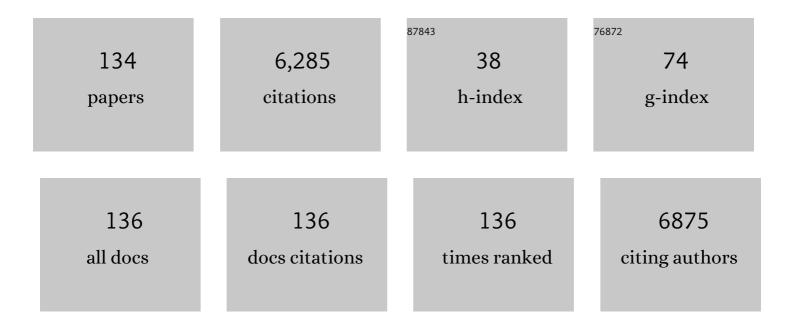
Young-Ki Paik

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6293636/publications.pdf Version: 2024-02-01



YOUNG-KI PAIK

#	Article	IF	CITATIONS
1	Deficiency in RCAT-1 Function Causes Dopamine Metabolism Related Behavioral Disorders in Caenorhabditis elegans. International Journal of Molecular Sciences, 2022, 23, 2393.	1.8	2
2	Progress Identifying and Analyzing the Human Proteome: 2021ÂMetrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2021, 20, 5227-5240.	1.8	30
3	Early Diagnostic Ability of Human Complement Factor B in Pancreatic Cancer Is Partly Linked to Its Potential Tumor-Promoting Role. Journal of Proteome Research, 2021, 20, 5315-5328.	1.8	2
4	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	5.8	152
5	Potential Regulatory Role of Human-Carboxylesterase-1 Glycosylation in Liver Cancer Cell Growth. Journal of Proteome Research, 2020, 19, 4867-4883.	1.8	19
6	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. Journal of Proteome Research, 2020, 19, 4735-4746.	1.8	38
7	A novel functional cross-interaction between opioid and pheromone signaling may be involved in stress avoidance in Caenorhabditis elegans. Scientific Reports, 2020, 10, 7524.	1.6	3
8	Identification of ALDH6A1 as a Potential Molecular Signature in Hepatocellular Carcinoma via Quantitative Profiling of the Mitochondrial Proteome. Journal of Proteome Research, 2020, 19, 1684-1695.	1.8	25
9	A Molecular Basis for Reciprocal Regulation between Pheromones and Hormones in Response to Dietary Cues in C. elegans. International Journal of Molecular Sciences, 2020, 21, 2366.	1.8	3
10	200+ Protein Concentrations in Healthy Human Blood Plasma: Targeted Quantitative SRM SIS Screening of Chromosomes 18, 13, Y, and the Mitochondrial Chromosome Encoded Proteome. Journal of Proteome Research, 2019, 18, 120-129.	1.8	17
11	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2019, 18, 4098-4107.	1.8	41
12	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116.	1.8	82
13	Ascaroside Pheromones: Chemical Biology and Pleiotropic Neuronal Functions. International Journal of Molecular Sciences, 2019, 20, 3898.	1.8	24
14	FusionPro, a Versatile Proteogenomic Tool for Identification of Novel Fusion Transcripts and Their Potential Translation Products in Cancer Cells*. Molecular and Cellular Proteomics, 2019, 18, 1651-1668.	2.5	8
15	Prognostic potential of the preoperative plasma complement factor B in resected pancreatic cancer: A pilot study. Cancer Biomarkers, 2019, 24, 335-342.	0.8	25
16	β-catenin activation down-regulates cell-cell junction-related genes and induces epithelial-to-mesenchymal transition in colorectal cancers. Scientific Reports, 2019, 9, 18440.	1.6	68
17	Advances in Identifying and Characterizing the Human Proteome. Journal of Proteome Research, 2019, 18, 4079-4084.	1.8	4
18	<i>O</i> -GlcNAcylation of the Tumor Suppressor FOXO3 Triggers Aberrant Cancer Cell Growth. Cancer Research, 2018, 78, 1214-1224.	0.4	34

#	Article	IF	CITATIONS
19	Toward Completion of the Human Proteome Parts List: Progress Uncovering Proteins That Are Missing or Have Unknown Function and Developing Analytical Methods. Journal of Proteome Research, 2018, 17, 4023-4030.	1.8	22
20	ASV-ID, a Proteogenomic Workflow To Predict Candidate Protein Isoforms on the Basis of Transcript Evidence. Journal of Proteome Research, 2018, 17, 4235-4242.	1.8	10
21	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. Journal of Proteome Research, 2018, 17, 4042-4050.	1.8	41
