

Proteome-wide analysis of protein carboxy termini: C t

Nature Methods

7, 508-511

DOI: [10.1038/nmeth.1467](https://doi.org/10.1038/nmeth.1467)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Who gets cut during cell death?. <i>Current Opinion in Cell Biology</i> , 2010, 22, 859-864.	2.6	7
2	Systems Biology and Synthetic Biology: Understanding Biological Complexity on the Critical Path to Personalized Medicine. <i>Current Pharmacogenomics and Personalized Medicine</i> , 2010, 8, 257-267.	0.2	3
3	Proteomic techniques and activity-based probes for the system-wide study of proteolysis. <i>Biochimie</i> , 2010, 92, 1705-1714.	1.3	54
4	Selecting protein N-terminal peptides by combined fractional diagonal chromatography. <i>Nature Protocols</i> , 2011, 6, 1130-1141.	5.5	164
6	Chemoenzymatic Labeling of Protein C-Termini for Positive Selection of C-Terminal Peptides. <i>ACS Chemical Biology</i> , 2011, 6, 1015-1020.	1.6	40
7	Network Biology. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	3
8	Online Nanoflow Reversed Phase-Strong Anion Exchange-Reversed Phase Liquid Chromatography-Tandem Mass Spectrometry Platform for Efficient and In-Depth Proteome Sequence Analysis of Complex Organisms. <i>Analytical Chemistry</i> , 2011, 83, 6996-7005.	3.2	62
9	C-terminal de novo sequencing of peptides using oxazolone-based derivatization with bromine signature. <i>Analytical Biochemistry</i> , 2011, 419, 211-216.	1.1	16
10	Selective isolation of N-blocked peptide by combining AspN digestion, transamination, and tosylhydrazine glass treatment. <i>Analytical Biochemistry</i> , 2011, 410, 214-223.	1.1	8
11	Broad Coverage Identification of Multiple Proteolytic Cleavage Site Sequences in Complex High Molecular Weight Proteins Using Quantitative Proteomics as a Complement to Edman Sequencing. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003533.	2.5	47
12	Rho Kinase II Phosphorylation of the Lipoprotein Receptor LR11/SORLA Alters Amyloid- β Production. <i>Journal of Biological Chemistry</i> , 2011, 286, 6117-6127.	1.6	50
13	TopFIND, a knowledgebase linking protein termini with function. <i>Nature Methods</i> , 2011, 8, 703-704.	9.0	91
14	Biological role of matrix metalloproteinases: a critical balance. <i>European Respiratory Journal</i> , 2011, 38, 191-208.	3.1	571
15	Protease signalling: the cutting edge. <i>EMBO Journal</i> , 2012, 31, 1630-1643.	3.5	242
16	Targeting Proteases in Cardiovascular Diseases by Mass Spectrometry-Based Proteomics. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 265-265.	5.1	7
17	TopFIND 2.0-linking protein termini with proteolytic processing and modifications altering protein function. <i>Nucleic Acids Research</i> , 2012, 40, D351-D361.	6.5	54
18	The Degradative Inventory of the Cell: Proteomic Insights. <i>Antioxidants and Redox Signaling</i> , 2012, 17, 803-812.	2.5	13
19	Isobaric cross-sequence labeling of peptides by using site-selective N-terminus dimethylation. <i>Chemical Communications</i> , 2012, 48, 6265.	2.2	34

