

# CITATION REPORT

List of articles citing

Thermal proximity coaggregation for system-wide profiling of protein complex dynamics in cells

DOI: 10.1126/science.aan0346  
Science, 2018, 359, 1170-1177.

**Source:** <https://exaly.com/paper-pdf/69083847/citation-report.pdf>

**Version:** 2024-04-29

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
130	Capturing dynamic protein interactions. <i>Science</i> , <b>2018</b> , 359, 1105-1106	33.3	35
129	Modulation of Protein-Interaction States through the Cell Cycle. <b>2018</b> , 173, 1481-1494.e13		80
128	Heating up cells to bring down complexes. <b>2018</b> , 15, 242-243		
127	Proteome-Wide Structural Biology: An Emerging Field for the Structural Analysis of Proteins on the Proteomic Scale. <b>2018</b> , 17, 3614-3627		34
126	In-Cell Titration of Small Solutes Controls Protein Stability and Aggregation. <b>2018</b> , 140, 10497-10503		24
125	Thermal proteome profiling in bacteria: probing protein state. <b>2018</b> , 14, e8242		82
124	Large Scale Proteomic Data and Network-Based Systems Biology Approaches to Explore the Plant World. <b>2018</b> , 6,		12
123	Chemoproteomics and Chemical Probes for Target Discovery. <b>2018</b> , 36, 1275-1286		57
122	High throughput discovery of functional protein modifications by Hotspot Thermal Profiling. <b>2019</b> , 16, 894-901		52
121	Ubiquitous expressed transcript promotes tumorigenesis by acting as a positive modulator of the polycomb repressive complex 2 in clear cell renal cell carcinoma. <b>2019</b> , 19, 874		3
120	A small-molecule inhibitor of BamA impervious to efflux and the outer membrane permeability barrier. <b>2019</b> , 116, 21748-21757		64
119	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. <b>2019</b> , 18, 2506-2515		34
118	Illuminating the dark phosphoproteome. <b>2019</b> , 12,		125
117	Protein Melting Temperature Cannot Fully Assess Whether Protein Folding Free Energy Underlies the Universal Abundance-Evolutionary Rate Correlation Seen in Proteins. <b>2019</b> , 36, 1955-1963		12
116	Quantitative proteomic analysis of prostate tissue specimens identifies deregulated protein complexes in primary prostate cancer. <b>2019</b> , 16, 15		8
115	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <b>2019</b> , 10, 1155		88
114	Monitoring structural modulation of redox-sensitive proteins in cells with MS-CETSA. <b>2019</b> , 24, 101168		23

113	Label-free target identification in drug discovery via phenotypic screening. <b>2019</b> , 50, 66-72	20
112	CETSA-based target engagement of taxanes as biomarkers for efficacy and resistance. <b>2019</b> , 9, 19384	10
111	Label-Free Techniques for Target Discovery and Validation. <b>2019</b> , 131-152	
110	Identifying purine nucleoside phosphorylase as the target of quinine using cellular thermal shift assay. <b>2019</b> , 11,	81
109	Proteome-wide Analysis of Protein Thermal Stability in the Model Higher Plant. <b>2019</b> , 18, 308-319	23
108	Modification-free approaches to screen drug targets at proteome level. <b>2020</b> , 124, 115574	8
107	Mass spectrometry-based Cellular Thermal Shift Assay (CETSA <sup>2</sup> ) for target deconvolution in phenotypic drug discovery. <b>2020</b> , 28, 115174	17
106	Perspective on CETSA Literature: Toward More Quantitative Data Interpretation. <b>2020</b> , 25, 118-126	16
105	Mass spectrometry analysis of the structural proteome. <b>2020</b> , 60, 57-65	13
104	CETSA in integrated proteomics studies of cellular processes. <b>2020</b> , 54, 54-62	16
103	A materials-science perspective on tackling COVID-19. <b>2020</b> , 1-14	123
102	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <b>2020</b> , 11, 5783	8
101	Mutant thermal proteome profiling for characterization of missense protein variants and their associated phenotypes within the proteome. <b>2020</b> , 295, 16219-16238	9
100	The Integrator Complex in Transcription and Development. <b>2020</b> , 45, 923-934	13
99	COVID-19: Nanomedicine Uncovers Blood-Clot Mystery. <b>2020</b> , 19, 4364-4373	9
98	The functional proteome landscape of Escherichia coli. <b>2020</b> , 588, 473-478	14
97	High-Throughput and Integrated Chemical Proteomic Approach for Profiling Phosphotyrosine Signaling Complexes. <b>2020</b> , 92, 8933-8942	3
96	Dynamic rewiring of the human interactome by interferon signaling. <b>2020</b> , 21, 140	12