22	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2018, 17, 4031-4041.	1.8	59
23	Identification of Missing Proteins in Human Olfactory Epithelial Tissue by Liquid Chromatography–Tandem Mass Spectrometry. Journal of Proteome Research, 2018, 17, 4320-4324.	1.8	14
24	Epsilon-Q: An Automated Analyzer Interface for Mass Spectral Library Search and Label-Free Protein Quantification. Journal of Proteome Research, 2017, 16, 4435-4445.	1.8	9
25	Systematic Proteogenomic Approach To Exploring a Novel Function for NHERF1 in Human Reproductive Disorder: Lessons for Exploring Missing Proteins. Journal of Proteome Research, 2017, 16, 4455-4467.	1.8	12
26	Next Generation Proteomic Pipeline for Chromosome-Based Proteomic Research Using NeXtProt and GENCODE Databases. Journal of Proteome Research, 2017, 16, 4425-4434.	1.8	14
27	Advances in the Chromosome-Centric Human Proteome Project: looking to the future. Expert Review of Proteomics, 2017, 14, 1059-1071.	1.3	25
28	Genetic deficiency in neuronal peroxisomal fatty acid β-oxidation causes the interruption of dauer development in Caenorhabditis elegans. Scientific Reports, 2017, 7, 9358.	1.6	12
29	The genetic basis of natural variation in a phoretic behavior. Nature Communications, 2017, 8, 273.	5.8	48
30	A conserved neuronal DAF-16/FoxO plays an important role in conveying pheromone signals to elicit repulsion behavior in Caenorhabditis elegans. Scientific Reports, 2017, 7, 7260.	1.6	17
31	MGL-1 on AIY neurons translates starvation to reproductive plasticity via neuropeptide signaling in Caenorhabditis elegans. Developmental Biology, 2017, 430, 80-89.	0.9	14
32	Progress and Future Direction of Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2017, 16, 4253-4258.	1.8	14
33	Integrated GlycoProteome Analyzer (I-GPA) for Automated Identification and Quantitation of Site-Specific N-Glycosylation. Scientific Reports, 2016, 6, 21175.	1.6	81
34	HSF-1 is involved in regulation of ascaroside pheromone biosynthesis by heat stress in <i>Caenorhabditis elegans</i> . Biochemical Journal, 2016, 473, 789-796.	1.7	13
35	gFinder: A Web-Based Bioinformatics Tool for the Analysis of <i>N</i> -Glycopeptides. Journal of Proteome Research, 2016, 15, 4116-4125.	1.8	12
36	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	1.8	158

#	Article	lF	CITATIONS
37	Integrated Proteomic Pipeline Using Multiple Search Engines for a Proteogenomic Study with a Controlled Protein False Discovery Rate. Journal of Proteome Research, 2016, 15, 4082-4090.	1.8	34
38	Progress in the Chromosome-Centric Human Proteome Project as Highlighted in the Annual Special Issue IV. Journal of Proteome Research, 2016, 15, 3945-3950.	1.8	17
39	Quantitative Profiling Identifies Potential Regulatory Proteins Involved in Development from Dauer Stage to L4 Stage in <i>Caenorhabditis elegans</i> . Journal of Proteome Research, 2016, 15, 531-539.	1.8	2
40	Synthesis of Photoaffinity‣abeled Daumone Analogs. Bulletin of the Korean Chemical Society, 2015, 36, 2177-2178.	1.0	0
41	Chromosome-Based Proteomic Study for Identifying Novel Protein Variants from Human Hippocampal Tissue Using Customized neXtProt and GENCODE Databases. Journal of Proteome Research, 2015, 14, 5028-5037.	1.8	4
42	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	1.8	53
43	Distinct Protein Expression Profiles of Solid-Pseudopapillary Neoplasms of the Pancreas. Journal of Proteome Research, 2015, 14, 3007-3014.	1.8	23