#	ARTICLE	IF	CITATIONS
20	Unbiased Selective Isolation of Protein N-terminal Peptides from Complex Proteome Samples Using Phospho Tagging (PTAG) and TiO ₂ -based Depletion. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 832-842.	2.5	51
21	Specific functions of lysosomal proteases in endocytic and autophagic pathways. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 34-43.	1.1	74
22	4.7 Rock, paper, and molecular scissors: regulating the game of extracellular matrix homeostasis, remodeling, and inflammation. , 2012, , 377-400.		0
23	Mass spectrometry-based proteomics strategies for protease cleavage site identification. <i>Proteomics</i> , 2012, 12, 516-529.	1.3	35
24	Profiling protease activities by dynamic proteomics workflows. <i>Proteomics</i> , 2012, 12, 587-596.	1.3	19
25	Qualitative improvement and quantitative assessment of N-terminomics. <i>Proteomics</i> , 2012, 12, 1207-1216.	1.3	17
26	Enhanced identification of peptides lacking basic residues by LC-ESI-MS/MS analysis of singly charged peptides. <i>Proteomics</i> , 2012, 12, 1303-1309.	1.3	16
27	New approaches for dissecting protease functions to improve probe development and drug discovery. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 9-16.	3.6	143
28	Applications of stable isotope dimethyl labeling in quantitative proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 991-1009.	1.9	61
29	N- and C-terminal degradomics: new approaches to reveal biological roles for plant proteases from substrate identification. <i>Physiologia Plantarum</i> , 2012, 145, 5-17.	2.6	45
30	Matrix metalloproteinase processing of signaling molecules to regulate inflammation. <i>Periodontology 2000</i> , 2013, 63, 123-148.	6.3	42
31	Alpha-synuclein Post-translational Modifications as Potential Biomarkers for Parkinson Disease and Other Synucleinopathies. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3543-3558.	2.5	159
32	Approach for Identification and Quantification of C-Terminal Peptides: Incorporation of Isotopic Arginine Labeling Based on Oxazolone Chemistry. <i>Analytical Chemistry</i> , 2013, 85, 10745-10753.	3.2	17
33	Proteases: Structure and Function. , 2013, , .		31
34	Contemporary positional proteomics strategies to study protein processing. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 66-72.	2.8	31
35	Functional decorations: post-translational modifications and heart disease delineated by targeted proteomics. <i>Genome Medicine</i> , 2013, 5, 20.	3.6	85
36	Protein TAILS: when termini tell tales of proteolysis and function. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 73-82.	2.8	80
37	Proteomic identification of protease cleavage sites: cell-biological and biomedical applications. <i>Expert Review of Proteomics</i> , 2013, 10, 421-433.	1.3	32

#	ARTICLE	IF	CITATIONS
38	Proteolytic Post-translational Modification of Proteins: Proteomic Tools and Methodology. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3532-3542.	2.5	127
39	Proteome-derived Peptide Libraries to Study the Substrate Specificity Profiles of Carboxypeptidases. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2096-2110.	2.5	40
40	C-Terminal Protein Characterization by Mass Spectrometry using Combined Micro Scale Liquid and Solid-Phase Derivatization. <i>Journal of Biomolecular Techniques</i> , 2013, 24, jbt.13-2401-003.	0.8	10
41	Network Analyses Reveal Pervasive Functional Regulation Between Proteases in the Human Protease Web. <i>PLoS Biology</i> , 2014, 12, e1001869.	2.6	137
42	Time-resolved Analysis of the Matrix Metalloproteinase 10 Substrate Degradome. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 580-593.	2.5	48
43	Mapping orphan proteases by proteomics: Meprip metalloproteases deciphered as potential therapeutic targets. <i>Proteomics - Clinical Applications</i> , 2014, 8, 382-388.	0.8	6
44	Ensembles of protein termini and specific proteolytic signatures as candidate biomarkers of disease. <i>Proteomics - Clinical Applications</i> , 2014, 8, 338-350.	0.8	28
45	Proteomics of protein post-translational modifications implicated in neurodegeneration. <i>Translational Neurodegeneration</i> , 2014, 3, 23.	3.6	59
46	Beyond gene expression: The impact of protein post-translational modifications in bacteria. <i>Journal of Proteomics</i> , 2014, 97, 265-286.	1.2	176
47	What Can Proteomics Tell Us About Platelets?. <i>Circulation Research</i> , 2014, 114, 1204-1219.	2.0	97
48	A novel method for identification and relative quantification of N-terminal peptides using metal-element-chelated tags coupled with mass spectrometry. <i>Science China Chemistry</i> , 2014, 57, 708-717.	4.2	4
49	Microwave-assisted acid hydrolysis of proteins combined with peptide fractionation and mass spectrometry analysis for characterizing protein terminal sequences. <i>Journal of Proteomics</i> , 2014, 100, 68-78.	1.2	6
50	Carboxyterminal Protein Processing in Health and Disease: Key Actors and Emerging Technologies. <i>Journal of Proteome Research</i> , 2014, 13, 4497-4504.	1.8	22
51	Holistic View on the Extended Substrate Specificities of Orthologous Granzymes. <i>Journal of Proteome Research</i> , 2014, 13, 1785-1793.	1.8	8
53	Streamlining Bottom-Up Protein Identification Based on Selective Ultraviolet Photodissociation (UVPD) of Chromophore-Tagged Histidine- and Tyrosine-Containing Peptides. <i>Analytical Chemistry</i> , 2014, 86, 6237-6244.	3.2	15
54	Magnetic Immunoaffinity Enrichment for Selective Capture and MS/MS Analysis of N-Terminal-TMPP-Labeled Peptides. <i>Journal of Proteome Research</i> , 2014, 13, 668-680.	1.8	32
55	Neutrophil Elastase in the capacity of the α -H2A-specific protease. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 51, 39-44.	1.2	11
56	The Human Proteome Organization Chromosome 6 Consortium: Integrating chromosome-centric and biology/disease driven strategies. <i>Journal of Proteomics</i> , 2014, 100, 60-67.	1.2	8