95	Approaching complexity: systems biology and ms-based techniques to address immune signaling. <b>2020</b> , 17, 341-354	1
94	Interaction profiling methods to map protein and pathway targets of bioactive ligands. <b>2020</b> , 54, 76-84	2
93	chaperonin TRiC/CCT identified as a target of the antihistamine clemastine using parallel chemoproteomic strategy. <b>2020</b> , 117, 5810-5817	19
92	Proteome Instability Is a Therapeutic Vulnerability in Mismatch Repair-Deficient Cancer. <b>2020</b> , 37, 371-386.e1228	
91	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <b>2020</b> , 38, 303-308	46
90	Thermal proteome profiling for interrogating protein interactions. <b>2020</b> , 16, e9232	53
89	Meltome atlas-thermal proteome stability across the tree of life. <b>2020</b> , 17, 495-503	53
88	Cellular thermal shift assay for the identification of drug-target interactions in the Plasmodium falciparum proteome. <b>2020</b> , 15, 1881-1921	27
87	Mass Spectrometry-Based Protein Complex Profiling in Time and Space. <b>2021</b> , 93, 598-619	3
86	Rtpca: an R package for differential thermal proximity coaggregation analysis. <b>2021</b> , 37, 431-433	3
85	Rationalizing the therapeutic potential of apigenin against cancer. <b>2021</b> , 267, 118814	20
84	Discovery of cellular substrates of human RNA-decapping enzyme DCP2 using a stapled bicyclic peptide inhibitor. <b>2021</b> , 28, 463-474.e7	3
83	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. <b>2021</b> , 184, 545-559.e22	28
82	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. <b>2021</b> , 18, 84-91	12
81	Mass spectrometry-based protein-protein interaction networks for the study of human diseases. <b>2021</b> , 17, e8792	30
80	Mass spectrometry-based protein-protein interaction techniques and their applications in studies of DNA damage repair. <b>2021</b> , 22, 1-20	2
79	PrInCE: an R/bioconductor package for protein-protein interaction network inference from co-fractionation mass spectrometry data. <b>2021</b> ,	3
78	Recent advances in bioanalytical methods to measure proteome stability in cells. <b>2021</b> , 146, 2097-2109	5

77	Hidden information on protein function in censuses of proteome foldedness.	0
76	Recent advances in proteome-wide label-free target deconvolution for bioactive small molecules. <b>2021</b> , 41, 2893-2926	1
75	TP-MAP - an Integrated Software Package for the Analysis of 1D and 2D Thermal Profiling Data.	0
74	A survey on computational models for predicting protein-protein interactions. <b>2021</b> , 22,	22
73	Discovery-Versus Hypothesis-Driven Detection of Protein-Protein Interactions and Complexes. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3 2
72	Subcellular proteomics. <b>2021</b> , 1,	13
71	Recent progress in mass spectrometry-based strategies for elucidating protein-protein interactions. <b>2021</b> , 78, 5325-5339	12
70	Chemoproteomics for Plasmodium Parasite Drug Target Discovery. <b>2021</b> , 22, 2591-2599	2
69	Systematic profiling of protein complex dynamics reveals DNA-PK phosphorylation of IFI16 en route to herpesvirus immunity. <b>2021</b> , 7,	4
68	A Bayesian semi-parametric model for thermal proteome profiling. <b>2021</b> , 4, 810	0
67	Impact of phosphorylation on thermal stability of proteins. <b>2021</b> , 18, 757-759	15
66	Engineering of Human Lactoferrin for Improved Anticancer Activity. <b>2021</b> , 4, 1476-1482	1
65	The rise of proteome-wide biophysics. <b>2021</b> , 17, e10442	1
64	Sensitive Measurement of Drug-Target Engagement by a Cellular Thermal Shift Assay with Multiplex Proximity Extension Readout. <b>2021</b> , 93, 10999-11009	4
63	ATP Can Efficiently Stabilize Protein through a Unique Mechanism. <b>2021</b> , 1, 1766-1777	4
62	Characterizing Endogenous Protein Complexes with Biological Mass Spectrometry. <b>2021</b> ,	5
61	Drug Target Identification in Tissues by Thermal Proteome Profiling. <b>2021</b> ,	2
60	The thermal proteome stability profile of <i>Trypanosoma cruzi</i> in epimastigote and trypomastigote life stages. <b>2021</b> , 248, 104339	1

