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Tracking cancer drugs in living cells by thermal profiling of the proteome

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674	2014: signaling breakthroughs of the year. 2015 , 8, eg1		
673	Inhibitors of protein methyltransferases as chemical tools. 2015 , 7, 1327-38		12
672	Hitting the target. 2015 , 12, 1127-8		
671	Target engagement and drug residence time can be observed in living cells with BRET. 2015 , 6, 10091		153
670	Joining time-resolved thermometry and magnetic-induced heating in a single nanoparticle unveils intriguing thermal properties. 2015 , 9, 3134-42		106
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667	Functional Identification of Target by Expression Proteomics (FITeXP) reveals protein targets and highlights mechanisms of action of small molecule drugs. 2015 , 5, 11176		30
666	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. 2015 , 14, 2394-404		210
665	Global analysis of protein folding thermodynamics for disease state characterization. 2015 , 14, 2287-97		23
664	Multidimensional proteomics for cell biology. 2015 , 16, 269-80		288
663	CETSA: a target engagement assay with potential to transform drug discovery. 2015 , 7, 975-8		32

662	Proteome-wide drug and metabolite interaction mapping by thermal-stability profiling. 2015 , 12, 1055-7	145
661	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. 2015 , 12, 1129-31	173
660	Assessing the Efficacy of Mdm2/Mdm4-Inhibiting Stapled Peptides Using Cellular Thermal Shift Assays. 2015 , 5, 12116	32
659	CRKL oncogene is downregulated by p53 through miR-200s. 2015 , 106, 1033-40	18
658	Identification of drug candidates and repurposing opportunities through compound-target interaction networks. 2015 , 10, 1333-45	39
657	Limited Proteolysis Combined with Stable Isotope Labeling Reveals Conformational Changes in Protein (Pseudo)kinases upon Binding Small Molecules. 2015 , 14, 4179-93	4
656	Generation of multiple reporter ions from a single isobaric reagent increases multiplexing capacity for quantitative proteomics. 2015 , 87, 9855-63	34
655	Next-generation sequencing: hype and hope for development of personalized radiation therapy?. 2015 , 10, 183	8
654	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. 2015 , 10, 1567-93	293
653	Are label-free investigations the best approach to drug discovery?. 2015 , 7, 1561-4	10
652	A Small Molecule that Induces Intrinsic Pathway Apoptosis with Unparalleled Speed. 2015 , 13, 2027-36	48
651	Functional genomics to uncover drug mechanism of action. 2015 , 11, 942-8	58
650	Quantitative proteomics of kinase inhibitor targets and mechanisms. 2015 , 10, 201-12	23
649	Biomarker Development in Targeting Cancer Epigenetic. 2016 , 123-142	
648	Real-Time Biological Annotation of Synthetic Compounds. 2016 , 138, 8920-7	27
647	ECBS & ICBS 2015 Joint Meeting: Bringing Chemistry to Life. 2016 , 17, 447-52	2
646	A Modular Probe Strategy for Drug Localization, Target Identification and Target Occupancy Measurement on Single Cell Level. 2016 , 11, 2541-50	53
645	Chemical Dimerizers in Three-Hybrid Systems for Small Molecule-Target Protein Profiling. 2016 , 11, 2075-90	3

644	Selectivity on-target of bromodomain chemical probes by structure-guided medicinal chemistry and chemical biology. 2016 , 8, 1655-80	41
643	Trapping mammalian protein complexes in viral particles. 2016 , 7, 11416	30
642	Sample Preparation for Mass Spectrometry-Based Proteomics; from Proteomes to Peptides. 2016 , 919, 43-62	20
641	CETSA screening identifies known and novel thymidylate synthase inhibitors and slow intracellular activation of 5-fluorouracil. 2016 , 7, 11040	96
640	Small-Molecule Target Engagement in Cells. 2016 , 23, 435-41	77
639	Novel approaches to map small molecule-target interactions. 2016 , 24, 3232-45	19
638	Cellular thermal shift and clickable chemical probe assays for the determination of drug-target engagement in live cells. 2016 , 14, 6179-83	19
637	Application of Mass Spectrometry Profiling to Establish Brusatol as an Inhibitor of Global Protein Synthesis. 2016 , 15, 1220-31	61
636	Systematic Identification of Protein-Metabolite Interactions in Complex Metabolite Mixtures by Ligand-Detected Nuclear Magnetic Resonance Spectroscopy. 2016 , 55, 2590-600	13
635	Chemical proteomics approaches for identifying the cellular targets of natural products. 2016 , 33, 681-708	225
634	An industry perspective on drug target validation. 2016 , 11, 623-5	18
633	Medicinal Bioprospecting of the Amazon Rainforest: A Modern Eldorado?. 2016 , 34, 781-790	21
632	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. 2016 , 12, 908-910	120
631	Lanthanides in Luminescent Thermometry. 2016 , 49, 339-427	196
630	An Unbiased Chemical Proteomics Method Identifies FabI as the Primary Target of 6-OH-BDE-47. 2016 , 50, 11329-11336	20
629	Biophysics in drug discovery: impact, challenges and opportunities. 2016 , 15, 679-98	209
628	Mass-spectrometric exploration of proteome structure and function. 2016 , 537, 347-55	1070
627	Mission critical: the need for proteomics in the era of next-generation sequencing and precision medicine. 2016 , 25, R182-R189	18

626	Early Perspective. 2016 , 21, 1019-1033	19
625	Targeted Mass Spectrometry-Based Approach for Protein-Ligand Binding Analyses in Complex Biological Mixtures Using a Phenacyl Bromide Modification Strategy. 2016 , 88, 10987-10993	11
624	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. 2016 , 23, 1490-1503	58
623	Validation and development of MTH1 inhibitors for treatment of cancer. 2016 , 27, 2275-2283	77
622	The diverse and expanding role of mass spectrometry in structural and molecular biology. 2016 , 35, 2634-2657	160
621	Large-Scale Analysis of Breast Cancer-Related Conformational Changes in Proteins Using Limited Proteolysis. 2016 , 15, 4666-4674	20
620	Trail-blazing new directions for conditional proteomics. 2016 , 13, 917-918	
619	Kinetic Insights into the Binding between the nSH3 Domain of CrkII and Proline-Rich Motifs in cAbl. 2016 , 111, 1843-1853	7
618	cAMP-dependent protein kinase (PKA) complexes probed by complementary differential scanning fluorimetry and ion mobility-mass spectrometry. 2016 , 473, 3159-75	33
617	Studying epigenetic complexes and their inhibitors with the proteomics toolbox. 2016 , 8, 76	12
616	Thermal proteome profiling: unbiased assessment of protein state through heat-induced stability changes. 2016 , 15, 13	62
615	Binding Mechanism of the N-Terminal SH3 Domain of CrkII and Proline-Rich Motifs in cAbl. 2016 , 110, 2630-2641	14
614	Functional interdependence of BRD4 and DOT1L in MLL leukemia. 2016 , 23, 673-81	69
613	The Cellular Thermal Shift Assay: A Novel Biophysical Assay for In Situ Drug Target Engagement and Mechanistic Biomarker Studies. 2016 , 56, 141-61	156
612	The contribution of mass spectrometry-based proteomics to understanding epigenetics. 2016 , 8, 429-45	28
611	Characterizing Protein-Protein Interactions Using Mass Spectrometry: Challenges and Opportunities. 2016 , 34, 825-834	99
610	Label-free technologies for target identification and validation. 2016 , 7, 769-777	8
609	A Biologist's Field Guide to Multiplexed Quantitative Proteomics. 2016 , 15, 1489-97	44

608	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. 2016 , 11, 1245-54	58
607	Strategies in functional proteomics: Unveiling the pathways to precision oncology. 2016 , 382, 86-94	7
606	A Perspective on Implementing a Quantitative Systems Pharmacology Platform for Drug Discovery and the Advancement of Personalized Medicine. 2016 , 21, 521-34	29
605	Characterization of the <i>Saccharomyces cerevisiae</i> ATP-Interactome using the iTRAQ-SPROX Technique. 2016 , 27, 233-43	26
604	Next-generation proteomics faces new challenges in environmental biotechnology. 2016 , 38, 174-82	36
603	Advances in identification and validation of protein targets of natural products without chemical modification. 2016 , 33, 719-30	64
602	Non-stoichiometric inhibition in integrated lead finding - a literature review. 2016 , 11, 149-62	6
601	The resurgence of phenotypic screening in drug discovery and development. 2016 , 11, 121-5	32
600	Whole/Intact Cell MALDI MS Biotyping in Mammalian Cell Analysis. 2016 , 249-262	2
599	Identifying compound efficacy targets in phenotypic drug discovery. 2016 , 21, 82-89	103
598	A timeline of stable isotopes and mass spectrometry in the life sciences. 2017 , 36, 58-85	47
597	Ligand and Target Discovery by Fragment-Based Screening in Human Cells. 2017 , 168, 527-541.e29	231
596	Target engagement: Shining a light. 2017 , 13, 133-134	5
595	A PDE6 β KRas Inhibitor Chemotype with up to Seven H-Bonds and Picomolar Affinity that Prevents Efficient Inhibitor Release by Arl2. 2017 , 56, 2423-2428	63
594	From genome to proteome: Looking beyond DNA and RNA in chronic lymphocytic leukemia. 2017 , 155, 73-84	5
593	Time, space, and disorder in the expanding proteome universe. 2017 , 17, 1600399	16
592	Tau interactome mapping-based identification of Otub1 as Tau deubiquitinase involved in accumulation of pathological Tau forms in vitro and in vivo. 2017 , 133, 731-749	49
591	A PDE6 β KRas Inhibitor Chemotype with up to Seven H-Bonds and Picomolar Affinity that Prevents Efficient Inhibitor Release by Arl2. 2017 , 129, 2463-2468	4