#	ARTICLE	IF	CITATIONS
57	Automation of C-terminal sequence analysis of 2D-PAGE separated proteins. <i>EuPA Open Proteomics</i> , 2014, 3, 250-261.	2.5	2
58	Metalloprotease meprin β^2 is activated by transmembrane serine protease matriptase-2 at the cell surface thereby enhancing APP shedding. <i>Biochemical Journal</i> , 2015, 470, 91-103.	1.7	39
61	Protein Termini and Their Modifications Revealed by Positional Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 1754-1764.	1.6	90
62	C-terminomics: Targeted analysis of natural and posttranslationally modified protein and peptide C-termini. <i>Proteomics</i> , 2015, 15, 903-914.	1.3	51
63	C-terminomics Screen for Natural Substrates of Cytosolic Carboxypeptidase 1 Reveals Processing of Acidic Protein C termini. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 177-190.	2.5	25
64	Systematic Optimization of C-Terminal Amine-Based Isotope Labeling of Substrates Approach for Deep Screening of C-Terminome. <i>Analytical Chemistry</i> , 2015, 87, 10354-10361.	3.2	24
65	Fishing the PTM proteome with chemical approaches using functional solid phases. <i>Chemical Society Reviews</i> , 2015, 44, 8260-8287.	18.7	70
66	Positive Enrichment of C-Terminal Peptides Using Oxazolone Chemistry and Biotinylation. <i>Analytical Chemistry</i> , 2015, 87, 9916-9922.	3.2	26
67	Matrix Metalloproteinase (MMP) Proteolysis of the Extracellular Loop of Voltage-gated Sodium Channels and Potential Alterations in Pain Signaling. <i>Journal of Biological Chemistry</i> , 2015, 290, 22939-22944.	1.6	11
68	Cysteine cathepsin proteases: regulators of cancer progression and therapeutic response. <i>Nature Reviews Cancer</i> , 2015, 15, 712-729.	12.8	481
69	Proteolysis mediated by cysteine cathepsins and legumain—recent advances and cell biological challenges. <i>Protoplasma</i> , 2015, 252, 755-774.	1.0	36
70	LysargiNase mirrors trypsin for protein C-terminal and methylation-site identification. <i>Nature Methods</i> , 2015, 12, 55-58.	9.0	128
71	Proteomic Substrate Identification for Membrane Proteases in the Brain. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 96.	1.4	26
72	Protein C-terminal enzymatic labeling identifies novel caspase cleavages during the apoptosis of multiple myeloma cells induced by kinase inhibition. <i>Proteomics</i> , 2016, 16, 60-69.	1.3	13
73	Mass Spectrometry-based Methodologies for Studying Proteolytic Networks and the Degradome. , 2016, , 568-581.		1
74	Stable isotope dimethyl labelling for quantitative proteomics and beyond. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20150364.	1.6	32
75	Quantitative proteomics and terminomics to elucidate the role of ubiquitination and proteolysis in adaptive immunity. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20150372.	1.6	8
76	Depletion of internal peptides by site-selective blocking, phosphate labeling, and TiO ₂ adsorption for in-depth analysis of C-terminome. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 3867-3874.	1.9	11