59	Design and synthesis of a new orthogonally protected glutamic acid analog and its use in the preparation of high affinity polo-like kinase 1 polo-box domain - binding peptide macrocycles. <b>2021</b> , 19, 7843-7854	1
58	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <b>2020</b> , 10, 133-155.e624	24
57	Temporal dynamics of protein complex formation and dissociation during human cytomegalovirus infection. <b>2020</b> , 11, 806	33
56	Impact of phosphorylation on thermal stability of proteins.	7
55	Three Essential Resources to Improve Differential Scanning Fluorimetry (DSF) Experiments.	6
54	Computational analysis of ligand dose range thermal proteome profiles.	1
53	Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins.	2
52	Analysis of Independent Differences (AID) detects complex thermal proteome profiles independent of shape and identifies candidate panobinostat targets.	1
51	Dynamic rewiring of the human interactome by interferon signalling.	2
50	Origin, fate, and risk assessment of emerging contaminants in groundwater bodies: a holistic review. <b>2021</b> , 4, 1275	1
49	A global screen for assembly state changes of the mitotic proteome by SEC-SWATH-MS.	1
48	Temperature sensitive Mutant Proteome Profiling: a novel tool for the characterization of the global impact of missense mutations on the proteome.	0
47	In-depth characterization of Staurosporine induced proteome thermal stability changes.	2
46	A Bayesian semi-parametric model for thermal proteome profiling.	
45	Chemoproteomic-enabled characterization of small GTPase Rab1a as a target of an -arylbenzimidazole ligand rescue of Parkinson-associated cell toxicity.. <b>2022</b> , 3, 96-111	2
44	Technique development of high-throughput and high-sensitivity sample preparation and separation for proteomics. <b>2022</b> , 14, 101-111	1
43	An integrative proteomics method identifies a regulator of translation during stem cell maintenance and differentiation. <b>2021</b> , 12, 6558	3
42	Comprehensive chemical proteomics analyses reveal that the new TRi-1 and TRi-2 compounds are more specific thioredoxin reductase 1 inhibitors than auranofin. <b>2021</b> , 48, 102184	3

