

Chris T A Evelo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4933825/publications.pdf>

Version: 2024-02-01

176
papers

17,996
citations

61984

43
h-index

16183

124
g-index

188
all docs

188
docs citations

188
times ranked

34379
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of In Utero Folate Exposure on DNA Methylation and Its Potential Relevance for Later-Life Health—Evidence from Mouse Models Translated to Human Cohorts. <i>Molecular Nutrition and Food Research</i> , 2022, 66, e2100789.	3.3	2
2	A systematically derived overview of the non-ubiquitous pathways and genes that define the molecular and genetic signature of the healthy trabecular meshwork. <i>Genomics</i> , 2022, , 110280.	2.9	1
3	The AOP-DB RDF: Applying FAIR Principles to the Semantic Integration of AOP Data Using the Research Description Framework. <i>Frontiers in Toxicology</i> , 2022, 4, 803983.	3.1	5
4	PSnpBind: a database of mutated binding site protein–ligand complexes constructed using a multithreaded virtual screening workflow. <i>Journal of Cheminformatics</i> , 2022, 14, 8.	6.1	5
5	Providing Adverse Outcome Pathways from the AOP-Wiki in a Semantic Web Format to Increase Usability and Accessibility of the Content. <i>Applied in Vitro Toxicology</i> , 2022, 8, 2-13.	1.1	10
6	A formalization of one of the main claims of “Overlap of vitamin A and vitamin D target genes with CAKUT-related processes” by Ozisik et al. 2021. <i>Data Science</i> , 2022, 5, 25-27.	0.9	0
7	Understanding signaling and metabolic paths using semantified and harmonized information about biological interactions. <i>PLoS ONE</i> , 2022, 17, e0263057.	2.5	1
8	A Community-Driven, Openly Accessible Molecular Pathway Integrating Knowledge on Malignant Pleural Mesothelioma. <i>Frontiers in Oncology</i> , 2022, 12, 849640.	2.8	4
9	A Simple Standard for Sharing Ontological Mappings (SSSOM). <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	23
10	Blunted nutrient-response pathways in adipose tissue following high fat meals in men with metabolic syndrome: A randomized postprandial transcriptomic study. <i>Clinical Nutrition</i> , 2021, 40, 1355-1366.	5.0	2
11	ELIXIR–EXCELERATE: establishing Europe’s data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021, 40, e107409.	7.8	18
12	Overlap of vitamin A and vitamin D target genes with CAKUT-related processes. <i>F1000Research</i> , 2021, 10, 395.	1.6	5
13	A resource to explore the discovery of rare diseases and their causative genes. <i>Scientific Data</i> , 2021, 8, 124.	5.3	11
14	Assessing the Contribution of Relative Macrophage Frequencies to Subcutaneous Adipose Tissue. <i>Frontiers in Nutrition</i> , 2021, 8, 675935.	3.7	2
15	Ten simple rules to make your publication look better. <i>PLoS Computational Biology</i> , 2021, 17, e1008938.	3.2	2
16	Integrative multiomics analysis of human atherosclerosis reveals a serum response factor–driven network associated with intraplaque hemorrhage. <i>Clinical and Translational Medicine</i> , 2021, 11, e458.	4.0	33
17	Tolerogenic effects of 1,25-dihydroxyvitamin D on dendritic cells involve induction of fatty acid synthesis. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2021, 211, 105891.	2.5	11
18	Ten simple rules for creating reusable pathway models for computational analysis and visualization. <i>PLoS Computational Biology</i> , 2021, 17, e1009226.	3.2	13