44	GenomewidePDB 2.0: A Newly Upgraded Versatile Proteogenomic Database for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3710-3719.	1.8	8
45	Combination of Multiple Spectral Libraries Improves the Current Search Methods Used to Identify Missing Proteins in the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 4959-4966.	1.8	14
46	Recent Advances in the Chromosome-Centric Human Proteome Project: Missing Proteins in the Spot Light. Journal of Proteome Research, 2015, 14, 3409-3414.	1.8	16
47	Characterization of gene expression and activated signaling pathways in solid-pseudopapillary neoplasm of pancreas. Modern Pathology, 2014, 27, 580-593.	2.9	97
48	Identification of Human Complement Factor B as a Novel Biomarker Candidate for Pancreatic Ductal Adenocarcinoma. Journal of Proteome Research, 2014, 13, 4878-4888.	1.8	42
49	Abundance-Ratio-Based Semiquantitative Analysis of Site-Specific N-Linked Glycopeptides Present in the Plasma of Hepatocellular Carcinoma Patients. Journal of Proteome Research, 2014, 13, 2328-2338.	1.8	39
50	Genome-wide Proteomics, Chromosome-centric Human Proteome Project (C-HPP), Part II. Journal of Proteome Research, 2014, 13, 1-4.	1.8	21
51	Mutation of the lbp-5 gene alters metabolic output in Caenorhabditis elegans. BMB Reports, 2014, 47, 15-20.	1.1	8
52	Alteration in cellular acetylcholine influences dauer formation in Caenorhabditis elegans. BMB Reports, 2014, 47, 80-85.	1.1	5
53	NSBP-1 mediates the effects of cholesterol on insulin/IGF-1 signaling in Caenorhabditis elegans. Cellular and Molecular Life Sciences, 2013, 70, 1623-1636.	2.4	13
54	A First Step Toward Completion of a Genome-Wide Characterization of the Human Proteome. Journal of Proteome Research, 2013, 12, 1-5.	1.8	77

#	Article	IF	CITATIONS
55	GenomewidePDB, a Proteomic Database Exploring the Comprehensive Protein Parts List and Transcriptome Landscape in Human Chromosomes. Journal of Proteome Research, 2013, 12, 106-111.	1.8	21
56	Comprehensive Genome-Wide Proteomic Analysis of Human Placental Tissue for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2013, 12, 2458-2466.	1.8	30
57	Chromosome 11-Centric Human Proteome Analysis of Human Brain Hippocampus Tissue. Journal of Proteome Research, 2013, 12, 97-105.	1.8	20
58	Development of a Method to Quantitate Nematode Pheromone for Study of Small-Molecule Metabolism in <i>Caenorhabditis elegans</i> . Analytical Chemistry, 2013, 85, 2681-2688.	3.2	12
59	Human liver carboxylesterase 1 outperforms alphaâ€fetoprotein as biomarker to discriminate hepatocellular carcinoma from other liver diseases in Korean patients. International Journal of Cancer, 2013, 133, 408-415.	2.3	33
60	Nictation, a dispersal behavior of the nematode Caenorhabditis elegans, is regulated by IL2 neurons. Nature Neuroscience, 2012, 15, 107-112.	7.1	157
61	Uniting ENCODE with genome-wide proteomics. Nature Biotechnology, 2012, 30, 1065-1067.	9.4	45
62	Normalization using a tagged-internal standard assay for analysis of antibody arrays and the evaluation of serological biomarkers for liver disease. Analytica Chimica Acta, 2012, 718, 92-98.	2.6	8
63	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	1.8	135
64	Differential Gel-Based Proteomic Approach for Cancer Biomarker Discovery Using Human Plasma. Methods in Molecular Biology, 2012, 854, 223-237.	0.4	3
65	PanelComposer: A Web-Based Panel Construction Tool for Multivariate Analysis of Disease Biomarker Candidates. Journal of Proteome Research, 2012, 11, 6277-6281.	1.8	9
