# Young-Ki Paik

## List of Publications by Year in descending order

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|---|---|---|---|
| 134 papers | 6,285 citations | 87888 38 h-index | 76900 74 g-index |
| 136 all docs | 136 docs citations | 136 times ranked | 6875 citing authors |

| # | 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. | 4.1 | 2 |
| 2 | Progress Identifying and Analyzing the Human Proteome: 2021ÂMetrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2021, 20, 5227-5240. | 3.7 | 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. | 3.7 | 2 |
| 4 | A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301. | 12.8 | 152 |
| 5 | Potential Regulatory Role of Human-Carboxylesterase-1 Glycosylation in Liver Cancer Cell Growth. Journal of Proteome Research, 2020, 19, 4867-4883. | 3.7 | 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. | 3.7 | 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. | 3.3 | 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. | 3.7 | 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. | 4.1 | 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. | 3.7 | 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. | 3.7 | 41 |
| 12 | Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116. | 3.7 | 82 |
| 13 | Ascaroside Pheromones: Chemical Biology and Pleiotropic Neuronal Functions. International Journal of Molecular Sciences, 2019, 20, 3898. | 4.1 | 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. | 3.8 | 8 |
| 15 | Prognostic potential of the preoperative plasma complement factor B in resected pancreatic cancer: A pilot study. Cancer Biomarkers, 2019, 24, 335-342. | 1.7 | 25 |
| 16 | Î²-catenin activation down-regulates cell-cell junction-related genes and induces epithelial-to-mesenchymal transition in colorectal cancers. Scientific Reports, 2019, 9, 18440. | 3.3 | 68 |
| 17 | Advances in Identifying and Characterizing the Human Proteome. Journal of Proteome Research, 2019, 18, 4079-4084. | 3.7 | 4 |
| 18 | O-GlcNAcylation of the Tumor Suppressor FOXO3 Triggers Aberrant Cancer Cell Growth. Cancer Research, 2018, 78, 1214-1224. | 0.9 | 34 |

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| 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. | 3.7 | 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. | 3.7 | 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. | 3.7 | 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. | 3.7 | 59 |
| 23 | Identification of Missing Proteins in Human Olfactory Epithelial Tissue by Liquid Chromatographyâ€“Tandem Mass Spectrometry. Journal of Proteome Research, 2018, 17, 4320-4324. | 3.7 | 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. | 3.7 | 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. | 3.7 | 12 |
| 26 | Next Generation Proteomic Pipeline for Chromosome-Based Proteomic Research Using NeXtProt and GENCODE Databases. Journal of Proteome Research, 2017, 16, 4425-4434. | 3.7 | 14 |
| 27 | Advances in the Chromosome-Centric Human Proteome Project: looking to the future. Expert Review of Proteomics, 2017, 14, 1059-1071. | 3.0 | 25 |
| 28 | Genetic deficiency in neuronal peroxisomal fatty acid Î²-oxidation causes the interruption of dauer development in Caenorhabditis elegans. Scientific Reports, 2017, 7, 9358. | 3.3 | 12 |
| 29 | The genetic basis of natural variation in a phoretic behavior. Nature Communications, 2017, 8, 273. | 12.8 | 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. | 3.3 | 17 |
| 31 | MGL-1 on AIY neurons translates starvation to reproductive plasticity via neuropeptide signaling in Caenorhabditis elegans. Developmental Biology, 2017, 430, 80-89. | 2.0 | 14 |
| 32 | Progress and Future Direction of Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2017, 16, 4253-4258. | 3.7 | 14 |
| 33 | Integrated GlycoProteome Analyzer (I-GPA) for Automated Identification and Quantitation of Site-Specific N-Glycosylation. Scientific Reports, 2016, 6, 21175. | 3.3 | 81 |
| 34 | HSF-1 is involved in regulation of ascaroside pheromone biosynthesis by heat stress in Caenorhabditis elegans. Biochemical Journal, 2016, 473, 789-796. | 3.7 | 13 |
| 35 | gFinder: A Web-Based Bioinformatics Tool for the Analysis of N-Glycopeptides. Journal of Proteome Research, 2016, 15, 4116-4125. | 3.7 | 12 |
| 36 | Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970. | 3.7 | 158 |