590	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. <i>Science</i> , 2017 , 355,	33.3	198
589	Technological advances and proteomic applications in drug discovery and target deconvolution: identification of the pleiotropic effects of statins. 2017 , 22, 848-869		19
588	Non-kinase targets of protein kinase inhibitors. 2017 , 16, 424-440		72
587	Plant Chemical Genetics: From Phenotype-Based Screens to Synthetic Biology. 2017 , 174, 5-20		43
586	System-wide detection of protein-small molecule complexes suggests extensive metabolite regulation in plants. 2017 , 7, 42387		26
585	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. 2017 , 2, 17047		74
584	Covalent Protein Labeling at Glutamic Acids. 2017 , 24, 589-597.e5		50
583	In silico polypharmacology of natural products. 2018 , 19, 1153-1171		64
582	Target Engagement Measures in Preclinical Drug Discovery: Theory, Methods, and Case Studies. 2017 , 41-80		2
581	Discovery of Nicotinamide Adenine Dinucleotide Binding Proteins in the Escherichia coli Proteome Using a Combined Energetic- and Structural-Bioinformatics-Based Approach. 2017 , 16, 470-480		8
580	Ferrochelatase is a therapeutic target for ocular neovascularization. 2017 , 9, 786-801		30
579	Measuring protein structural changes on a proteome-wide scale using limited proteolysis-coupled mass spectrometry. 2017 , 12, 2391-2410		83
578	Optimization of Experimental Parameters in Data-Independent Mass Spectrometry Significantly Increases Depth and Reproducibility of Results. 2017 , 16, 2296-2309		186
577	Quantitative proteomics of model organisms. 2017 , 6, 58-66		7
576	A Primer on Concepts and Applications of Proteomics in Neuroscience. 2017 , 96, 558-571		41
575	Biomarkers of Cancer. 2017 , 273-462		1
574	Combined CRISPRi/a-Based Chemical Genetic Screens Reveal that Rigosertib Is a Microtubule-Destabilizing Agent. 2017 , 68, 210-223.e6		127
573	Sensitive and Accurate Quantitation of Phosphopeptides Using TMT Isobaric Labeling Technique. 2017 , 16, 4244-4252		16

572	Structural coverage of the proteome for pharmaceutical applications. 2017 , 22, 1792-1799	34
571	ATP alters protein folding and function of Escherichia coli uridine phosphorylase. 2017 , 634, 11-20	3
570	A network integration approach for drug-target interaction prediction and computational drug repositioning from heterogeneous information. 2017 , 8, 573	295
569	Genome-Scale Architecture of Small Molecule Regulatory Networks and the Fundamental Trade-Off between Regulation and Enzymatic Activity. 2017 , 20, 2666-2677	43
568	Mass spectrometry methods to study protein-metabolite interactions. 2017 , 12, 1271-1280	6
567	Nanoparticle Surface Functionality Dictates Cellular and Systemic Toxicity. 2017 , 29, 6578-6595	73
566	Towards detecting regulatory protein-metabolite interactions. 2017 , 39, 16-23	28
565	Cellular Assays. 2017 , 313-333	1
564	The target landscape of clinical kinase drugs. <i>Science</i> , 2017 , 358,	33-3 389
563	Chemical Biology in Drug Discovery. 2017 , 335-370	2
562	Prediction of intracellular exposure bridges the gap between target- and cell-based drug discovery. 2017 , 114, E6231-E6239	60
561	Biophysics: for HTS hit validation, chemical lead optimization, and beyond. 2017 , 12, 897-907	12
560	Measurement of drug-target engagement in live cells by two-photon fluorescence anisotropy imaging. 2017 , 12, 1472-1497	14
559	Emerging Methods in Chemoproteomics with Relevance to Drug Discovery. 2017 , 1513, 11-22	15
558	Label-free target identification using in-gel fluorescence difference thermal stability shift. 2017 , 8, 1127-1133	25
557	Detergents: Friends not foes for high-performance membrane proteomics toward precision medicine. 2017 , 17, 1600209	5
556	Dual blockade of the lipid kinase PIP4Ks and mitotic pathways leads to cancer-selective lethality. 2017 , 8, 2200	46
555	Label-Free Screening Technologies. 2017 , 416-433	0

554	Novel Molecular Challenges in Targeting Anaplastic Lymphoma Kinase in ALK-Expressing Human Cancers. 2017 , 9,	4
553	Contemporary Considerations for Discovering a Successful Medicine. 2017 , 560-576	
552	Capturing dynamic protein interactions. <i>Science</i> , 2018 , 359, 1105-1106	33-3 35
551	Targeting CDK2 overcomes melanoma resistance against BRAF and Hsp90 inhibitors. 2018 , 14, e7858	35
550	Advancing translational research and precision medicine with targeted proteomics. 2018 , 189, 1-10	44
549	Homogeneous Assay for Target Engagement Utilizing Bioluminescent Thermal Shift. 2018 , 9, 546-551	22
548	New use for CETSA: monitoring innate immune receptor stability via post-translational modification by OGT. 2018 , 50, 231-240	10
547	Thermal proteome profiling of breast cancer cells reveals proteasomal activation by CDK4/6 inhibitor palbociclib. 2018 , 37,	52
546	Global profiling of protein-DNA and protein-nucleosome binding affinities using quantitative mass spectrometry. 2018 , 9, 1653	36
545	Modulation of Protein-Interaction States through the Cell Cycle. 2018 , 173, 1481-1494.e13	80
544	Systematic analysis of protein turnover in primary cells. 2018 , 9, 689	145
543	Methods to validate Hsp90 inhibitor specificity, to identify off-target effects, and to rethink approaches for further clinical development. 2018 , 23, 467-482	58
542	Application of targeted mass spectrometry in bottom-up proteomics for systems biology research. 2018 , 189, 75-90	49
541	Structure-guided design of a potent peptide inhibitor targeting the interaction between CRK and ABL kinase. 2018 , 9, 519-524	1
540	An integrative overview of genomic, transcriptomic and proteomic analyses in organohalide respiration research. 2018 , 94,	23
539	ProteomicsDB. 2018 , 46, D1271-D1281	113
538	Targeted NUDT5 inhibitors block hormone signaling in breast cancer cells. 2018 , 9, 250	28
537	Thermal proximity coaggregation for system-wide profiling of protein complex dynamics in cells. <i>Science</i> , 2018 , 359, 1170-1177	33-3 90

536	Metabolism as a signal generator across trans-omic networks at distinct time scales. 2018 , 8, 59-66	18
535	New Perspectives, Opportunities, and Challenges in Exploring the Human Protein Kinome. 2018 , 78, 15-29	81
534	CRISPR Approaches to Small Molecule Target Identification. 2018 , 13, 366-375	41
533	A Map of Protein-Metabolite Interactions Reveals Principles of Chemical Communication. 2018 , 172, 358-372.e23	192
532	Emerging Approaches for the Identification of Protein Targets of Small Molecules - A Practitioners' Perspective. 2018 , 61, 8504-8535	38
531	Pervasive Protein Thermal Stability Variation during the Cell Cycle. 2018 , 173, 1495-1507.e18	109
530	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. 2018 , 173, 260-274.e25	125
529	Bioactive Compound Collections: From Design to Target Identification. 2018 , 4, 705-730	29
528	Kinase inhibitors: the road ahead. 2018 , 17, 353-377	447
527	Toxoplasma Calcium-Dependent Protein Kinase 1 Inhibitors: Probing Activity and Resistance Using Cellular Thermal Shift Assays. 2018 , 62,	11
526	Cell Density Affects the Detection of Chk1 Target Engagement by the Selective Inhibitor V158411. 2018 , 23, 144-153	2
525	A High-Throughput Dose-Response Cellular Thermal Shift Assay for Rapid Screening of Drug Target Engagement in Living Cells, Exemplified Using SMYD3 and IDO1. 2018 , 23, 34-46	28
524	A Vinyl Sulfone-Based Fluorogenic Probe Capable of Selective Labeling of PHGDH in Live Mammalian Cells. 2018 , 57, 579-583	27
523	A Vinyl Sulfone-Based Fluorogenic Probe Capable of Selective Labeling of PHGDH in Live Mammalian Cells. 2018 , 130, 588-592	8
522	Demonstrating In-Cell Target Engagement Using a Pirin Protein Degradation Probe (CCT367766). 2018 , 61, 918-933	61
521	Small-Molecule Kinase Downregulators. 2018 , 25, 30-35	45
520	A Step-Up LC-MS/MS for Proteomics. 2018 , 377-414	
519	Ber bisherige Denkweisen hinaus Ihre Wirkstoffe zur Berwindung der Antibiotika-Krise. 2018 , 130, 14642-14682	15

518	Chemo-Selection Strategy for Limited Proteolysis Experiments on the Proteomic Scale. 2018 , 90, 14039-14047	9
517	An efficient proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions. 2018 , 13, e0208273	22
516	Identification of Protein Targets of Bioactive Small Molecules Using Randomly Photomodified Probes. 2018 , 13, 3333-3342	7
515	Reagents for Isobaric Labeling Peptides in Quantitative Proteomics. 2018 , 90, 12366-12371	21
514	Covalent inhibitors of EGFR family protein kinases induce degradation of human Tribbles 2 (TRIB2) pseudokinase in cancer cells. 2018 , 11,	43
513	Thinking Outside the Box- Novel Antibacterials To Tackle the Resistance Crisis. 2018 , 57, 14440-14475	75
512	Proteome-Wide Structural Biology: An Emerging Field for the Structural Analysis of Proteins on the Proteomic Scale. 2018 , 17, 3614-3627	34
511	Small Molecule Targeting of Specific BAF (mSWI/SNF) Complexes for HIV Latency Reversal. 2018 , 25, 1443-1455.e14	25
510	Detection of Chemical Engagement of Solute Carrier Proteins by a Cellular Thermal Shift Assay. 2018 , 13, 1480-1486	20
509	Impact of Mass Spectrometry-Based Technologies and Strategies on Chemoproteomics as a Tool for Drug Discovery. 2018 , 9, 785-791	14
508	Identification of the Natural Product Rotihibin A as a TOR Kinase Signaling Inhibitor by Unbiased Transcriptional Profiling. 2018 , 24, 12500-12504	2
507	Thermal proteome profiling in bacteria: probing protein state. 2018 , 14, e8242	82
506	Natural Products for Drug Discovery in the 21st Century: Innovations for Novel Drug Discovery. 2018 , 19,	380
505	Innovations in improving lipid production: Algal chemical genetics. 2018 , 71, 101-123	20
504	A high content, high throughput cellular thermal stability assay for measuring drug-target engagement in living cells. 2018 , 13, e0195050	14
503	Chemical Denaturation and Protein Precipitation Approach for Discovery and Quantitation of Protein-Drug Interactions. 2018 , 90, 9249-9255	21
502	Chemoproteomics and Chemical Probes for Target Discovery. 2018 , 36, 1275-1286	57
501	Chemical proteomics, an integrated research engine for exploring drug-target-phenotype interactions. 2018 , 16, 1	5