66	PDHK-2 Deficiency Is Associated with Attenuation of Lipase-Mediated Fat Consumption for the Increased Survival of Caenorhabditis elegans Dauers. PLoS ONE, 2012, 7, e41755.	1.1	6
67	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	9.4	281
68	Quantitative Proteomic Analysis of Human Embryonic Stem Cell Differentiation by 8-Plex iTRAQ Labelling. PLoS ONE, 2012, 7, e38532.	1.1	23
69	Methods for Evaluating the Caenorhabditis elegans Dauer State: Standard Dauer-Formation Assay Using Synthetic Daumones and Proteomic Analysis of O-GlcNAc Modifications. Methods in Cell Biology, 2011, 106, 445-460.	0.5	4
70	Proteomics, Human Proteome Project, and Chromosomes. Journal of Proteome Research, 2011, 10, 210-210.	1.8	38
71	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	2.5	294
72	Proteomic analysis of pancreatic juice for the identification of biomarkers of pancreatic cancer. Journal of Cancer Research and Clinical Oncology, 2011, 137, 1229-1238.	1.2	33

#	Article	IF	CITATIONS
73	Enhanced peptide quantification using spectral count clustering and cluster abundance. BMC Bioinformatics, 2011, 12, 423.	1.2	10
74	A new versatile peptideâ€based size exclusion chromatography platform for global profiling and quantitation of candidate biomarkers in hepatocellular carcinoma specimens. Proteomics, 2011, 11, 1976-1984.	1.3	5
75	Novel Functions of Lipid-binding Protein 5 in Caenorhabditis elegans Fat Metabolism. Journal of Biological Chemistry, 2011, 286, 28111-28118.	1.6	22
76	Contribution of sams-1 and pmt-1 to lipid homoeostasis in adult Caenorhabditis elegans. Journal of Biochemistry, 2011, 149, 529-538.	0.9	49
77	STR-33, a Novel G Protein-coupled Receptor That Regulates Locomotion and Egg Laying in Caenorhabditis elegans. Journal of Biological Chemistry, 2011, 286, 39860-39870.	1.6	4
78	The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , .	2.5	37
79	A Potential Biochemical Mechanism Underlying the Influence of Sterol Deprivation Stress on Caenorhabditis elegans Longevity. Journal of Biological Chemistry, 2011, 286, 7248-7256.	1.6	13
80	A potential role for fatty acid biosynthesis genes during molting and cuticle formation in Caenorhabditis elegans. BMB Reports, 2011, 44, 285-290.	1.1	31
81	Data management and functional annotation of the Korean reference plasma proteome. Proteomics, 2010, 10, 1250-1255.	1.3	8
82	<i>Caenorhabditis elegans</i> proteomics comes of age. Proteomics, 2010, 10, 846-857.	1.3	17
83	The loss of phenol sulfotransferase 1 in hepatocellular carcinogenesis. Proteomics, 2010, 10, 266-276.	1.3	15
84	Contribution of the Peroxisomal acox Gene to the Dynamic Balance of Daumone Production in Caenorhabditis elegans*. Journal of Biological Chemistry, 2010, 285, 29319-29325.	1.6	63
85	FISH: Finding of identical spectra set for Homogenous peptide using two-stage clustering algorithm. , 2010, , .		0
86	Regulation of Dauer Formation by O-GlcNAcylation in Caenorhabditis elegans. Journal of Biological Chemistry, 2010, 285, 2930-2939.	1.6	35
87	Simple Method for Quantitative Analysis of N-Linked Glycoproteins in Hepatocellular Carcinoma Specimens. Journal of Proteome Research, 2010, 9, 308-318.	1.8	43
88	Identification and Characterization of a Dual-Acting Antinematodal Agent against the Pinewood Nematode, Bursaphelenchus xylophilus. PLoS ONE, 2009, 4, e7593.	1.1	17
89	BiomarkerDigger: A versatile disease proteome database and analysis platform for the identification of plasma cancer biomarkers. Proteomics, 2009, 9, 3729-3740.	1.3	19