#	ARTICLE	IF	CITATIONS
77	Positional proteomics in the era of the human proteome project on the doorstep of precision medicine. <i>Biochimie</i> , 2016, 122, 110-118.	1.3	42
78	Protease Inhibitors in View of Peptide Substrate Databases. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1228-1235.	2.5	4
79	Comprehensive analysis of protein glycosylation by solid-phase extraction of N-linked glycans and glycosite-containing peptides. <i>Nature Biotechnology</i> , 2016, 34, 84-88.	9.4	213
80	C-Terminal Charge-Reversal Derivatization and Parallel Use of Multiple Proteases Facilitates Identification of Protein C-Termini by C-Terminomics. <i>Journal of Proteome Research</i> , 2016, 15, 1369-1378.	1.8	26
81	Current trends and challenges in proteomic identification of protease substrates. <i>Biochimie</i> , 2016, 122, 77-87.	1.3	38
82	Matrix metalloproteinases – From the cleavage data to the prediction tools and beyond. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 1952-1963.	1.9	39
84	ProC-TEL: Profiling of Protein C-Termini by Enzymatic Labeling. <i>Methods in Molecular Biology</i> , 2017, 1574, 135-144.	0.4	6
85	ArgC-Like Digestion: Complementary or Alternative to Tryptic Digestion?. <i>Journal of Proteome Research</i> , 2017, 16, 978-987.	1.8	12
86	The [PSI +] yeast prion does not wildly affect proteome composition whereas selective pressure exerted on [PSI +] cells can promote aneuploidy. <i>Scientific Reports</i> , 2017, 7, 8442.	1.6	12
88	Top-down proteomics for the analysis of proteolytic events - Methods, applications and perspectives. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 2191-2199.	1.9	42
89	Site-Specific Profiling of Serum Glycoproteins Using N-Linked Glycan and Glycosite Analysis Revealing Atypical N-Glycosylation Sites on Albumin and Î±1B-Glycoprotein. <i>Analytical Chemistry</i> , 2018, 90, 6292-6299.	3.2	44
90	Proteomic approaches beyond expression profiling and PTM analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 4051-4060.	1.9	9
91	Proteolytic Cleavage – Mechanisms, Function, and – Approaches for a Near-Ubiquitous Posttranslational Modification. <i>Chemical Reviews</i> , 2018, 118, 1137-1168.	23.0	145
92	Identification of Protease Cleavage Sites and Substrates in Cancer by Carboxy-TAILS (C-TAILS). <i>Methods in Molecular Biology</i> , 2018, 1731, 15-28.	0.4	3
93	A review of the role of chemical modification methods in contemporary mass spectrometry-based proteomics research. <i>Analytica Chimica Acta</i> , 2018, 1000, 2-19.	2.6	26
94	Enzyme and Chemical Assisted N-Terminal Blocked Peptides Analysis, ENCHANT, as a Selective Proteomics Approach Complementary to Conventional Shotgun Approach. <i>Journal of Proteome Research</i> , 2018, 17, 212-221.	1.8	11
95	An Approach to Incorporate Multi-Enzyme Digestion into C-TAILS for C-Terminomics Studies. <i>Proteomics</i> , 2018, 18, 1700034.	1.3	21
96	Digging for Missing Proteins Using Low-Molecular-Weight Protein Enrichment and a – Mirror Protease – Strategy. <i>Journal of Proteome Research</i> , 2018, 17, 4178-4185.	1.8	12

#	ARTICLE	IF	CITATIONS
97	Degradomics in Biomarker Discovery. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800138.	0.8	9
98	LysargiNase and Chemical Derivatization Based Strategy for Facilitating In-Depth Profiling of C-Terminome. <i>Analytical Chemistry</i> , 2019, 91, 14522-14529.	3.2	15
99	ADAM15 mediates upregulation of Claudin-1 expression in breast cancer cells. <i>Scientific Reports</i> , 2019, 9, 12540.	1.6	18
100	Combination of SCX Fractionation and Charge-Reversal Derivatization Facilitates the Identification of Nontryptic Peptides in C-Terminomics. <i>Journal of Proteome Research</i> , 2019, 18, 2954-2964.	1.8	17
101	In-Depth Analysis of C Terminomes Based on LysC Digestion and Site-Selective Dimethylation. <i>Analytical Chemistry</i> , 2019, 91, 6498-6506.	3.2	16
102	New beginnings and new ends: methods for large-scale characterization of protein termini and their use in plant biology. <i>Journal of Experimental Botany</i> , 2019, 70, 2021-2038.	2.4	37
103	Dual chemical probes enable quantitative system-wide analysis of protein prenylation and prenylation dynamics. <i>Nature Chemistry</i> , 2019, 11, 552-561.	6.6	80
104	Quantitative Multiplex Substrate Profiling of Peptidases by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 968a-981.	2.5	28
105	Proteomics turns functional. <i>Journal of Proteomics</i> , 2019, 198, 36-44.	1.2	74
106	Deuterium-Free, Three-Plexed Peptide Diethylation for Highly Accurate Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 1078-1087.	1.8	17
107	Positional proteomics for identification of secreted proteoforms released by site-specific processing of membrane proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 140138.	1.1	23
108	Targeted Metagenomics of Retting in Flax: The Beginning of the Quest to Harness the Secret Powers of the Microbiota. <i>Frontiers in Genetics</i> , 2020, 11, 581664.	1.1	13
109	What Room for Two-Dimensional Gel-Based Proteomics in a Shotgun Proteomics World?. <i>Proteomes</i> , 2020, 8, 17.	1.7	42
110	Carboxypeptidase B-Assisted Charge-Based Fractional Diagonal Chromatography for Deep Screening of C-Terminome. <i>Analytical Chemistry</i> , 2020, 92, 8005-8009.	3.2	10
111	Development of Multiplexed Immuno-N-Terminomics to Reveal the Landscape of Proteolytic Processing in Early Embryogenesis of <i>Drosophila melanogaster</i> . <i>Analytical Chemistry</i> , 2020, 92, 4926-4934.	3.2	7
112	Basic Strong Cation Exchange Chromatography, BaSCX, a Highly Efficient Approach for C-Terminomic Studies Using LysargiNase Digestion. <i>Analytical Chemistry</i> , 2020, 92, 4742-4748.	3.2	13
113	Tyrosine-EDC Conjugation, an Undesirable Side Effect of the EDC-Catalyzed Carboxyl Labeling Approach. <i>Analytical Chemistry</i> , 2021, 93, 697-703.	3.2	5
114	Proteomics approaches for the identification of protease substrates during virus infection. <i>Advances in Virus Research</i> , 2021, 109, 135-161.	0.9	5