500	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. 2018 , 17, 2284-2296	133
499	A widely-applicable high-throughput cellular thermal shift assay (CETSA) using split Nano Luciferase. 2018 , 8, 9472	42
498	Polypharmacology by Design: A Medicinal Chemist's Perspective on Multitargeting Compounds. 2019 , 62, 420-444	188
497	Thermal proteome profiling allows quantitative assessment of interactions between tetrachloroethene reductive dehalogenase and trichloroethene. 2019 , 192, 10-17	17
496	An Antitumor Bis(N-Heterocyclic Carbene)Platinum(II) Complex That Engages Asparagine Synthetase as an Anticancer Target. 2019 , 131, 11030-11034	8
495	High throughput discovery of functional protein modifications by Hotspot Thermal Profiling. 2019 , 16, 894-901	52
494	Application of Bioactive Thermal Proteome Profiling to Decipher the Mechanism of Action of the Lipid Lowering 13-Hydroxy-pheophytin Isolated from a Marine Cyanobacteria. 2019 , 17,	10
493	Target engagement approaches for pharmacological evaluation in animal models. 2019 , 55, 9241-9250	1
492	CETSA beyond Soluble Targets: a Broad Application to Multipass Transmembrane Proteins. 2019 , 14, 1913-1920	31
491	Advances in exploring the therapeutic potential of marine natural products. 2019 , 147, 104373	39
490	Mechanistic MALDI-TOF Cell-Based Assay for the Discovery of Potent and Specific Fatty Acid Synthase Inhibitors. 2019 , 26, 1322-1331.e4	7
489	ACT001, a novel PAI-1 inhibitor, exerts synergistic effects in combination with cisplatin by inhibiting PI3K/AKT pathway in glioma. 2019 , 10, 757	56
488	Target Discovery Using Thermal Proteome Profiling. 2019 , 267-291	3
487	ProteomicsDB: a multi-omics and multi-organism resource for life science research. 2020 , 48, D1153-D1163	67
486	Hydralazine targets cAMP-dependent protein kinase leading to sirtuin1/5 activation and lifespan extension in <i>C. elegans</i> . 2019 , 10, 4905	16
485	Differential PROTAC substrate specificity dictated by orientation of recruited E3 ligase. 2019 , 10, 131	188
484	Anticancer Effect of Deuterium Depleted Water - Redox Disbalance Leads to Oxidative Stress. 2019 , 18, 2373-2387	18
483	Epigenetic drug target deconvolution by mass spectrometry-based technologies. 2019 , 26, 854-857	3

482	Chemical proteomics reveals target selectivity of clinical Jak inhibitors in human primary cells. 2019 , 9, 14159	22
481	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. 2019 , 18, 2506-2515	34
480	Proteome Integral Solubility Alteration: A High-Throughput Proteomics Assay for Target Deconvolution. 2019 , 18, 4027-4037	56
479	Illuminating the dark phosphoproteome. 2019 , 12,	125
478	Effect of Sec61 interaction with Mpd1 on endoplasmic reticulum-associated degradation. 2019 , 14, e0211180	4
477	Plasma proteomic and autoantibody profiles reveal the proteomic characteristics involved in longevity families in Bama, China. 2019 , 16, 22	6
476	Mechanistic Basis of Cabotegravir-Glucuronide Disposition in Humans. 2019 , 370, 269-277	3
475	Emerging strategies for the identification of protein-metabolite interactions. 2019 , 70, 4605-4618	15
474	An Antitumor Bis(N-Heterocyclic Carbene)Platinum(II) Complex That Engages Asparagine Synthetase as an Anticancer Target. 2019 , 58, 10914-10918	31
473	Posttranslational Modifications Drive Protein Stability to Control the Dynamic Beer Brewing Proteome. 2019 , 18, 1721-1731	19
472	DO-MS: Data-Driven Optimization of Mass Spectrometry Methods. 2019 , 18, 2493-2500	31
471	Melting Down Protein Stability: PAPS Synthase 2 in Patients and in a Cellular Environment. 2019 , 6, 31	8
470	Quantifying drug-target engagement in live cells using sulfonyl fluoride chemical probes. 2019 , 622, 201-220	2
469	Chemical Epigenetics: The Impact of Chemical and Chemical Biology Techniques on Bromodomain Target Validation. 2019 , 58, 17930-17952	20
468	Global analysis of methionine oxidation provides a census of folding stabilities for the human proteome. 2019 , 116, 6081-6090	38
467	Engagement with tNOX (ENOX2) to Inhibit SIRT1 and Activate p53-Dependent and -Independent Apoptotic Pathways by Novel 4,11-Diaminoanthra[2,3]-furan-5,10-diones in Hepatocellular Carcinoma Cells. 2019 , 11,	9
466	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. 2019 , 10, 1155	88
465	Chemische Epigenetik: der Einfluss chemischer und chemo-biologischer Techniken auf die Zielstruktur-Validierung von Bromodomänen. 2019 , 131, 18096-18120	1

464	Monitoring structural modulation of redox-sensitive proteins in cells with MS-CETSA. 2019 , 24, 101168	23
463	Advanced proteomics approaches to unravel protein homeostasis. 2019 , 31, 99-108	11
462	Label-free target identification in drug discovery via phenotypic screening. 2019 , 50, 66-72	20
461	Horizontal Cell Biology: Monitoring Global Changes of Protein Interaction States with the Proteome-Wide Cellular Thermal Shift Assay (CETSA). 2019 , 88, 383-408	39
460	Protein corona formed on silver nanoparticles in blood plasma is highly selective and resistant to physicochemical changes of the solution. 2019 , 6, 1089-1098	36
459	Proteomics in Drug Development: The Dawn of a New Era?. 2019 , 13, e1800087	30
458	Mass Spectrometry and Chemical Biology in Epigenetics Drug Discovery. 2019 , 79-106	
457	Chemical Probes. 2019 , 133-152	
456	Identification of bioactive metabolites using activity metabolomics. 2019 , 20, 353-367	258
455	Label-free target identification reveals oxidative DNA damage as the mechanism of a selective cytotoxic agent. 2019 , 10, 3449-3458	14
454	CETSA-based target engagement of taxanes as biomarkers for efficacy and resistance. 2019 , 9, 19384	10
453	PROMIS: Global Analysis of PROtein-Metabolite Interactions. 2019 , 4, e20101	8
452	A new era for proteomics. 2019 , 11, 1731-1735	4
451	Label-Free Techniques for Target Discovery and Validation. 2019 , 131-152	
450	ProTargetMiner as a proteome signature library of anticancer molecules for functional discovery. 2019 , 10, 5715	16
449	Target deconvolution from phenotype-based drug discovery by using chemical proteomics approaches. 2019 , 1867, 22-27	40
448	Screening Strategies and Methods for Better Off-Target Liability Prediction and Identification of Small-Molecule Pharmaceuticals. 2019 , 24, 1-24	17
447	A one-pot analysis approach to simplify measurements of protein stability and folding kinetics. 2019 , 1867, 184-193	13

446	Identifying purine nucleoside phosphorylase as the target of quinine using cellular thermal shift assay. 2019 , 11,	81
445	Plasma proteome profiling of high-altitude polycythemia using TMT-based quantitative proteomics approach. 2019 , 194, 60-69	16
444	Monitoring and deciphering protein degradation pathways inside cells. 2019 , 31, 61-68	31
443	Proteome-wide Analysis of Protein Thermal Stability in the Model Higher Plant. 2019 , 18, 308-319	23
442	Perturbation-Based Proteomic Correlation Profiling as a Target Deconvolution Methodology. 2019 , 26, 137-143.e8	5
441	TMT-Based Quantitative Proteomic Analysis Reveals Proteomic Changes Involved in Longevity. 2019 , 13, e1800024	9
440	Lysine-Targeted Inhibitors and Chemoproteomic Probes. 2019 , 88, 365-381	42
439	A Review on Quantitative Multiplexed Proteomics. 2019 , 20, 1210-1224	110
438	Quantitative, Real-Time Measurements of Intracellular Target Engagement Using Energy Transfer. 2019 , 1888, 45-71	19
437	Target Engagement of Small Molecules: Thermal Profiling Approaches on Different Levels. 2019 , 1888, 73-98	5
436	Fluorescence anisotropy imaging in drug discovery. 2019 , 151-152, 262-288	29
435	High-Throughput Cellular Thermal Shift Assays in Research and Drug Discovery. 2020 , 25, 137-147	22
434	The future of cystic fibrosis care: a global perspective. 2020 , 8, 65-124	259
433	Tools of the Ethylene Trade: A Chemical Kit to Influence Ethylene Responses in Plants and Its Use in Agriculture. 2020 , 4, 1900267	5
432	Systematic mapping of protein-metabolite interactions with mass spectrometry-based techniques. 2020 , 64, 24-31	9
431	Modification-free approaches to screen drug targets at proteome level. 2020 , 124, 115574	8
430	Der zytotoxische Naturstoff Vioprolid A interagiert mit dem für die Ribosomen-Biogenese essentiellen nukleolären Protein 14. 2020 , 132, 1611-1617	2
429	Mass spectrometry-based Cellular Thermal Shift Assay (CETSA) for target deconvolution in phenotypic drug discovery. 2020 , 28, 115174	17