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| 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. | 3.7 | 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. | 3.7 | 17 |
| 39 | Quantitative Profiling Identifies Potential Regulatory Proteins Involved in Development from Dauer Stage to L4 Stage in Caenorhabditis elegans. Journal of Proteome Research, 2016, 15, 531-539. | 3.7 | 2 |
| 40 | Synthesis of Photoaffinityâ€Labeled Daumone Analogs. Bulletin of the Korean Chemical Society, 2015, 36, 2177-2178. | 1.9 | 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. | 3.7 | 4 |
| 42 | Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431. | 3.7 | 53 |
| 43 | Distinct Protein Expression Profiles of Solid-Pseudopapillary Neoplasms of the Pancreas. Journal of Proteome Research, 2015, 14, 3007-3014. | 3.7 | 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. | 3.7 | 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. | 3.7 | 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. | 3.7 | 16 |
| 47 | Characterization of gene expression and activated signaling pathways in solid-pseudopapillary neoplasm of pancreas. Modern Pathology, 2014, 27, 580-593. | 5.5 | 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. | 3.7 | 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. | 3.7 | 39 |
| 50 | Genome-wide Proteomics, Chromosome-centric Human Proteome Project (C-HPP), Part II. Journal of Proteome Research, 2014, 13, 1-4. | 3.7 | 21 |
| 51 | Mutation of the lbp-5 gene alters metabolic output in Caenorhabditis elegans. BMB Reports, 2014, 47, 15-20. | 2.4 | 8 |
| 52 | Alteration in cellular acetylcholine influences dauer formation in Caenorhabditis elegans. BMB Reports, 2014, 47, 80-85. | 2.4 | 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. | 5.4 | 13 |
| 54 | A First Step Toward Completion of a Genome-Wide Characterization of the Human Proteome. Journal of Proteome Research, 2013, 12, 1-5. | 3.7 | 77 |

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| 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. | 3.7 | 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. | 3.7 | 30 |
| 57 | Chromosome 11-Centric Human Proteome Analysis of Human Brain Hippocampus Tissue. Journal of Proteome Research, 2013, 12, 97-105. | 3.7 | 20 |
| 58 | Development of a Method to Quantitate Nematode Pheromone for Study of Small-Molecule Metabolism in Caenorhabditis elegans. Analytical Chemistry, 2013, 85, 2681-2688. | 6.5 | 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. | 5.1 | 33 |
| 60 | Nictation, a dispersal behavior of the nematode Caenorhabditis elegans, is regulated by IL2 neurons. Nature Neuroscience, 2012, 15, 107-112. | 14.8 | 157 |
| 61 | Uniting ENCODE with genome-wide proteomics. Nature Biotechnology, 2012, 30, 1065-1067. | 17.5 | 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. | 5.4 | 8 |
| 63 | Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013. | 3.7 | 135 |
| 64 | Differential Gel-Based Proteomic Approach for Cancer Biomarker Discovery Using Human Plasma. Methods in Molecular Biology, 2012, 854, 223-237. | 0.9 | 3 |
| 65 | PanelComposer: A Web-Based Panel Construction Tool for Multivariate Analysis of Disease Biomarker Candidates. Journal of Proteome Research, 2012, 11, 6277-6281. | 3.7 | 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. | 2.5 | 6 |
| 67 | The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223. | 17.5 | 281 |
| 68 | Quantitative Proteomic Analysis of Human Embryonic Stem Cell Differentiation by 8-Plex iTRAQ Labelling. PLoS ONE, 2012, 7, e38532. | 2.5 | 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. | 1.1 | 4 |
| 70 | Proteomics, Human Proteome Project, and Chromosomes. Journal of Proteome Research, 2011, 10, 210-210. | 3.7 | 38 |
| 71 | The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993. | 3.8 | 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. | 2.5 | 33 |