90	Quantitative analysis of phosphopeptides in search of the disease biomarker from the hepatocellular carcinoma specimen. Proteomics, 2009, 9, 3395-3408.	1.3	53

#	Article	IF	CITATIONS
91	Human plasma carboxylesterase 1, a novel serologic biomarker candidate for hepatocellular carcinoma. Proteomics, 2009, 9, 3989-3999.	1.3	100
92	Proteomic profiling of yeast―and hyphalâ€specific responses of <i>Candida albicans</i> to the antifungal agent, HWYâ€289. Proteomics - Clinical Applications, 2009, 3, 452-461.	0.8	5
93	Endogenous cGMP regulates adult longevity via the insulin signaling pathway in <i>Caenorhabditis elegans</i> . Aging Cell, 2009, 8, 473-483.	3.0	38
94	Proteomic Analysis of Caenorhabditis elegans. Methods in Molecular Biology, 2009, 519, 145-169.	0.4	13
95	<i>Caenorhabditis elegans</i> utilizes dauer pheromone biosynthesis to dispose of toxic peroxisomal fatty acids for cellular homoeostasis. Biochemical Journal, 2009, 422, 61-71.	1.7	76
96	Molecular Time-Course and the Metabolic Basis of Entry into Dauer in Caenorhabditis elegans. PLoS ONE, 2009, 4, e4162.	1.1	58
97	Proteomic Analysis of the Sterol-Mediated Signaling Pathway in Caenorhabditis elegans. Methods in Molecular Biology, 2009, 462, 1-15.	0.4	5
98	Effects of Sterols on the Development and Aging of Caenorhabditis elegans. Methods in Molecular Biology, 2009, 462, 1-13.	0.4	3
99	Establishment of a PF2Dâ€MS/MS platform for rapid profiling and semiquantitative analysis of membrane protein biomarkers. Proteomics, 2008, 8, 2168-2177.	1.3	21
100	Application of a peptideâ€based PF2D platform for quantitative proteomics in disease biomarker discovery. Proteomics, 2008, 8, 3371-3381.	1.3	32
101	IntelliMS: A platform to efficiently manage and visualize tandem mass spectral data. Proteomics, 2008, 8, 4910-4913.	1.3	3
102	Overview and Introduction to Clinical Proteomics. Methods in Molecular Biology, 2008, 428, 1-31.	0.4	26
103	Developmental and reproductive consequences of prolonged non-aging dauer in Caenorhabditis elegans. Biochemical and Biophysical Research Communications, 2008, 368, 588-592.	1.0	24
104	Protein Profiling of Human Plasma Samples by Two-Dimensional Electrophoresis. Methods in Molecular Biology, 2008, 428, 57-75.	0.4	18
105	C. elegans: an invaluable model organism for the proteomics studies of the cholesterol-mediated signaling pathway. Expert Review of Proteomics, 2006, 3, 439-453.	1.3	15
106	Efficient prefractionation of low-abundance proteins in human plasma and construction of a two-dimensional map. , 2006, , 201-219.		0
107	Alteration of the glutamate and GABA transporters in the hippocampus of the Niemann-Pick disease, typeâ€C mouse using proteomic analysis. Proteomics, 2006, 6, 1230-1236.	1.3	27
108	Proteomic analysis of mammalian basic proteins by liquid-based two-dimensional column chromatography. Proteomics, 2006, 6, 1143-1150.	1.3	40

#	Article	IF	CITATIONS
109	Guidelines for the next 10 years of proteomics. Proteomics, 2006, 6, 4-8.	1.3	314
110	Disease Biomarker Discovery in Korea. Proteomics, 2006, 6, 1091-1093.	1.3	0
111	Biomarker discovery from the plasma proteome using multidimensional fractionation proteomics. Current Opinion in Chemical Biology, 2006, 10, 42-49.	2.8	104
112	Chemical structure and biological activity of the Caenorhabditis elegans dauer-inducing pheromone. Nature, 2005, 433, 541-545.	13.7	322
113	Efficient prefractionation of low-abundance proteins in human plasma and construction of a two-dimensional map. Proteomics, 2005, 5, 3386-3396.	1.3	121