#	ARTICLE	IF	CITATIONS
115	N-terminomics – its past and recent advancements. <i>Journal of Proteomics</i> , 2021, 233, 104089.	1.2	25
116	Proteomic approaches to assist in diagnosis and prognosis of oral cancer. <i>Expert Review of Proteomics</i> , 2021, 18, 261-284.	1.3	8
117	Proteolysis and inflammation of the kidney glomerulus. <i>Cell and Tissue Research</i> , 2021, 385, 489-500.	1.5	4
118	Fractionation-free negative enriching for in-depth C-terminome analysis. <i>Chinese Chemical Letters</i> , 2021, , .	4.8	2
120	Insights into protease sequence similarities by comparing substrate sequences and phylogenetic dynamics. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 837-850.	1.0	0
121	Preparation of <i>Arabidopsis thaliana</i> Seedling Proteomes for Identifying Metacaspase Substrates by N-terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2014, 1133, 255-261.	0.4	8
122	Identification and Relative Quantification of Native and Proteolytically Generated Protein C-Termini from Complex Proteomes: C-Terminome Analysis. <i>Methods in Molecular Biology</i> , 2011, 781, 59-69.	0.4	23
124	Microbial proteomics: how far have we come?. <i>Microbiology Australia</i> , 2011, 32, 169.	0.1	1
125	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. <i>PLoS ONE</i> , 2012, 7, e50300.	1.1	265
126	The Functional Human C-Terminome. <i>PLoS ONE</i> , 2016, 11, e0152731.	1.1	11
127	Engineered peptide ligases for cell signaling and bioconjugation. <i>Biochemical Society Transactions</i> , 2020, 48, 1153-1165.	1.6	6
128	Shedding light on both ends: An update on analytical approaches for N- and C-terminomics. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022, 1869, 119137.	1.9	6
129	The protease web. , 2022, , 229-250.		0
130	–omics–approaches to determine protease degradomes in complex biological matrices. , 2022, , 209-228.		0
131	One-Step Isolation of Protein C-Terminal Peptides from V8 Protease-Digested Proteins by Metal Oxide-Based Ligand-Exchange Chromatography. <i>Analytical Chemistry</i> , 2022, 94, 944-951.	3.2	7
133	Ac-LysargiNase efficiently helps genome reannotation of <i>Mycobacterium smegmatis</i> MC2 155. <i>Journal of Proteomics</i> , 2022, 264, 104622.	1.2	1
134	Proteolysis: a key post-translational modification regulating proteoglycans. <i>American Journal of Physiology - Cell Physiology</i> , 2022, 323, C651-C665.	2.1	14
135	Validation of Top-Down Proteomics Data by Bottom-Up-Based N-Terminomics Reveals Pitfalls in Top-Down-Based Terminomics Workflows. <i>Journal of Proteome Research</i> , 2022, 21, 2185-2196.	1.8	4

#	ARTICLE	IF	CITATIONS
136	Separation methods for system-wide profiling of protein terminome. <i>Proteomics</i> , 2023, 23, .	1.3	3
137	NAPT, an unbiased approach for sequential analysis of the protein N- and C-terminome. <i>Chemical Communications</i> , 2022, 58, 9397-9400.	2.2	1
138	PBC, an easy and efficient strategy for high-throughput protein C-terminome profiling. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
139	Degradomics technologies in matrisome exploration. <i>Matrix Biology</i> , 2022, 114, 1-17.	1.5	5
140	Mass Spectrometry-based Methodologies for Studying Proteolytic Networks and the Degradome. , 2016, , 396-410.		0
141	Mass spectrometry-based candidate substrate and site identification of PTM enzymes. <i>TrAC - Trends in Analytical Chemistry</i> , 2023, 160, 116991.	5.8	0