428	Perspective on CETSA Literature: Toward More Quantitative Data Interpretation. 2020 , 25, 118-126	16
427	The Cytotoxic Natural Product Vioprolide A Targets Nucleolar Protein 14, Which Is Essential for Ribosome Biogenesis. 2020 , 59, 1595-1600	24
426	Multiscale modelling of drug mechanism and safety. 2020 , 25, 519-534	10
425	Drug Target Engagement Using Coupled Cellular Thermal Shift Assay-Acoustic Reverse-Phase Protein Array. 2020 , 25, 207-214	3
424	Label-Free Proteome Profiling as a Quantitative Target Identification Technique for Bioactive Small Molecules. 2020 , 59, 213-215	0
423	Mass spectrometry analysis of the structural proteome. 2020 , 60, 57-65	13
422	Chemoproteomic profiling of protein-metabolite interactions. 2020 , 54, 28-36	7
421	The functional landscape of the human phosphoproteome. 2020 , 38, 365-373	106
420	CETSA in integrated proteomics studies of cellular processes. 2020 , 54, 54-62	16
419	Solvent-Induced Protein Precipitation for Drug Target Discovery on the Proteomic Scale. 2020 , 92, 1363-1371	21
418	Image-Based Morphological Profiling Identifies a Lysosomotropic, Iron-Sequestering Autophagy Inhibitor. 2020 , 59, 5721-5729	27
417	Identification of a Small Compound Targeting PKM2-Regulated Signaling Using 2D Gel Electrophoresis-Based Proteome-wide CETSA. 2020 , 27, 186-196.e4	21
416	The Druggability of Solute Carriers. 2020 , 63, 3834-3867	25
415	An anticancer gold(III)-activated porphyrin scaffold that covalently modifies protein cysteine thiols. 2020 , 117, 1321-1329	26
414	Hit Triage and Validation in Phenotypic Screening: Considerations and Strategies. 2020 , 27, 1332-1346	17
413	Detectives and helpers: Natural products as resources for chemical probes and compound libraries. 2020 , 216, 107688	4
412	Profiling of post-translational modifications by chemical and computational proteomics. 2020 , 56, 13506-13519	9
411	Thermal Proteome Profiling and Meltome Analysis of a Thermophilic Bacterial Strain, ARTRW1: Toward Industrial Applications. 2020 , 24, 756-765	2

410	A mass spectrometry-based proteome map of drug action in lung cancer cell lines. 2020 , 16, 1111-1119	13
409	The glyphosate formulation Roundup [®] LB plus influences the global metabolome of pig gut microbiota in vitro. 2020 , 745, 140932	8
408	Pooled protein tagging, cellular imaging, and in situ sequencing for monitoring drug action in real time. 2020 , 30, 1846-1855	3
407	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. 2020 , 11, 5783	8
406	Mutant thermal proteome profiling for characterization of missense protein variants and their associated phenotypes within the proteome. 2020 , 295, 16219-16238	9
405	Direct label-free methods for identification of target proteins in agrochemicals. 2020 , 164, 1475-1483	1
404	Selective Modulation of Dynamic Protein Complexes. 2020 , 27, 986-997	10
403	COVID-19: Nanomedicine Uncovers Blood-Clot Mystery. 2020 , 19, 4364-4373	9
402	Genetic screens reveal a central role for heme metabolism in artemisinin susceptibility. 2020 , 11, 4813	10
401	A machine learning-based chemoproteomic approach to identify drug targets and binding sites in complex proteomes. 2020 , 11, 4200	34
400	Analysis of selective target engagement by small-molecule sphingosine kinase inhibitors using the Cellular Thermal Shift Assay (CETSA). 2020 , 21, 841-852	3
399	Microparticle-Assisted Precipitation Screening Method for Robust Drug Target Identification. 2020 , 92, 13912-13921	5
398	On-Chip Acousto Thermal Shift Assay for Rapid and Sensitive Assessment of Protein Thermodynamic Stability. 2020 , 16, e2003506	4
397	Novel Broad-Spectrum Antiviral Inhibitors Targeting Host Factors Essential for Replication of Pathogenic RNA Viruses. 2020 , 12,	9
396	From Phenotypic Hit to Chemical Probe: Chemical Biology Approaches to Elucidate Small Molecule Action in Complex Biological Systems. 2020 , 25,	8
395	Culture-Independent Omics-Techniques for Microbiome-Based Molecular Therapeutics Against Infectious Diseases. 2020 , 95-114	
394	Thermostability profiling of MHC-bound peptides: a new dimension in immunopeptidomics and aid for immunotherapy design. 2020 , 11, 6305	2
393	The functional proteome landscape of Escherichia coli. 2020 , 588, 473-478	14

392	The GOLIATH Project: Towards an Internationally Harmonised Approach for Testing Metabolism Disrupting Compounds. 2020 , 21,	13
391	New approaches to antibacterial drug discovery. 2020 , 223-248	
390	A Dual-Mechanism Antibiotic Kills Gram-Negative Bacteria and Avoids Drug Resistance. 2020 , 181, 1518-1532.	88
389	Target identification of natural medicine with chemical proteomics approach: probe synthesis, target fishing and protein identification. 2020 , 5, 72	29
388	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. 2020 , 5, 1119-1133	17
387	TMTpro reagents: a set of isobaric labeling mass tags enables simultaneous proteome-wide measurements across 16 samples. 2020 , 17, 399-404	123
386	Cell-Based Ligand Discovery for the ENL YEATS Domain. 2020 , 15, 895-903	14
385	Interaction profiling methods to map protein and pathway targets of bioactive ligands. 2020 , 54, 76-84	2
384	Validation of the Applicability of In-Cell Fast Photochemical Oxidation of Proteins across Multiple Eukaryotic Cell Lines. 2020 , 31, 1372-1379	3
383	Comprehensive chemical proteomics for target deconvolution of the redox active drug auranofin. 2020 , 32, 101491	27
382	Characterizing Drug-Target Interactions: Shifting towards the Clinic. 2020 , 41, 295-297	1
381	Quantifying Target Occupancy of Small Molecules Within Living Cells. 2020 , 89, 557-581	20
380	Multiparametric Assays for Accelerating Early Drug Discovery. 2020 , 41, 318-335	8
379	Selection of Heating Temperatures Improves the Sensitivity of the Proteome Integral Solubility Alteration Assay. 2020 , 19, 2159-2166	8
378	Phenotypic Screening of Chemical Libraries Enriched by Molecular Docking to Multiple Targets Selected from Glioblastoma Genomic Data. 2020 , 15, 1424-1444	3
377	Proteomic and interactomic insights into the molecular basis of cell functional diversity. 2020 , 21, 327-340	68
376	Importance of Quantifying Drug-Target Engagement in Cells. 2020 , 11, 403-406	11
375	Monitoring protein communities and their responses to therapeutics. 2020 , 19, 414-426	19

374	Identifying the Target of an Antiparasitic Compound in Using Thermal Proteome Profiling. 2020 , 15, 1801-1807	15
373	A Simplified Thermal Proteome Profiling Approach to Screen Protein Targets of a Ligand. 2020 , 20, e1900372	4
372	Data, Reagents, Assays and Merits of Proteomics for SARS-CoV-2 Research and Testing. 2020 , 19, 1503-1522	52
371	Lysine-specific demethylase 1A restricts ex vivo propagation of human HSCs and is a target of UM171. 2020 , 136, 2151-2161	12
370	Comparative Analysis of Mass-Spectrometry-Based Proteomic Methods for Protein Target Discovery Using a One-Pot Approach. 2020 , 31, 217-226	11
369	Chemical Biology Framework to Illuminate Proteostasis. 2020 , 89, 529-555	12
368	Image-Based Morphological Profiling Identifies a Lysosomotropic, Iron-Sequestering Autophagy Inhibitor. 2020 , 132, 5770-5778	10
367	An isothermal shift assay for proteome scale drug-target identification. 2020 , 3, 75	18
366	Progress and pitfalls of using isobaric mass tags for proteome profiling. 2020 , 17, 149-161	13
365	Click Chemistry in Proteomic Investigations. 2020 , 180, 605-632	92
364	High-throughput quantitative top-down proteomics. 2020 , 16, 91-99	34
363	Chaperone mediated detection of small molecule target binding in cells. 2020 , 11, 465	1
362	Pifithrin-1 alters p53 post-translational modifications pattern and differentially inhibits p53 target genes. 2020 , 10, 1049	14
361	A misprocessed form of Apolipoprotein A-I is specifically associated with recurrent Focal Segmental Glomerulosclerosis. 2020 , 10, 1159	7
360	Identifying drug targets in tissues and whole blood with thermal-shift profiling. 2020 , 38, 303-308	46
359	Thermal Proteome Profiling Identifies Oxidative-Dependent Inhibition of the Transcription of Major Oncogenes as a New Therapeutic Mechanism for Select Anticancer Compounds. 2020 , 80, 1538-1550	9
358	Proteomic Technologies for Deciphering Local and Global Protein Interactions. 2020 , 45, 454-455	4
357	Thermal proteome profiling for interrogating protein interactions. 2020 , 16, e9232	53

356	Ethacrynic acid inhibits STAT3 activity through the modulation of SHP2 and PTP1B tyrosine phosphatases in DU145 prostate carcinoma cells. 2020 , 175, 113920	5
355	Towards a functional understanding of the plant metabolome. 2020 , 55, 47-51	20
354	Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics. 2020 , 92, 6478-6485	24
353	Meltome atlas-thermal proteome stability across the tree of life. 2020 , 17, 495-503	53
352	Cellular thermal shift assay for the identification of drug-target interactions in the Plasmodium falciparum proteome. 2020 , 15, 1881-1921	27
351	Proteome-scale studies of protein stability. 2020 , 71-90	0
350	Loss of N-Glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines. 2020 , 10, 1585-1597	5
349	Turning liabilities into opportunities: Off-target based drug repurposing in cancer. 2021 , 68, 209-229	11
348	Design of next-generation covalent inhibitors: Targeting residues beyond cysteine. 2021 , 56, 95-134	2
347	Rtpca: an R package for differential thermal proximity coaggregation analysis. 2021 , 37, 431-433	3
346	CETSA MS Profiling for a Comparative Assessment of FDA-Approved Antivirals Repurposed for COVID-19 Therapy Identifies TRIP13 as a Remdesivir Off-Target. 2021 , 26, 336-344	6
345	Isocotoin suppresses hepatitis E virus replication through inhibition of heat shock protein 90. 2021 , 185, 104997	4
344	Protein Folding Stability Changes Across the Proteome Reveal Targets of Cu Toxicity in. 2021 , 16, 214-224	7
343	Target Validation Using PROTACs: Applying the Four Pillars Framework. 2021 , 26, 474-483	7
342	ProThermDB: thermodynamic database for proteins and mutants revisited after 15 years. 2021 , 49, D420-D424	3
341	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. 2021 , 184, 545-559.e22	28
340	Thermal Proteome Profiling in Zebrafish Reveals Effects of Napabucasin on Retinoic Acid Metabolism. 2021 , 20, 100033	3
339	Applicability of Chromatographic Co-Elution for Antibiotic Target Identification. 2021 , 21, e2000038	1