#	ARTICLE	IF	CITATIONS
19	Investigating the Molecular Processes behind the Cell-Specific Toxicity Response to Titanium Dioxide Nanobelts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9432.	4.1	1
20	A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. <i>Scientific Data</i> , 2021, 8, 10.	5.3	12
21	WikiPathways: connecting communities. <i>Nucleic Acids Research</i> , 2021, 49, D613-D621.	14.5	519
22	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
23	Comparison of metabolic states using genome-scale metabolic models. <i>PLoS Computational Biology</i> , 2021, 17, e1009522.	3.2	4
24	An interferon-related signature characterizes the whole blood transcriptome profile of insulin-resistant individuals—the CODAM study. <i>Genes and Nutrition</i> , 2021, 16, 22.	2.5	3
25	Comprehensive bioinformatics analysis of trabecular meshwork gene expression data to unravel the molecular pathogenesis of primary open-angle glaucoma. <i>Acta Ophthalmologica</i> , 2020, 98, 48-57.	1.1	18
26	Integrated analysis of human transcriptome data for Rett syndrome finds a network of involved genes. <i>World Journal of Biological Psychiatry</i> , 2020, 21, 712-725.	2.6	19
27	FAIR Principles: Interpretations and Implementation Considerations. <i>Data Intelligence</i> , 2020, 2, 10-29.	1.5	149
28	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	5.3	99
29	Stratifying cellular metabolism during weight loss: an interplay of metabolism, metabolic flexibility and inflammation. <i>Scientific Reports</i> , 2020, 10, 1651.	3.3	8
30	EFMviz: A COBRA Toolbox Extension to Visualize Elementary Flux Modes in Genome-Scale Metabolic Models. <i>Metabolites</i> , 2020, 10, 66.	2.9	7
31	Identification of Biological Pathways Contributing to Marbling in Skeletal Muscle to Improve Beef Cattle Breeding. <i>Frontiers in Genetics</i> , 2020, 10, 1370.	2.3	14
32	The Molecular Processes in the Trabecular Meshwork After Exposure to Corticosteroids and in Corticosteroid-Induced Ocular Hypertension. , 2020, 61, 24.		13
33	The need for standardisation in life science research - an approach to excellence and trust.. <i>F1000Research</i> , 2020, 9, 1398.	1.6	7
34	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
35	The need for standardisation in life science research - an approach to excellence and trust.. <i>F1000Research</i> , 2020, 9, 1398.	1.6	1
36	Review and gap analysis: molecular pathways leading to fetal alcohol spectrum disorders. <i>Molecular Psychiatry</i> , 2019, 24, 10-17.	7.9	52