114	A functional annotation of subproteomes in human plasma. Proteomics, 2005, 5, 3506-3519.	1.3	82
115	Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database. Proteomics, 2005, 5, 3226-3245.	1.3	766
116	Cholesterol-producing transgenic Caenorhabditis elegans lives longer due to newly acquired enhanced stress resistance. Biochemical and Biophysical Research Communications, 2005, 328, 929-936.	1.0	33
117	Alterations of protein expression in macrophages in response to Candida albicans infection. Molecules and Cells, 2005, 20, 271-9.	1.0	17
118	Proteomic analysis of diet-induced hypercholesterolemic mice. Proteomics, 2004, 4, 514-523.	1.3	37
119	A simple pattern classification method for alcohol-responsive proteins that are differentially expressed in mouse brain. Proteomics, 2004, 4, 3369-3375.	1.3	19
120	A strain-specific alteration of proteomic expression in mouse liver fructose 1,6-bisphosphatase isoforms by alcohol. Proteomics, 2004, 4, 3413-3421.	1.3	6
121	Molecular cloning and biochemical characterization of Candida albicans acyl-CoA:sterol acyltransferase, a potential target of antifungal agents. Biochemical and Biophysical Research Communications, 2004, 319, 911-919.	1.0	13
122	Strategies for the enrichment and identification of basic proteins in proteome projects. Proteomics, 2003, 3, 569-579.	1.3	68
123	Single-step perfusion chromatography with a throughput potential for enhanced peptide detection by matrix-assisted laser desorption/ ionization-mass spectrometry. Proteomics, 2003, 3, 1955-1961.	1.3	53
124	Differential expression of the liver proteome in senescence accelerated mice. Proteomics, 2003, 3, 1883-1894.	1.3	73
125	Proteomic Changes during Disturbance of Cholesterol Metabolism by Azacoprostane Treatment in Caenorhabditis elegans. Molecular and Cellular Proteomics, 2003, 2, 1086-1095.	2.5	40
126	An integrated proteome database for two-dimensional electrophoresis data analysis and laboratory information management system. Proteomics, 2002, 2, 1104-1113.	1.3	46

#	Article	IF	CITATIONS
127	Proteomic alterations of the variants of human aldehyde dehydrogenase isozymes correlate with hepatocellular carcinoma. International Journal of Cancer, 2002, 97, 261-265.	2.3	89
128	Role of cholesterol in germ-line development ofCaenorhabditis elegans. Molecular Reproduction and Development, 2002, 61, 358-366.	1.0	64
129	Proteomic analysis and molecular characterization of tissue ferritin light chain in hepatocellular carcinoma. Hepatology, 2002, 35, 1459-1466.	3.6	98
130	Cholesterol biosynthesis from lanosterol: molecular cloning, chromosomal localization, functional expression and liver-specific gene regulation of rat sterol Δ8-isomerase, a cholesterogenic enzyme with multiple functions. Biochemical Journal, 2001, 353, 689-699.	1.7	17
131	Cholesterol Biosynthesis from Lanosterol. Journal of Biological Chemistry, 1999, 274, 14624-14631.	1.6	61
132	Cholesterol biosynthesis from lanosterol: development of a novel assay method and characterization of rat liver microsomal lanosterol Δ24-reductase. Biochemical Journal, 1997, 326, 609-616.	1.7	85
133	Characterization of an Upstream Regulatory Element of the Human Apolipoprotein E Gene, and Purification of Its Binding Protein from the Human Placenta1. Journal of Biochemistry, 1995, 117, 915-922.	0.9	15
134	Cholesterol Biosynthesis from Lanosterol: Regulation and Purification of Rat Hepatic Sterol 8-Isomerase1. Journal of Biochemistry, 1995, 117, 819-823.	0.9	18