338	Target Validation Prosecuting the Target. 2021,	
337	Affinity Enrichment Chemoproteomics for Target Deconvolution and Selectivity Profiling. 2021, 2228, 237-252	1
336	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatography-Mass Spectrometry (SEC-MS). 2021, 2259, 269-294	1
335	The right tools for the job: the central role for next generation chemical probes and chemistry-based target deconvolution methods in phenotypic drug discovery. 2021, 12, 646-665	2
334	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. 2021, 18, 84-91	12
333	Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. 2021, 20, 1133-1152	18
332	Selective cross-linking of coinciding protein assemblies by in-gel cross-linking mass spectrometry. 2021, 40, e106174	8
331	Mass spectrometry-based protein-protein interaction networks for the study of human diseases. 2021, 17, e8792	30
330	A Tale of Two Tails: Efficient Profiling of Protein Degraders by Specific Functional and Target Engagement Readouts. 2021, 26, 534-546	7
329	Mass spectrometry-based protein-protein interaction techniques and their applications in studies of DNA damage repair. 2021, 22, 1-20	2
328	Dynamic supramolecular self-assembly of platinum(ii) complexes perturbs an autophagy-lysosomal system and triggers cancer cell death.. 2021, 12, 15229-15238	4
327	The Relationship between the Misfolding Avoidance Hypothesis and Protein Evolutionary Rates in the Light of Empirical Evidence. 2021, 13,	4
326	System Biology-Guided Chemical Proteomics to Discover Protein Targets of Monoethylhexyl Phthalate in Regulating Cell Cycle. 2021, 55, 1842-1851	6
325	"Structuromics": another step toward a holistic view of the cell. 2021, 184, 301-303	2
324	Reproducibility in the unfolding process of protein induced by an external electric field. 2020, 12, 2030-2038	1
323	Photoaffinity labelling strategies for mapping the small molecule-protein interactome. 2021, 19, 7792-7809	8
322	Probing the methotrexate-protein interactions by proteomics and thermostability assay for drug resistance study. 2021, 13, 411-418	
321	Chemoproteomic methods for covalent drug discovery. 2021, 50, 8361-8381	5

320	Recent advances in bioanalytical methods to measure proteome stability in cells. 2021 , 146, 2097-2109	5
319	Prediction and collection of protein-metabolite interactions. 2021 , 22,	19
318	Global mapping of protein-metabolite interactions in <i>Saccharomyces cerevisiae</i> reveals that Ser-Leu dipeptide regulates phosphoglycerate kinase activity. 2021 , 4, 181	12
317	Improved Proteomics-Based Drug Mechanism-of-Action Studies Using 16-Plex Isobaric Mass Tags. 2021 , 20, 1792-1801	5
316	System-wide identification and prioritization of enzyme substrates by thermal analysis. 2021 , 12, 1296	16
315	Hidden information on protein function in censuses of proteome foldedness.	0
314	Recent advances in proteome-wide label-free target deconvolution for bioactive small molecules. 2021 , 41, 2893-2926	1
313	Reply to Ma and Wang: Reliability of various in vitro activity assays on SARS-CoV-2 main protease inhibitors. 2021 , 118,	6
312	SARS-CoV-2 infection remodels the host protein thermal stability landscape. 2021 , 17, e10188	5
311	TP-MAP - an Integrated Software Package for the Analysis of 1D and 2D Thermal Profiling Data.	0
310	Identification of Celecoxib-Targeted Proteins Using Label-Free Thermal Proteome Profiling on Rat Hippocampus. 2021 , 99, 308-318	2
309	Thermal proteome profiling identifies the membrane-bound purinergic receptor P2X4 as a target of the autophagy inhibitor indophagolin. 2021 ,	9
308	A MALDI-TOF assay identifies nilotinib as an inhibitor of inflammation in acute myeloid leukaemia.	0
307	Chemical Phosphoproteomics Sheds New Light on the Targets and Modes of Action of AKT Inhibitors. 2021 , 16, 631-641	5
306	Global Profiling of Lysine Accessibility to Evaluate Protein Structure Changes in Alzheimer's Disease. 2021 , 32, 936-945	4
305	Chemoproteomic-enabled phenotypic screening. 2021 , 28, 371-393	7
304	Probes for Photoaffinity Labelling of Kinases. 2021 , 22, 2206-2218	2
303	Infect: Optimizing Computational Workflows for Thermal Proteome Profiling Data Analysis. 2021 , 20, 1874-1888	2

302	Recent advances in identifying protein targets in drug discovery. 2021 , 28, 394-423	17
301	Progress of tubulin polymerization activity detection methods. 2021 , 37, 127698	9
300	Boosting Detection of Low-Abundance Proteins in Thermal Proteome Profiling Experiments by Addition of an Isobaric Trigger Channel to TMT Multiplexes. 2021 , 93, 7000-7010	1
299	Chemoproteomic Profiling of Covalent XPO1 Inhibitors to Assess Target Engagement and Selectivity. 2021 , 22, 2116-2123	1
298	Chd8 regulates X chromosome inactivation in mouse through fine-tuning control of Xist expression. 2021 , 4, 485	0
297	Discovery-Versus Hypothesis-Driven Detection of Protein-Protein Interactions and Complexes. 2021 , 22,	2
296	Subcellular proteomics. 2021 , 1,	13
295	A New Drug Discovery Approach Based on Thermal Proteome Profiling to Develop More Effective Drugs. 2021 , 8,	
294	Quantitative Mass Spectrometry-Based Proteomics for Biomarker Development in Ovarian Cancer. 2021 , 26,	4
293	Chemoproteomic-enabled characterization of small GTPase Rab1a as a target of an N-arylbenzimidazole ligand rescue of Parkinson-associated cell toxicity.	1
292	Hyperthermia Selectively Destabilizes Oncogenic Fusion Proteins. 2021 , 2, 388-401	13
291	Recent progress in mass spectrometry-based strategies for elucidating protein-protein interactions. 2021 , 78, 5325-5339	12
290	Thermal proteome profiling efficiently identifies ribosome destabilizing oxazolidinones. 2021 , 87, 132118	1
289	Why and How to Dig into Plant Metabolite-Protein Interactions. 2021 , 26, 472-483	12
288	Diverse Hotspot Thermal Profiling Methods Detect Phosphorylation-Dependent Changes in Protein Stability.	1
287	Principled decision-making workflow with hierarchical Bayesian models of high throughput dose-response measurements.	
286	Identification of phosphosites that alter protein thermal stability. 2021 , 18, 760-762	12
285	Thermal Analysis of a Mixture of Ribosomal Proteins by vT-ESI-MS: Toward a Parallel Approach for Characterizing the. 2021 , 93, 8484-8492	3

284	New applications of advanced instrumental techniques for the characterization of food allergenic proteins. 2021 , 1-17	3
283	Principled Decision-Making Workflow with Hierarchical Bayesian Models of High-Throughput Dose-Response Measurements. 2021 , 23,	1
282	Chemoproteomics for Plasmodium Parasite Drug Target Discovery. 2021 , 22, 2591-2599	2
281	Quantitative Chemical Proteomics Reveals Interspecies Variations on Binding Schemes of L-FABP with Perfluorooctanesulfonate. 2021 , 55, 9012-9023	0
280	Fundamentals to function: Quantitative and scalable approaches for measuring protein stability. 2021 , 12, 547-560	2
279	Systematic profiling of protein complex dynamics reveals DNA-PK phosphorylation of IFI16 en route to herpesvirus immunity. 2021 , 7,	4
278	Discovery of a β receptor antagonist by combination of unbiased cell painting and thermal proteome profiling. 2021 , 28, 848-854.e5	5
277	Receptor tyrosine kinases and cancer: oncogenic mechanisms and therapeutic approaches. 2021 , 40, 4079-4093	16
276	Tyr-Asp inhibition of glyceraldehyde 3-phosphate dehydrogenase affects plant redox metabolism. 2021 , 40, e106800	8
275	Thermal Proteome Profiling Reveals Glutathione Peroxidase 4 as the Target of the Autophagy Inducer Conophylline. 2021 , 100, 181-192	0
274	Conservation of metabolic regulation by phosphorylation and non-covalent small-molecule interactions. 2021 , 12, 538-546	2
273	A Bayesian semi-parametric model for thermal proteome profiling. 2021 , 4, 810	0
272	Thermal proteome profiling identifies PIP4K2A and ZADH2 as off-targets of Polo-like kinase 1 inhibitor volasertib. 2021 , 35, e21741	0
271	Protein mimetic amyloid inhibitor potently abrogates cancer-associated mutant p53 aggregation and restores tumor suppressor function. 2021 , 12, 3962	5
270	Impact of phosphorylation on thermal stability of proteins. 2021 , 18, 757-759	15
269	P38 β MAPK phosphorylates Snapin and reduces Snapin-mediated BACE1 transportation in APP-transgenic mice. 2021 , 35, e21691	0
268	Emerging Therapeutic Potential of SIRT6 Modulators. 2021 , 64, 9732-9758	7
267	Assessing target engagement using proteome-wide solvent shift assays.	0

266	Rapid Evaluation of Small Molecule Cellular Target Engagement with a Luminescent Thermal Shift Assay. 2021 , 12, 1288-1294	4
265	The Impact of Assay Design on Medicinal Chemistry: Case Studies. 2021 , 26, 1243-1255	0
264	Proteomics in the pharmaceutical and biotechnology industry: a look to the next decade. 2021 , 18, 503-526	5
263	Mechanical stress induced protein precipitation method for drug target screening. 2021 , 1168, 338612	3
262	Characterization of the Heat-Stable Proteome during Seed Germination in Arabidopsis with Special Focus on LEA Proteins. 2021 , 22,	2
261	Intracellular Protein-Drug Interactions Probed by Direct Mass Spectrometry of Cell Lysates. 2021 , 60, 19637-19642	3
260	The rise of proteome-wide biophysics. 2021 , 17, e10442	1
259	Degradation of CCNK/CDK12 is a druggable vulnerability of colorectal cancer. 2021 , 36, 109394	9
258	Proteomics-based target identification of natural products affecting cancer metabolism. 2021 , 74, 639-650	2
257	IFN- γ Drives Human Monocyte Differentiation into Highly Proinflammatory Macrophages That Resemble a Phenotype Relevant to Psoriasis. 2021 , 207, 555-568	2
256	Intracellular Protein-Drug Interactions Probed by Direct Mass Spectrometry of Cell Lysates. 2021 , 133, 19789-19794	
255	Sensitive Measurement of Drug-Target Engagement by a Cellular Thermal Shift Assay with Multiplex Proximity Extension Readout. 2021 , 93, 10999-11009	4
254	A Comparison of Two Stability Proteomics Methods for Drug Target Identification in OnePot 2D Format. 2021 , 16, 1445-1455	2
253	Alectinib treatment improves photodynamic therapy in cancer cell lines of different origin. 2021 , 21, 971	0
252	Characterizing Endogenous Protein Complexes with Biological Mass Spectrometry. 2021 ,	5
251	A Pan-Cancer Analysis of Transcriptome and Survival Reveals Prognostic Differentially Expressed LncRNAs and Predicts Novel Drugs for Glioblastoma Multiforme Therapy. 2021 , 12, 723725	
250	Global Mapping of Metalloproteomes. 2021 , 60, 3507-3514	1
249	Y box binding protein 1 inhibition as a targeted therapy for ovarian cancer. 2021 , 28, 1206-1220.e6	6