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| 73 | Enhanced peptide quantification using spectral count clustering and cluster abundance. BMC Bioinformatics, 2011, 12, 423. | 2.6 | 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. | 2.2 | 5 |
| 75 | Novel Functions of Lipid-binding Protein 5 in Caenorhabditis elegans Fat Metabolism. Journal of Biological Chemistry, 2011, 286, 28111-28118. | 3.4 | 22 |
| 76 | Contribution of sams-1 and pmt-1 to lipid homoeostasis in adult Caenorhabditis elegans. Journal of Biochemistry, 2011, 149, 529-538. | 1.7 | 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. | 3.4 | 4 |
| 78 | The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , . | 3.8 | 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. | 3.4 | 13 |
| 80 | A potential role for fatty acid biosynthesis genes during molting and cuticle formation in Caenorhabditis elegans. BMB Reports, 2011, 44, 285-290. | 2.4 | 31 |
| 81 | Data management and functional annotation of the Korean reference plasma proteome. Proteomics, 2010, 10, 1250-1255. | 2.2 | 8 |
| 82 | Caenorhabditis elegans proteomics comes of age. Proteomics, 2010, 10, 846-857. | 2.2 | 17 |
| 83 | The loss of phenol sulfotransferase 1 in hepatocellular carcinogenesis. Proteomics, 2010, 10, 266-276. | 2.2 | 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. | 3.4 | 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. | 3.4 | 35 |
| 87 | Simple Method for Quantitative Analysis of N-Linked Glycoproteins in Hepatocellular Carcinoma Specimens. Journal of Proteome Research, 2010, 9, 308-318. | 3.7 | 43 |
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| 89 | BiomarkerDigger: A versatile disease proteome database and analysis platform for the identification of plasma cancer biomarkers. Proteomics, 2009, 9, 3729-3740. | 2.2 | 19 |
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| 94 | Proteomic Analysis of Caenorhabditis elegans. Methods in Molecular Biology, 2009, 519, 145-169. | 0.9 | 13 |
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| 97 | Proteomic Analysis of the Sterol-Mediated Signaling Pathway in Caenorhabditis elegans. Methods in Molecular Biology, 2009, 462, 1-15. | 0.9 | 5 |
| 98 | Effects of Sterols on the Development and Aging of Caenorhabditis elegans. Methods in Molecular Biology, 2009, 462, 1-13. | 0.9 | 3 |
| 99 | Establishment of a PF2Dâ€•MS/MS platform for rapid profiling and semiquantitative analysis of membrane protein biomarkers. Proteomics, 2008, 8, 2168-2177. | 2.2 | 21 |
| 100 | Application of a peptideâ€•based PF2D platform for quantitative proteomics in disease biomarker discovery. Proteomics, 2008, 8, 3371-3381. | 2.2 | 32 |
| 101 | IntelliMS: A platform to efficiently manage and visualize tandem mass spectral data. Proteomics, 2008, 8, 4910-4913. | 2.2 | 3 |
| 102 | Overview and Introduction to Clinical Proteomics. Methods in Molecular Biology, 2008, 428, 1-31. | 0.9 | 26 |
| 103 | Developmental and reproductive consequences of prolonged non-aging dauer in Caenorhabditis elegans. Biochemical and Biophysical Research Communications, 2008, 368, 588-592. | 2.1 | 24 |
| 104 | Protein Profiling of Human Plasma Samples by Two-Dimensional Electrophoresis. Methods in Molecular Biology, 2008, 428, 57-75. | 0.9 | 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. | 3.0 | 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. | 2.2 | 27 |
| 108 | Proteomic analysis of mammalian basic proteins by liquid-based two-dimensional column chromatography. Proteomics, 2006, 6, 1143-1150. | 2.2 | 40 |