41	Experimental study of proteome halophilicity using nanoDSF: a proof of concept. <b>2021</b> , 26, 1		
40	Precipitate-Supported Thermal Proteome Profiling Coupled with Deep Learning for Comprehensive Screening of Drug Target Proteins.. <b>2022</b> ,		2
39	An Ensemble Learning Framework for Detecting Protein Complexes From PPI Networks.. <b>2022</b> , 13, 839949		1
38	Selective Removal of Unhydrolyzed Monolinked Peptides from Enriched Crosslinked Peptides To Improve the Coverage of Protein Complex Analysis.. <b>2022</b> ,		0
37	ProSAP: a GUI software tool for statistical analysis and assessment of thermal stability data.. <b>2022</b> ,		0
36	Metabolite interactions in the bacterial Calvin cycle and implications for flux regulation.		0
35	Thermal Proteome Profiling Reveals the O-GlcNAc-Dependent Meltome.. <b>2022</b> ,		3
34	Protein-Peptide Turnover Profiling reveals wiring of phosphorylation during protein maturation.		1
33	Hidden information on protein function in censuses of proteome foldedness.. <b>2022</b> , 13, 1992		1
32	Matrix Thermal Shift Assay for Fast Construction of Multidimensional Ligand-Target Space.. <b>2022</b> ,		0
31	Ion-Based Proteome-Integrated Solubility Alteration Assays for Systemwide Profiling of Protein-Molecule Interactions.. <b>2022</b> , 94, 7066-7074		0
30	Systems Biology of Virus-Host Protein Interactions: From Hypothesis Generation to Mechanisms of Replication and Pathogenesis.. <i>Annual Review of Virology</i> , <b>2022</b> ,	14.6	1
29	Small Molecule Arranged Thermal Proximity Coaggregation (smarTPCA) A Novel Approach to Characterize Protein-Protein Interactions in Living Cells by Similar Isothermal Dose-Responses. <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23, 5605	6.3	0
28	Protein painting reveals pervasive remodeling of conserved proteostasis machinery in response to pharmacological stimuli..		
27	Deep thermal proteome profiling for detection of proteoforms and drug sensitivity biomarkers.		
26	Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3.		
25	Network analysis of genome-wide association studies for drug target prioritisation. <b>2022</b> , 71, 102206		0
24	Highly effective identification of drug targets at proteome level by pH-dependent protein precipitation.		0

- 23 CycleDNN - A Novel Deep Neural Network Model for CETSA Feature Prediction cross Cell Lines. **2022**, ○
- 22 CETSA Feature Based Clustering for Protein Outlier Discovery by Protein-to-Protein Interaction Prediction. **2022**, ○
- 21 Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3. **2022**, 13, ○
- 20 Thermal proteome profiling: Insights into protein modifications, associations, and functions. **2022**, 71, 102225 ○
- 19 Profiling disease-selective drug targets: From proteomics to ligandomics. **2023**, 28, 103430 ○
- 18 Proteomic analysis of antiviral innate immunity. **2023**, 58, 101291 ○
- 17 Protein painting reveals pervasive remodeling of conserved proteostasis machinery in response to pharmacological stimuli. **2022**, 8, ○
- 16 Protein-Peptide Turnover Profiling reveals the order of PTM addition and removal during protein maturation. **2022**, 13, ○
- 15 FKBP35 secures ribosome homeostasis in *Plasmodium falciparum*. ○
- 14 Proteome-wide structural changes measured with limited proteolysis-mass spectrometry: an advanced protocol for high-throughput applications. ○
- 13 Proteomic discovery of chemical probes that perturb protein complexes in human cells. 1
- 12 Phenotype-based screening rediscovered benzopyran-embedded microtubule inhibitors as anti-neuroinflammatory agents by modulating the tubulin $\beta$ 65 interaction. **2022**, 54, 2200-2209 ○
- 11 Elucidating Protein-Ligand Interactions in Cell Lysates Using High-Throughput Hydrogen-Deuterium Exchange Mass Spectrometry with Integrated Protein Thermal Depletion. ○
- 10 Multi-comparative Thermal Proteome Profiling Uncovers New O-GlcNAc Proteins in a System-wide Method. ○
- 9 Global analysis of aging-related protein structural changes uncovers enzyme polymerization-based control of longevity. ○
- 8 A partially shared joint clustering framework for detecting protein complexes from multiple state-specific signed interaction networks. ○
- 7 Analysis of affinity purification-related proteomic data for studying protein-protein interaction networks in cells. ○
- 6 Potential of dissimilarity measure-based computation of protein thermal stability data for determining protein interactions. ○



- 5 Improved in situ Characterization of Proteome-wide Protein Complex Dynamics with Thermal Proximity Co-Aggregation.
- 4 Deep thermal profiling for detection of functional proteoform groups.
- 3 DeepSTABp: A Deep Learning Approach for the Prediction of Thermal Protein Stability. **2023**, 24, 7444
- 2 A partially shared joint clustering framework for detecting protein complexes from multiple state-specific signed interaction networks. **2023**, 106936
- 1 Proteomic discovery of chemical probes that perturb protein complexes in human cells. **2023**,