248	Application of omics- and multi-omics-based techniques for natural product target discovery. 2021 , 141, 111833	4
247	Natural-Product-Based Solutions for Tropical Infectious Diseases. 2021 , e0034820	1
246	Chemical Probes for Understudied Kinases: Challenges and Opportunities. 2021 ,	1
245	Kidney toxicity of the BRAF-kinase inhibitor vemurafenib is driven by off-target ferrochelatase inhibition. 2021 , 100, 1214-1226	2
244	Callyspongiolide kills cells by inducing mitochondrial dysfunction via cellular iron depletion. 2021 , 4, 1123	0
243	Discovery and Pharmacological Characterization of JNJ-64619178, a Novel Small-Molecule Inhibitor of PRMT5 with Potent Antitumor Activity. 2021 , 20, 2317-2328	5
242	Therapeutic Response Assessment of High-Grade Gliomas During Early-Phase Drug Development in the Era of Molecular and Immunotherapies. 2021 , 27, 395-403	
241	Novel perspectives of environmental proteomics. 2021 , 788, 147588	0
240	Hsp40 Affinity to Identify Proteins Destabilized by Cellular Toxicant Exposure.	
239	Drug Target Identification in Tissues by Thermal Proteome Profiling. 2021 ,	2
238	Utilizing thermal proteome profiling to identify the molecular targets of anti-leishmanial compounds. 2021 , 2, 100704	1
237	Systematic analysis of chemical-protein interactions from zebrafish embryo by proteome-wide thermal shift assay, bridging the gap between molecular interactions and toxicity pathways. 2021 , 249, 104382	2
236	Flavonoid 4,4'-dimethoxychalcone suppresses cell proliferation via dehydrogenase inhibition and oxidative stress aggravation. 2021 , 175, 206-215	1
235	Organometallic Receptors and Conjugates With Biomolecules in Bioorganometallic Chemistry. 2021 ,	
234	Nephrotoxicity of the BRAF-kinase inhibitor Vemurafenib is driven by off-target Ferrochelatase inhibition.	1
233	Label-Free Target Identification and Confirmation Using Thermal Stability Shift Assays. 2021 , 2213, 163-173	1
232	Profiling of Small Molecules by Chemical Proteomics. 2016 , 1394, 211-218	10
231	Quantitative, Wide-Spectrum Kinase Profiling in Live Cells for Assessing the Effect of Cellular ATP on Target Engagement. 2018 , 25, 206-214.e11	109

230	Target identification and validation of natural products with label-free methodology: A critical review from 2005 to 2020. 2020 , 216, 107690	12
229	Temporal dynamics of protein complex formation and dissociation during human cytomegalovirus infection. 2020 , 11, 806	33
228	Chapter 8:Fluorescent Thermal Shift Assays for Identifying Small Molecule Ligands. 208-238	2
227	Chapter 5:Contemporary Techniques for Target Deconvolution and Mode of Action Elucidation. 2020 , 83-103	1
226	Mass spectrometry-based methods for structural biology on a proteome-wide scale. 2020 , 48, 945-954	1
225	The small non-coding vault RNA1-1 acts as a riboregulator of autophagy.	1
224	Impact of phosphorylation on thermal stability of proteins.	7
223	Identification of phosphosites that alter protein thermal stability.	4
222	Computational analysis of ligand dose range thermal proteome profiles.	1
221	CETSA-MS profiling for a comparative assessment of FDA approved antivirals repurposed for COVID-19 therapy identifies Trip13 as a Remdesivir off-target.	1
220	Thermal proteome profiling of breast cancer cells reveals proteasomal activation by CDK4/6 inhibitor palbociclib.	0
219	Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins.	2
218	System-wide identification and prioritization of enzyme substrates by thermal analysis (SIESTA).	2
217	Rapid discovery of drug target engagement by isothermal shift assay.	2
216	The outer membrane lipoprotein Nlpl nucleates hydrolases within peptidoglycan multi-enzyme complexes in <i>Escherichia coli</i> .	5
215	Analysis of Independent Differences (AID) detects complex thermal proteome profiles independent of shape and identifies candidate panobinostat targets.	1
214	Towards a systematic map of the functional role of protein phosphorylation.	6
213	Computational-experimental approach to drug-target interaction mapping: A case study on kinase inhibitors. 2017 , 13, e1005678	51

212	Outer membrane lipoprotein Nlpl scaffolds peptidoglycan hydrolases within multi-enzyme complexes in Escherichia coli. 2020 , 39, e102246	36
211	Systematic mapping of protein-metabolite interactions in central metabolism of Escherichia coli. 2019 , 15, e9008	22
210	Drug mechanism-of-action discovery through the integration of pharmacological and CRISPR screens. 2020 , 16, e9405	22
209	Aggregation and disaggregation features of the human proteome. 2020 , 16, e9500	9
208	Phenotypic proteomic profiling identifies a landscape of targets for circadian clock-modulating compounds. 2019 , 2,	9
207	Analysis of Brain Protein Stability Changes in Mouse Models of Normal Aging and Synucleinopathy Reveals Age- and Disease-Related Differences. 2021 , 20, 5156-5168	2
206	Evaluation of FOXO1 Target Engagement Using a Single-Cell Microfluidic Platform. 2021 , 93, 14659-14666	0
205	Non-conserved metabolic regulation by LKB1 distinguishes human and mouse lung adenocarcinoma.	
204	High-throughput functional characterization of protein phosphorylation sites in yeast. 2021 ,	3
203	Mapping paths: new approaches to dissect eukaryotic signaling circuitry. 2016 , 5,	
202	Genome-Scale Architecture of Small Molecule Regulatory Networks and the Fundamental Trade-Off Between Regulation and Enzymatic Activity.	
201	Repurposing covalent EGFR/HER2 inhibitors for on-target degradation of human Tribbles 2 (TRIB2) pseudokinase.	
200	A novel LC system embeds analytes in pre-formed gradients for rapid, ultra-robust proteomics.	2
199	Post-translational modifications drive protein stability to control the dynamic beer brewing proteome.	0
198	ProTargetMiner: A proteome signature library of anticancer molecules for functional discovery.	1
197	Effect of Sec61 interaction with Mpd1 on Endoplasmic Reticulum- Associated Degradation.	
196	DO-MS: Data-Driven Optimization of Mass Spectrometry Methods.	0
195	TargetSeeker-MS: A Computational Method for Drug Target Discovery using Protein Separation Coupled to Mass Spectrometry.	1

194	The relationship between misfolding avoidance hypothesis and protein evolutionary rates in the light of empirical evidence.	0
193	LiP-Quant, an automated chemoproteomic approach to identify drug targets in complex proteomes.	
192	Temperature sensitive Mutant Proteome Profiling: a novel tool for the characterization of the global impact of missense mutations on the proteome.	0
191	The GFP thermal shift assay for screening ligand and lipid interactions to solute carrier transporters. 2021 , 16, 5357-5376	1
190	Experimental methods for dissecting the terra-incognita of protein-metabolite interactomes. 2021 , 100403	1
189	Boosting detection of low abundance proteins in thermal proteome profiling experiments by addition of an isobaric trigger channel to TMT multiplexes.	0
188	CHAPTER 10:Assays to Characterize the Cellular Pharmacology of a Chemical Probe. 2020 , 247-275	0
187	Aggregation and Disaggregation Features of the Human Proteome.	1
186	In-depth characterization of Staurosporine induced proteome thermal stability changes.	2
185	A dual-mechanism antibiotic targets Gram-negative bacteria and avoids drug resistance.	1
184	Identifying Protein-Drug Interactions in Cell Lysates Using Histidine Hydrogen Deuterium Exchange. 2021 , 93, 14985-14995	0
183	Selective cross-linking of coinciding protein assemblies by in-gel cross-linking mass-spectrometry.	
182	A tale of two tails - efficient profiling of protein degraders by specific functional and target engagement readouts.	
181	Off-target identification by chemical proteomics for the understanding of drug side effects. 2020 , 17, 695-697	1
180	Inflect: Optimizing Computational Workflows for Thermal Proteome Profiling Data Analysis.	
179	A Bayesian semi-parametric model for thermal proteome profiling.	
178	Showing NAFLD, as a key connector disease between Alzheimer's disease and diabetes via analysis of systems biology. 2020 , 13, S89-S97	
177	Chemoproteomic-enabled characterization of small GTPase Rab1a as a target of an -arylbenzimidazole ligand's rescue of Parkinson's-associated cell toxicity.. 2022 , 3, 96-111	2

