurodegenerative Diseases</i> , 2007, 4, 270-280.	1.4	19
88	Kruidenier et al. reply. <i>Nature</i> , 2014, 514, E2-E2.	27.8	18
89	Advanced proteomics approaches to unravel protein homeostasis. <i>Drug Discovery Today: Technologies</i> , 2019, 31, 99-108.	4.0	17
90	Discovery of Novel Small Molecules that Activate Satellite Cell Proliferation and Enhance Repair of Damaged Muscle. <i>ACS Chemical Biology</i> , 2016, 11, 518-529.	3.4	16

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91	Optimization of Orally Bioavailable PI3K ^Î Inhibitors and Identification of Vps34 as a Key Selectivity Target. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 638-655.	6.4	15
92	An improved two-step calibration method for matrix-assisted laser desorption/ionization time-of-flight mass spectra for proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 1892-1895.	1.5	14
93	Loss of N-Glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1585-1597.	1.8	14
94	CDK12 inhibition reduces abnormalities in cells from patients with myotonic dystrophy and in a mouse model. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	12
95	Probing the tertiary structure of multidomain proteins by limited proteolysis and mass spectrometry. <i>European Journal of Mass Spectrometry</i> , 1998, 4, 279.	0.7	11
96	Rational design and molecular characterization of a chimaeric response regulator protein. <i>Journal of Molecular Biology</i> , 2001, 310, 283-290.	4.2	10
97	Mutational Analysis of Glycogen Synthase Kinase 3 ^Î Protein Kinase Together with Kinome-Wide Binding and Stability Studies Suggests Context-Dependent Recognition of Kinases by the Chaperone Heat Shock Protein 90. <i>Molecular and Cellular Biology</i> , 2016, 36, 1007-1018.	2.3	9
98	Patient-derived gene and protein expression signatures of NGLY1 deficiency. <i>Journal of Biochemistry</i> , 2022, 171, 187-199.	1.7	9
99	Structure-function relationships in the Bvg and Evg two-component phosphorelay systems. <i>International Journal of Medical Microbiology</i> , 2000, 290, 317-323.	3.6	8
100	Evaluation of Data Analysis Strategies for Improved Mass Spectrometry-Based Phosphoproteomics. <i>Analytical Chemistry</i> , 2010, 82, 9843-9849.	6.5	8
101	Mass Spectrometry-Based Chemoproteomic Approaches. <i>Methods in Molecular Biology</i> , 2012, 803, 3-13.	0.9	8
102	Wilhelm et al. reply. <i>Nature</i> , 2017, 547, E23-E23.	27.8	7
103	A Bayesian semi-parametric model for thermal proteome profiling. <i>Communications Biology</i> , 2021, 4, 810.	4.4	6
104	Inhibition of BET Recruitment to Chromatin As An Effective Treatment for MLL-Fusion Leukaemia. <i>Blood</i> , 2011, 118, 55-55.	1.4	5
105	Discovery and Characterisation of Highly Cooperative FAK ^Î Degrading PROTACs. <i>Angewandte Chemie</i> , 2021, 133, 23515-23522.	2.0	4
106	Mapping Protein Complexes Using Covalently Linked Antibodies and Isobaric Mass Tags. <i>Methods in Molecular Biology</i> , 2014, 1156, 279-291.	0.9	4
107	Affinity Enrichment for Target Deconvolution and. <i>Methods in Molecular Biology</i> , 2021, 2228, 237-252.	0.9	3
108	The multi-target aspect of an Mmpl3 inhibitor: The BM212 series of compounds bind EthR2, a transcriptional regulator of ethionamide activation. <i>Cell Surface</i> , 2021, 7, 100068.	3.0	3

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109	Determination of Kinase Inhibitor Potencies in Cell Extracts by Competition Binding Assays and Isobaric Mass Tags. <i>Methods in Molecular Biology</i> , 2012, 803, 141-155.	0.9	2
110	Interval-Based Secretomics Unravels Acute-Phase Response in Hepatocyte Model Systems. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100241.	3.8	2
111	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.	0.9	1
112	New Allosteric Inhibitors of Mutant IDH1 in Acute Myeloid Leukemia. <i>Blood</i> , 2015, 126, 787-787.	1.4	1
113	Affinity Purification of Proteins Binding to Kinase Inhibitors Immobilized on Self-Assembling Monolayers. <i>Methods in Molecular Biology</i> , 2012, 795, 149-160.	0.9	0
114	Monitoring Dynamic Changes of the Cell Surface Glycoproteome by Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2017, 1647, 47-59.	0.9	0