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| 109 | Guidelines for the next 10 years of proteomics. Proteomics, 2006, 6, 4-8. | 2.2 | 314 |
| 110 | Disease Biomarker Discovery in Korea. Proteomics, 2006, 6, 1091-1093. | 2.2 | 0 |
| 111 | Biomarker discovery from the plasma proteome using multidimensional fractionation proteomics. Current Opinion in Chemical Biology, 2006, 10, 42-49. | 6.1 | 104 |
| 112 | Chemical structure and biological activity of the Caenorhabditis elegans dauer-inducing pheromone. Nature, 2005, 433, 541-545. | 27.8 | 322 |
| 113 | Efficient prefractionation of low-abundance proteins in human plasma and construction of a two-dimensional map. Proteomics, 2005, 5, 3386-3396. | 2.2 | 121 |
| 114 | A functional annotation of subproteomes in human plasma. Proteomics, 2005, 5, 3506-3519. | 2.2 | 82 |
| 115 | Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35â€‰collaborating laboratories and multiple analytical groups, generating a core dataset of 3020â€‰proteins and a publiclyâ€available database. Proteomics, 2005, 5, 3226-3245. | 2.2 | 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. | 2.1 | 33 |
| 117 | Alterations of protein expression in macrophages in response to Candida albicans infection. Molecules and Cells, 2005, 20, 271-9. | 2.6 | 17 |
| 118 | Proteomic analysis of dietâ€induced hypercholesterolemic mice. Proteomics, 2004, 4, 514-523. | 2.2 | 37 |
| 119 | A simple pattern classification method for alcohol-responsive proteins that are differentially expressed in mouse brain. Proteomics, 2004, 4, 3369-3375. | 2.2 | 19 |
| 120 | A strain-specific alteration of proteomic expression in mouse liver fructose 1,6-bisphosphatase isoforms by alcohol. Proteomics, 2004, 4, 3413-3421. | 2.2 | 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. | 2.1 | 13 |
| 122 | Strategies for the enrichment and identification of basic proteins in proteome projects. Proteomics, 2003, 3, 569-579. | 2.2 | 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. | 2.2 | 53 |
| 124 | Differential expression of the liver proteome in senescence accelerated mice. Proteomics, 2003, 3, 1883-1894. | 2.2 | 73 |
| 125 | Proteomic Changes during Disturbance of Cholesterol Metabolism by Azacoprostane Treatment in Caenorhabditis elegans. Molecular and Cellular Proteomics, 2003, 2, 1086-1095. | 3.8 | 40 |
| 126 | An integrated proteome database for two-dimensional electrophoresis data analysis and laboratory information management system. Proteomics, 2002, 2, 1104-1113. | 2.2 | 46 |

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| 127 | Proteomic alterations of the variants of human aldehyde dehydrogenase isozymes correlate with hepatocellular carcinoma. International Journal of Cancer, 2002, 97, 261-265. | 5.1 | 89 |
| 128 | Role of cholesterol in germ-line development ofCaenorhabditis elegans. Molecular Reproduction and Development, 2002, 61, 358-366. | 2.0 | 64 |
| 129 | Proteomic analysis and molecular characterization of tissue ferritin light chain in hepatocellular carcinoma. Hepatology, 2002, 35, 1459-1466. | 7.3 | 98 |
| 130 | Cholesterol biosynthesis from lanosterol: molecular cloning, chromosomal localization, functional expression and liver-specific gene regulation of rat sterol Î”8-isomerase, a cholesterogenic enzyme with multiple functions. Biochemical Journal, 2001, 353, 689-699. | 3.7 | 17 |
| 131 | Cholesterol Biosynthesis from Lanosterol. Journal of Biological Chemistry, 1999, 274, 14624-14631. | 3.4 | 61 |
| 132 | Cholesterol biosynthesis from lanosterol: development of a novel assay method and characterization of rat liver microsomal lanosterol Î”24-reductase. Biochemical Journal, 1997, 326, 609-616. | 3.7 | 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. | 1.7 | 15 |
| 134 | Cholesterol Biosynthesis from Lanosterol: Regulation and Purification of Rat Hepatic Sterol 8-Isomerase1. Journal of Biochemistry, 1995, 117, 819-823. | 1.7 | 18 |