- 176 Technique development of high-throughput and high-sensitivity sample preparation and separation for proteomics. **2022**, 14, 101-111 1
- 175 An integrative proteomics method identifies a regulator of translation during stem cell maintenance and differentiation. **2021**, 12, 6558 3
- 174 Illustrative Tutorials for ProThermDB: Thermodynamic Database for Proteins and Mutants. **2021**, 1, e306
- 173 Unexpected cause of vemurafenib-induced nephrotoxicity: ferrochelatase. **2021**, 100, 1158-1160
- 172 Comprehensive chemical proteomics analyses reveal that the new TRi-1 and TRi-2 compounds are more specific thioredoxin reductase 1 inhibitors than auranofin. **2021**, 48, 102184 3
- 171 Thermal Proteome Profiling to Identify Protein-ligand Interactions in the Apicomplexan Parasite. **2021**, 11, e4207 0
- 170 Inhibition of prolyl oligopeptidase: A promising pathway to prevent the progression of age-related macular degeneration. **2021**, 146, 112501
- 169 Experimental study of proteome halophilicity using nanoDSF: a proof of concept. **2021**, 26, 1
- 168 Quantitative Proteomics Using Isobaric Labeling: A Practical Guide.. **2022**, 6
- 167 An update of label-free protein target identification methods for natural active products.. **2022**, 12, 1829-1854 1
- 166 Precipitate-Supported Thermal Proteome Profiling Coupled with Deep Learning for Comprehensive Screening of Drug Target Proteins.. **2022**, 2
- 165 A real-time cellular thermal shift assay (RT-CETSA) to monitor target engagement.
- 164 A novel role of 3,5-BE-AMP in the regulation of actin cytoskeleton in Arabidopsis.
- 163 Integrated analysis reveals FOXA1 and Ku70/Ku80 as direct targets of ivermectin in prostate cancer.
- 162 SU086, an inhibitor of HSP90, impairs glycolysis and represents a treatment strategy for advanced prostate cancer.. **2022**, 3, 100502 3
- 161 The antimicrobial drug pyrimethamine inhibits STAT3 transcriptional activity by targeting the enzyme dihydrofolate reductase.. **2021**, 101531 4
- 160 Proteome-Wide Deconvolution of Drug Targets and Binding Sites by Lysine Reactivity Profiling.. **2022**,
- 159 Characterization of a small molecule inhibitor of disulfide reductases that induces oxidative stress and lethality in lung cancer cells.. **2022**, 38, 110343 1

158	High-Throughput Cellular Thermal Shift Assay Using Acoustic Transfer of Protein Lysates.. 2022,	2
157	Mass Spectrometry-Based Technologies for Probing the Three-Dimensional World of Plant Proteins.. 2022,	0
156	Hsp40 Affinity to Identify Proteins Destabilized by Cellular Toxicant Exposure. 2021,	0
155	A study of protein-drug interaction based on solvent-induced protein aggregation by fluorescence correlation spectroscopy.. 2022,	
154	Kurarinone alleviated Parkinson's disease via stabilization of epoxyeicosatrienoic acids in animal model.. 2022, 119,	6
153	Metabolomics paves the way for improved drug target identification.. 2022, 18, e10914	0
152	ProSAP: a GUI software tool for statistical analysis and assessment of thermal stability data.. 2022,	0
151	Past accomplishments and future challenges of the multi-omics characterization of leaf growth.. 2022,	0
150	Deep Neural Network-Assisted Drug Recommendation Systems for Identifying Potential Drug-Target Interactions.. 2022, 7, 12138-12146	2
149	Evaluating Client Protein Recovery by the Hsp40s DNAJB8 and DNAJB1 with AP-MS.	0
148	The emerging role of mass spectrometry-based proteomics in drug discovery.. 2022,	10
147	In-Cell Structural Biology by NMR: The Benefits of the Atomic Scale.. 2022,	3
146	Secretomics-A Key to a Comprehensive Picture of Unconventional Protein Secretion.. 2022, 10, 878027	0
145	Proteome-wide cellular thermal shift assay reveals unexpected cross-talk between brassinosteroid and auxin signaling.. 2022, 119, e2118220119	3
144	Regulation of Plant Primary Metabolism [How Results From Novel Technologies Are Extending Our Understanding From Classical Targeted Approaches. 1-20	0
143	Learning deep representations of enzyme thermal adaptation.	
142	Drug Mechanism Enrichment Analysis: A tool to link molecular signatures with sensitivity to drug mechanisms of action.	
141	A Recent Update on Small-molecule Kinase inhibitors for Targeted Cancer Therapy and Their Therapeutic Insights from Mass Spectrometry-based Proteomic Analysis.. 2022,	3

140	Metabolite interactions in the bacterial Calvin cycle and implications for flux regulation.	0
139	Thermal Proteome Profiling Reveals the O-GlcNAc-Dependent Meltome.. 2022 ,	3
138	NMS-873 Leads to Dysfunctional Glycometabolism in A p97-Independent Manner in HCT116 Colon Cancer Cells.. 2022 , 14,	0
137	High-Content Screening Pipeline for Natural Products Targeting Oncogenic Signaling in Melanoma.. 2022 ,	0
136	Validating Small Molecule Chemical Probes for Biological Discovery.. 2022 ,	3
135	Photoaffinity labeling and bioorthogonal ligation: Two critical tools for designing "Fish Hooks" to scout for target proteins.. 2022 , 62, 116721	3
134	Structural Alternation in Heat Shock Proteins of Activated Macrophages.. 2021 , 10,	1
133	Glycolytic flux-signaling controls mouse embryo mesoderm development.	
132	Proteome-wide cellular thermal shift assay reveals novel crosstalk between brassinosteroid and auxin signaling.	
131	Discovery of AL-GDa62 as a Potential Synthetic Lethal Lead for the Treatment of Gastric Cancer. 2021 ,	3
130	A specific inhibitor of ALDH1A3 regulates retinoic acid biosynthesis in glioma stem cells.. 2021 , 4, 1420	3
129	Assessing target engagement using proteome-wide solvent shift assays. 2021 , 10,	3
128	An overview of kinase downregulators and recent advances in discovery approaches.. 2021 , 6, 423	3
127	Mechanistic Insights into a CDK9 Inhibitor Via Orthogonal Proteomics Methods.. 2021 ,	1
126	Hidden information on protein function in censuses of proteome foldedness.. 2022 , 13, 1992	1
125	Activity-based annotation: the emergence of systems biochemistry.. 2022 ,	2
124	Matrix Thermal Shift Assay for Fast Construction of Multidimensional Ligand-Target Space.. 2022 ,	0
123	Proteome-wide identification of amino acid substitutions deleterious for protein function.	0

122	Unmodified methodologies in target discovery for small molecule drugs: A rising star. 2022,	
121	Chapter 5. Mass Spectrometry in Biophysics: from High Throughput Screening to Structural Biology. 87-119	
120	Ainsliadimer A Induces ROS-Mediated Apoptosis in Colorectal Cancer Cells via Directly Targeting Peroxiredoxin 1 and 2.	
119	Comprehensive Target Screening and Cellular Profiling of the Cancer-Active Compound b-AP15 Indicate Abrogation of Protein Homeostasis and Organelle Dysfunction as the Primary Mechanism of Action.. 2022, 12, 852980	0
118	PACTS-Assisted Thermal Proteome Profiling for Use in Identifying Peptide-Interacting Proteins.. 2022,	0
117	Integrated genomics and chemical biology herald an era of sophisticated antibacterial discovery, from defining essential genes to target elucidation.. 2022,	1
116	Ion-Based Proteome-Integrated Solubility Alteration Assays for Systemwide Profiling of Protein-Molecule Interactions.. 2022, 94, 7066-7074	0
115	Selective chemical probes can untangle the complexity of the plant cell endomembrane system.. 2022, 68, 102223	0
114	Xlink Mapping and AnalySis (XMAS) - Smooth Integrative Modeling in ChimeraX.	1
113	Rgs16 promotes antitumor CD8 + T cell exhaustion. 2022, 7,	1
112	Small Molecule Arranged Thermal Proximity Coaggregation (smarTPCA) A Novel Approach to Characterize Protein-Protein Interactions in Living Cells by Similar Isothermal Dose-Responses. 2022, 23, 5605	0
111	De novo mapping of the apicomplexan Ca ²⁺ -responsive proteome.	
110	Analytical methods for obtaining binding parameters of drug-protein interactions: A review. 2022, 340012	0
109	Deep thermal proteome profiling for detection of proteoforms and drug sensitivity biomarkers.	
108	Recent advances in isobaric labeling and applications in quantitative proteomics. 2100256	2
107	Flavonoid 4,4'-dimethoxychalcone induced ferroptosis in cancer cells by synergistically activating Keap1/Nrf2/HMOX1 pathway and inhibiting FECH. 2022, 188, 14-23	2
106	System-wide profiling by proteome integral solubility alteration assay of drug residence times for target characterization.	
105	Current Advances in CETSA. 9,	1

104	FL-DTD: an integrated pipeline to predict the drug interacting targets by feedback loop-based network analysis. 2022 , 23,	
103	Integrating knowledge and omics to decipher mechanisms via large-scale models of signaling networks. 2022 , 18,	2
102	KOPI: Kinase inhibitOr Proteome Impact analysis. 2022 , 12,	
101	Recent advances in proteomics and metabolomics in plants. 2022 , 2,	0
100	Optimization of Ultrafast Proteomics Using an LC-Quadrupole-Orbitrap Mass Spectrometer with Data-Independent Acquisition.	0
99	Temporal and thermal profiling of the Toxoplasma proteome implicates parasite Protein Phosphatase 1 in the regulation of Ca ²⁺ -responsive pathways. 11,	0
98	Exploring direct and indirect targets of current antileishmanial drugs using a novel thermal proteomics profiling approach. 12,	0
97	Quantitative Proteomics Explore the Potential Targets and Action Mechanisms of Hydroxychloroquine. 2022 , 27, 5175	
96	Evaluation of a Pooling Chemoproteomics Strategy with an FDA-Approved Drug Library.	
95	Mapping the GALNT1 substrate landscape with versatile proteomics tools.	0
94	OPDA, more than just a jasmonate precursor. 2022 , 204, 113432	3
93	Polypharmacology and Natural Products. 2022 , 625-646	0
92	The In-Cell Western immunofluorescence assay to monitor PROTAC mediated protein degradation. 2022 ,	0
91	Highly effective identification of drug targets at proteome level by pH-dependent protein precipitation.	0
90	Quantitative Detection of Protein Splice Variants by Selected Reaction Monitoring (SRM) Mass Spectrometry. 2022 , 231-246	0
89	Polypharmacology in Drug Design and DiscoveryBasis for Rational Design of Multitarget Drugs. 2022 , 397-533	0
88	Chapter 1. Chemical Approaches for Beta-cell Biology. 2022 , 1-52	0
87	Discovery and Structural Characterization of Small Molecule Binders of the Human CTLH E3 Ligase Subunit GID4.	1