#	ARTICLE	IF	CITATIONS
37	Network Analysis of Genome-Wide Association Studies for Chronic Obstructive Pulmonary Disease in the Context of Biological Pathways. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 1439-1441.	5.6	2
38	Logical modelling reveals the PDC-PDK interaction as the regulatory switch driving metabolic flexibility at the cellular level. <i>Genes and Nutrition</i> , 2019, 14, 27.	2.5	9
39	A bioinformatics workflow to decipher transcriptomic data from vitamin D studies. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 189, 28-35.	2.5	6
40	Beyond Pathway Analysis: Identification of Active Subnetworks in Rett Syndrome. <i>Frontiers in Genetics</i> , 2019, 10, 59.	2.3	10
41	Subcutaneous Adipose Tissue and Systemic Inflammation Are Associated With Peripheral but Not Hepatic Insulin Resistance in Humans. <i>Diabetes</i> , 2019, 68, 2247-2258.	0.6	35
42	Prader-Willi syndrome and Angelman syndrome: Visualisation of the molecular pathways for two chromosomal disorders. <i>World Journal of Biological Psychiatry</i> , 2019, 20, 670-682.	2.6	13
43	WikiPathways: a multifaceted pathway database bridging metabolomics to other omics research. <i>Nucleic Acids Research</i> , 2018, 46, D661-D667.	14.5	708
44	Advancing food, nutrition, and health research in Europe by connecting and building research infrastructures in a DISH-RI: Results of the EuroDISH project. <i>Trends in Food Science and Technology</i> , 2018, 73, 58-66.	15.1	19
45	<i>MECP2</i> variation in Rett syndrome-An overview of current coverage of genetic and phenotype data within existing databases. <i>Human Mutation</i> , 2018, 39, 914-924.	2.5	15
46	A Data Fusion Pipeline for Generating and Enriching Adverse Outcome Pathway Descriptions. <i>Toxicological Sciences</i> , 2018, 162, 264-275.	3.1	51
47	Integration among databases and data sets to support productive nanotechnology: Challenges and recommendations. <i>NanoImpact</i> , 2018, 9, 85-101.	4.5	56
48	Pathway analysis of transcriptomic data shows immunometabolic effects of vitamin D. <i>Journal of Molecular Endocrinology</i> , 2018, 60, 95-108.	2.5	26
49	Introducing WikiPathways as a Data-Source to Support Adverse Outcome Pathways for Regulatory Risk Assessment of Chemicals and Nanomaterials. <i>Frontiers in Genetics</i> , 2018, 9, 661.	2.3	34
50	Biological Pathways Leading From <i>ANGPTL8</i> to Diabetes Mellitus—A Co-expression Network Based Analysis. <i>Frontiers in Physiology</i> , 2018, 9, 1841.	2.8	8
51	Profiling Cellular Processes in Adipose Tissue during Weight Loss Using Time Series Gene Expression. <i>Genes</i> , 2018, 9, 525.	2.4	4
52	Exploring the cellular network of metabolic flexibility in the adipose tissue. <i>Genes and Nutrition</i> , 2018, 13, 17.	2.5	12
53	Role of $1\alpha,25$ -Dihydroxyvitamin D ₃ in Adipogenesis of SCBS Cells: New Insights into Human Preadipocyte Proliferation. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 397-408.	1.6	18
54	Differential protein expression of hippocampal cells associated with heavy metals (Pb, As, and MeHg) neurotoxicity: Deepening into the molecular mechanism of neurodegenerative diseases. <i>Journal of Proteomics</i> , 2018, 187, 106-125.	2.4	38

#	ARTICLE	IF	CITATIONS
55	From SNPs to pathways: Biological interpretation of type 2 diabetes (T2DM) genome wide association study (GWAS) results. PLoS ONE, 2018, 13, e0193515.	2.5	34
56	Explicit interaction information from WikiPathways in RDF facilitates drug discovery in the Open PHACTS Discovery Platform. F1000Research, 2018, 7, 75.	1.6	7
57	Explicit interaction information from WikiPathways in RDF facilitates drug discovery in the Open PHACTS Discovery Platform. F1000Research, 2018, 7, 75.	1.6	6
58	CyTargetLinker app update: A flexible solution for network extension in Cytoscape. F1000Research, 2018, 7, 743.	1.6	26
59	CyTargetLinker app update: A flexible solution for network extension in Cytoscape. F1000Research, 2018, 7, 743.	1.6	18
60	Maternal folate depletion during early development and high fat feeding from weaning elicit similar changes in gene expression, but not in DNA methylation, in adult offspring. Molecular Nutrition and Food Research, 2017, 61, 1600713.	3.3	8
61	Sexual Dimorphism, Age, and Fat Mass Are Key Phenotypic Drivers of Proteomic Signatures. Journal of Proteome Research, 2017, 16, 4122-4133.	3.7	14
62	Visualizing the regulatory role of Angiopoietin-like protein 8 (ANGPTL8) in glucose and lipid metabolic pathways. Genomics, 2017, 109, 408-418.	2.9	38
63	The Chemistry Development Kit (CDK) v2.0: atom typing, depiction, molecular formulas, and substructure searching. Journal of Cheminformatics, 2017, 9, 33.	6.1	275
64	A Review of Pathway-Based Analysis Tools That Visualize Genetic Variants. Frontiers in Genetics, 2017, 8, 174.	2.3	67
65	Organ-Specific Gene Expression Changes in the Fetal Liver and Placenta in Response to Maternal Folate Depletion. Nutrients, 2016, 8, 661.	4.1	9
66	Using the Semantic Web for Rapid Integration of WikiPathways with Other Biological Online Data Resources. PLoS Computational Biology, 2016, 12, e1004989.	3.2	33
67	Hypoxia increases genome-wide bivalent epigenetic marking by specific gain of H3K27me3. Epigenetics and Chromatin, 2016, 9, 46.	3.9	63
68	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
69	WikiPathways: capturing the full diversity of pathway knowledge. Nucleic Acids Research, 2016, 44, D488-D494.	14.5	380
70	The systems biology format converter. BMC Bioinformatics, 2016, 17, 154.	2.6	30
71	New insights in Rett syndrome using pathway analysis for transcriptomics data. Wiener Medizinische Wochenschrift, 2016, 166, 346-352.	1.1	9
72	Gene promoter DNA methylation patterns have a limited role in orchestrating transcriptional changes in the fetal liver in response to maternal folate depletion during pregnancy. Molecular Nutrition and Food Research, 2016, 60, 2031-2042.	3.3	21

#	ARTICLE	IF	CITATIONS
73	Rett syndrome " biological pathways leading from MECP2 to disorder phenotypes. Orphanet Journal of Rare Diseases, 2016, 11, 158.	2.7	63
74	XMetDB: an open access database for xenobiotic metabolism. Journal of Cheminformatics, 2016, 8, 47.	6.1	13
75	Quantitative analysis of ChIP-seq data uncovers dynamic and sustained H3K4me3 and H3K27me3 modulation in cancer cells under hypoxia. Epigenetics and Chromatin, 2016, 9, 48.	3.9	23
76	Reactome from a WikiPathways Perspective. PLoS Computational Biology, 2016, 12, e1004941.	3.2	35
77	diXa: a data infrastructure for chemical safety assessment. Bioinformatics, 2015, 31, 1505-1507.	4.1	40
78	PathVisio 3: An Extendable Pathway Analysis Toolbox. PLoS Computational Biology, 2015, 11, e1004085.	3.2	393
79	Integrative network-based analysis of mRNA and microRNA expression in 1,25-dihydroxyvitamin D3-treated cancer cells. Genes and Nutrition, 2015, 10, 35.	2.5	11
80	Automatically visualise and analyse data on pathways using PathVisioRPC from any programming environment. BMC Bioinformatics, 2015, 16, 267.	2.6	13
81	A user-friendly workflow for analysis of Illumina gene expression bead array data available at the arrayanalysis.org portal. BMC Genomics, 2015, 16, 482.	2.8	14
82	The Dutch Techcentre for Life Sciences: Enabling data-intensive life science research in the Netherlands. F1000Research, 2015, 4, 33.	1.6	8
83	The Dutch Techcentre for Life Sciences: Enabling data-intensive life science research in the Netherlands. F1000Research, 2015, 4, 33.	1.6	7
84	The Application of the Open Pharmacological Concepts Triple Store (Open PHACTS) to Support Drug Discovery Research. PLoS ONE, 2014, 9, e115460.	2.5	31
85	A network biology workflow to study transcriptomics data of the diabetic liver. BMC Genomics, 2014, 15, 971.	2.8	29
86	Consensus statement understanding health and malnutrition through a systems approach: the ENOUGH program for early life. Genes and Nutrition, 2014, 9, 378.	2.5	26
87	Transcriptome analysis of peripheral blood mononuclear cells in human subjects following a 36h fast provides evidence of effects on genes regulating inflammation, apoptosis and energy metabolism. Genes and Nutrition, 2014, 9, 432.	2.5	11
88	Applying linked data approaches to pharmacology: Architectural decisions and implementation. Semantic Web, 2014, 5, 101-113.	1.9	41
89	Integrated visualization of a multi-omics study of starvation in mouse intestine. Journal of Integrative Bioinformatics, 2014, 11, 1-16.	1.5	9
90	Scientific Lenses to Support Multiple Views over Linked Chemistry Data. Lecture Notes in Computer Science, 2014, , 98-113.	1.3	16