86	Clinical application of advanced multi-omics tumor profiling: Shaping precision oncology of the future. 2022 , 40, 920-938	2
85	Mass Spectrometry-Based Chemical Proteomics for Drug Target Discoveries. 2022 , 87, 983-994	0
84	Metabolization and sequestration of plant specialized metabolites in insect herbivores: Current and emerging approaches. 13,	0
83	Divergent polo boxes in KKT2 bind KKT1 to initiate the kinetochore assembly cascade in <i>Trypanosoma brucei</i> .	0
82	Integrated analysis reveals FOXA1 and Ku70/Ku80 as targets of ivermectin in prostate cancer. 2022 , 13,	0
81	A Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Assay Identifies Nilotinib as an Inhibitor of Inflammation in Acute Myeloid Leukemia. 2022 , 65, 12014-12030	0
80	Cellular Target Deconvolution of Small Molecules Using a Selection-Based Genetic Screening Platform.	0
79	Coupling cellular drug-target engagement to downstream pharmacology with CeTEAM.	0
78	Real-Time Cellular Thermal Shift Assay to Monitor Target Engagement. 2022 , 17, 2471-2482	1
77	Polypharmacology-based approach for screening TCM against coinfection of <i>Mycoplasma gallisepticum</i> and <i>Escherichia coli</i> . 9,	0
76	Integrated changes in thermal stability and proteome abundance during altered nutrient states in <i>Escherichia coli</i> and human cells. 2100254	1
75	Databases and Tools to Investigate Protein-Metabolite Interactions. 2023 , 231-249	0
74	Monitoring drug-target interactions through target engagement-mediated amplification on arrays and <i>in situ</i> .	0
73	Orthogonally-tunable and ER-targeting fluorophores detect avian influenza virus early infection. 2022 , 13,	0
72	Limited Proteolysis-Mass Spectrometry to Identify Metabolite-Protein Interactions. 2023 , 69-89	0
71	Cellular Thermal Shift Assay for the Detection of Small Molecule-Target Interactions in Arabidopsis Cells. 2023 , 21-34	0
70	Chemoproteomic Mapping of Glycolytic Targetome in Cancer Cells.	0
69	Label-free LC-MS based assay to characterize small molecule compound binding to cells. 2022 , 27, 405-412	0

- 68 PROMIS: Co-fractionation Mass Spectrometry for Analysis of ProteinMetabolite Interactions. **2023**, 141-153 ○
- 67 Proteome Integral Solubility Alteration (PISA) for High-Throughput Ligand Target Deconvolution with Increased Statistical Significance and Reduced Sample Amount. **2023**, 91-106 ○
- 66 Solvent-Induced Protein Precipitation for Drug Target Discovery. **2023**, 35-45 ○
- 65 Parallel Analysis of ProteinProtein and ProteinMetabolite Complexes Using a Single-Step Affinity Purification. **2023**, 107-122 1
- 64 Divergent polo boxes in KKT2 and KKT3 initiate the kinetochore assembly cascade inTrypanosoma brucei. ○
- 63 Learning deep representations of enzyme thermal adaptation. ○
- 62 Switching of Photocatalytic Tyrosine/Histidine Labeling and Application to Photocatalytic Proximity Labeling. **2022**, 23, 11622 ○
- 61 Nonionic surfactants can modify the thermal stability of globular and membrane proteins interfering with the thermal proteome profiling principles to identify protein targets. ○
- 60 Thermal proteome profiling reveals Haemonchus orphan protein HCO_011565 as a target of the nematocidal small molecule UMW-868. 13, ○
- 59 Rewiring of the proteinproteinmetabolite interactome during the diauxic shift in yeast. **2022**, 79, ○
- 58 Mitochondrial dysfunction rapidly modulates the abundance and thermal stability of cellular proteins. ○
- 57 Proteome integral solubility alteration assay combined with multi-criteria decision-making analysis for developing adverse outcome pathways. ○
- 56 Merits of Diazirine Photo-Immobilization for Target Profiling of Natural Products and Cofactors. ○
- 55 System-Wide Profiling by Proteome Integral Solubility Alteration Assay of Drug Residence Times for Target Characterization. ○
- 54 Multi-target-based polypharmacology prediction (mTPP): An approach using virtual screening and machine learning for multi-target drug discovery. **2022**, 368, 110239 ○
- 53 Label-free target protein characterization for small molecule drugs: recent advances in methods and applications. **2023**, 223, 115107 1
- 52 Proteomic characterization of post-translational modifications in drug discovery. ○
- 51 The mycotoxin viriditoxin induces leukemia- and lymphoma-specific apoptosis by targeting mitochondrial metabolism. **2022**, 13, ○

50	Current and emerging target identification methods for novel antimalarials. 2022 ,	1
49	Preclinical efficacy of azacitidine and venetoclax for infant KMT2A-rearranged acute lymphoblastic leukemia reveals a new therapeutic strategy.	1
48	Thermal proteome profiling: Insights into protein modifications, associations, and functions. 2022 , 71, 102225	0
47	On the Feasibility of Using an Ultra-Fast DirectMS1 Method of Proteome-Wide Analysis for Searching Drug Targets in Chemical Proteomics. 2022 , 87, 1342-1353	1
46	Site-Specific Activity-Based Protein Profiling Using Phosphonate Handles. 2023 , 22, 100455	0
45	Photoaffinity Labeling Chemistries Used to Map Biomolecular Interactions.	0
44	Proteome-wide structural changes measured with limited proteolysis-mass spectrometry: an advanced protocol for high-throughput applications.	0
43	Glycolytic flux-signaling controls mouse embryo mesoderm development. 11,	0
42	Drug discovery inspired by bioactive small molecules from nature. 1-12	1
41	Mega-scale experimental analysis of protein folding stability in biology and protein design.	0
40	Analysis of Copper-Induced Protein Precipitation across the E. coli Proteome.	0
39	Discovery of a small molecule ligand of FRS2 that inhibits invasion and tumor growth.	0
38	Profiling Protein Targets of Cellular Toxicant Exposure.	0
37	Chemical Biology Approaches Confirm MCT4 as the Therapeutic Target of a Cellular Optimized Hit.	0
36	Massive solubility changes of neuronal proteins upon simulated traumatic brain injury reveal the role of shockwave in irreversible damage.	0
35	Control of protein stability by post-translational modifications. 2023 , 14,	0
34	Elucidating Protein-Ligand Interactions in Cell Lysates Using High-Throughput Hydrogen-Deuterium Exchange Mass Spectrometry with Integrated Protein Thermal Depletion.	0
33	Tandem mass tag-based thermal proteome profiling for the discovery of drug-protein interactions in cancer cells. 2023 , 4, 102012	0

32	Methods to identify protein targets of metal-based drugs. 2023 , 73, 102257	1
31	Obtaining Increased Functional Proteomics Insights from Thermal Proteome Profiling through Optimized Melt Shift Calculation and Statistical Analysis.	0
30	Mass spectrometric exploration of phytohormone profiles and signaling networks. 2022 ,	0
29	Multi-comparative Thermal Proteome Profiling Uncovers New O-GlcNAc Proteins in a System-wide Method.	0
28	EFMC Trends that Link Medicinal Chemistry and Chemical Biology to Translational Drug Discovery.	0
27	Advancing Targeted Protein Degradation via Multiomics Profiling and Artificial Intelligence. 2023 , 145, 2711-2732	0
26	Rhodojaponin VI indirectly targets Cav2.2 channels via N-ethylmaleimide-sensitive fusion protein to alleviate neuropathic pain. 2023 ,	0
25	PerTurboID: A targeted in situ method to measure changes in a local protein environment reveals the impact of kinase deletion on cytoadhesion in malaria causing parasites.	0
24	Solvent-induced proteome profiling for proteomic quantitation and target discovery of small molecular drugs. 2200281	0
23	Decrypting drug actions and protein modifications by dose- and time-resolved proteomics. 2023 , 380, 93-101	0
22	Mass spectrometry for mitochondrial multi-omics. 2023 , 117063	0
21	Extraction of active, contaminant degrading enzymes from soil. 2023 , 187, 104841	0
20	Global profiling of AMG510 modified proteins identified tumor suppressor KEAP1 as an off-target. 2023 , 26, 106080	0
19	Concentration-Dependent Enrichment Identifies Primary Protein Targets of Multitarget Bioactive Molecules. 2023 , 22, 802-811	0
18	Bioinformatics toolbox for exploring target mutation-induced drug resistance. 2023 , 24,	0
17	Nonionic Surfactants can Modify the Thermal Stability of Globular and Membrane Proteins Interfering with the Thermal Proteome Profiling Principles to Identify Protein Targets. 2023 , 95, 4033-4042	1
16	Improved in situ Characterization of Proteome-wide Protein Complex Dynamics with Thermal Proximity Co-Aggregation.	0
15	A Comparison of Quantitative Mass Spectrometric Methods for Drug Target Identification by Thermal Proteome Profiling.	0

- 14 Comparative Analysis of Protein Folding Stability-Based Profiling Methods for Characterization of Biological Phenotypes. **2023**, 34, 383-393 ○
- 13 Prediction of Molecular Initiating Events for Adverse Outcome Pathways Using High-Throughput Identification of Chemical Targets. **2023**, 11, 189 ○
- 12 Challenges and Perspectives in Target Identification and Mechanism Illustration for Chinese Medicine. ○
- 11 A novel antifolate suppresses growth of FPGS-deficient cells and overcomes methotrexate resistance. ○
- 10 The Promises of Proteomics and Metabolomics for Unravelling the Mechanism and Side Effect Landscape of Beta-Adrenoceptor Antagonists in Cardiovascular Therapeutics. **2023**, 27, 87-92 ○
- 9 Ainsliadimer A induces ROS-mediated apoptosis in colorectal cancer cells via directly targeting peroxiredoxin 1 and 2. **2023**, 30, 295-307.e5 ○
- 8 Multidimensional proteomics identifies molecular trajectories of cellular aging and rejuvenation. ○
- 7 Lactate regulates cell cycle by remodelling the anaphase promoting complex. ○
- 6 A Shift in Thinking: Cellular Thermal Shift Assay-Enabled Drug Discovery. **2023**, 14, 369-375 ○
- 5 Mitochondrial dysfunction rapidly modulates the abundance and thermal stability of cellular proteins. **2023**, 6, e202201805 1
- 4 The toxic natural product tutin causes epileptic seizures in mice by activating calcineurin. **2023**, 8, ○
- 3 Deep thermal profiling for detection of functional proteoform groups. ○
- 2 Experimental strategies to improve drug-target identification in mass spectrometry-based thermal stability assays. **2023**, 6, ○
- 1 DeepSTABp: A Deep Learning Approach for the Prediction of Thermal Protein Stability. **2023**, 24, 7444 ○