#	ARTICLE	IF	CITATIONS
91	WikiPathways App for Cytoscape: Making biological pathways amenable to network analysis and visualization. <i>F1000Research</i> , 2014, 3, 152.	1.6	57
92	Integrated visualization of a multi-omics study of starvation in mouse intestine. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 235.	1.5	6
93	A pathway approach to investigate the function and regulation of SREBPs. <i>Genes and Nutrition</i> , 2013, 8, 289-300.	2.5	50
94	User-friendly solutions for microarray quality control and pre-processing on ArrayAnalysis.org. <i>Nucleic Acids Research</i> , 2013, 41, W71-W76.	14.5	127
95	CyTargetLinker: A Cytoscape App to Integrate Regulatory Interactions in Network Analysis. <i>PLoS ONE</i> , 2013, 8, e82160.	2.5	117
96	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	21.4	362
97	GO-Elite: a flexible solution for pathway and ontology over-representation. <i>Bioinformatics</i> , 2012, 28, 2209-2210.	4.1	268
98	WikiPathways: building research communities on biological pathways. <i>Nucleic Acids Research</i> , 2012, 40, D1301-D1307.	14.5	479
99	An evaluation of two-channel ChIP-on-chip and DNA methylation microarray normalization strategies. <i>BMC Genomics</i> , 2012, 13, 42.	2.8	17
100	Open PHACTS: semantic interoperability for drug discovery. <i>Drug Discovery Today</i> , 2012, 17, 1188-1198.	6.4	274
101	Marginal selenium deficiency down-regulates inflammation-related genes in splenic leukocytes of the mouse. <i>Journal of Nutritional Biochemistry</i> , 2012, 23, 1170-1177.	4.2	31
102	Molecular Pathways Involved in Prostate Carcinogenesis: Insights from Public Microarray Datasets. <i>PLoS ONE</i> , 2012, 7, e49831.	2.5	17
103	Effect of supplementation with an 80:20 <i>cis</i> : <i>trans</i> 11 conjugated linoleic acid blend on the human platelet proteome. <i>Molecular Nutrition and Food Research</i> , 2012, 56, 1148-1159.	3.3	14
104	Bilberries potentially alleviate stress-related retinal gene expression induced by a high-fat diet in mice. <i>Molecular Vision</i> , 2012, 18, 2338-51.	1.1	16
105	Measuring impact in online resources with the CI-number (the CitedIn Number for online impact). <i>Nature Precedings</i> , 2011, , .	0.1	1
106	Answering biological questions: querying a systems biology database for nutrigenomics. <i>Genes and Nutrition</i> , 2011, 6, 81-87.	2.5	4
107	Exploring pathway interactions in insulin resistant mouse liver. <i>BMC Systems Biology</i> , 2011, 5, 127.	3.0	17
108	2D-electrophoresis and multiplex immunoassay proteomic analysis of different body fluids and cellular components reveal known and novel markers for extended fasting. <i>BMC Medical Genomics</i> , 2011, 4, 24.	1.5	26

#	ARTICLE	IF	CITATIONS
109	Alterations in hepatic one-carbon metabolism and related pathways following a high-fat dietary intervention. <i>Physiological Genomics</i> , 2011, 43, 408-416.	2.3	64
110	From Nanotechnology to Nanomedicine: Applications to Cancer Research. <i>Current Molecular Medicine</i> , 2010, 10, 640-652.	1.3	148
111	Challenges of molecular nutrition research 6: the nutritional phenotype database to store, share and evaluate nutritional systems biology studies. <i>Genes and Nutrition</i> , 2010, 5, 189-203.	2.5	64
112	Connecting the Human Variome Project to nutrigenomics. <i>Genes and Nutrition</i> , 2010, 5, 275-283.	2.5	6
113	The Micronutrient Genomics Project: a community-driven knowledge base for micronutrient research. <i>Genes and Nutrition</i> , 2010, 5, 285-296.	2.5	47
114	The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. <i>BMC Bioinformatics</i> , 2010, 11, 5.	2.6	180
115	Biotransformation pathway maps in WikiPathways enable direct visualization of drug metabolism related expression changes. <i>Drug Discovery Today</i> , 2010, 15, 851-858.	6.4	33
116	Nature Europe site should highlight most productive countries. <i>Nature</i> , 2010, 465, 685-685.	27.8	1
117	The nutritional phenotype database*. A real data structure for systems biology. <i>Nature Precedings</i> , 2010, , .	0.1	0
118	Time-Resolved and Tissue-Specific Systems Analysis of the Pathogenesis of Insulin Resistance. <i>PLoS ONE</i> , 2010, 5, e8817.	2.5	126
119	A Combined Transcriptomics and Lipidomics Analysis of Subcutaneous, Epididymal and Mesenteric Adipose Tissue Reveals Marked Functional Differences. <i>PLoS ONE</i> , 2010, 5, e11525.	2.5	79
120	Finding the Right Questions: Exploratory Pathway Analysis to Enhance Biological Discovery in Large Datasets. <i>PLoS Biology</i> , 2010, 8, e1000472.	5.6	49
121	Identification of novel ER- α target genes in breast cancer cells: Gene- and cell-selective co-regulator recruitment at target promoters determines the response to 17 β -estradiol and tamoxifen. <i>Molecular and Cellular Endocrinology</i> , 2010, 314, 90-100.	3.2	28
122	Community curation on WikiPathways: How we assist knowledge collection. <i>Nature Precedings</i> , 2009, , .	0.1	1
123	Four selenoproteins, protein biosynthesis, and Wnt signalling are particularly sensitive to limited selenium intake in mouse colon. <i>Molecular Nutrition and Food Research</i> , 2009, 53, 1561-1572.	3.3	102
124	An integrated bioinformatics approach to improve two-color microarray quality-control: impact on biological conclusions. <i>Genes and Nutrition</i> , 2009, 4, 123-127.	2.5	0
125	Pathway Enrichment Based on Text Mining and Its Validation on Carotenoid and Vitamin A Metabolism. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 367-379.	2.0	14
126	Reduction of colonic inflammation in HLA-B27 transgenic rats by feeding Marie M \ddot{a} rtinard apples, rich in polyphenols. <i>British Journal of Nutrition</i> , 2009, 102, 1620.	2.3	43

#	ARTICLE	IF	CITATIONS
127	Mining Biological Pathways Using WikiPathways Web Services. PLoS ONE, 2009, 4, e6447.	2.5	100
128	Validating nutrient-related gene expression changes from microarrays using RT2 PCR-arrays. Genes and Nutrition, 2008, 3, 153-157.	2.5	22
129	Bioinformatic interrogation of expression array data to identify nutritionally regulated genes potentially modulated by DNA methylation. Genes and Nutrition, 2008, 3, 167-171.	2.5	6
130	The role of bioinformatics in pathway curation. Genes and Nutrition, 2008, 3, 139-142.	2.5	14
131	Bioinformatics for the NuGO proof of principle study: analysis of gene expression in muscle of ApoE3*Leiden mice on a high-fat diet using PathVisio. Genes and Nutrition, 2008, 3, 185-191.	2.5	5
132	The NuGO proof of principle study package: a collaborative research effort of the European Nutrigenomics Organisation. Genes and Nutrition, 2008, 3, 147-151.	2.5	22
133	Presenting and exploring biological pathways with PathVisio. BMC Bioinformatics, 2008, 9, 399.	2.6	305
134	The public road to high-quality curated biological pathways. Drug Discovery Today, 2008, 13, 856-862.	6.4	44
135	WikiPathways: Pathway Editing for the People. PLoS Biology, 2008, 6, e184.	5.6	542
136	Impact of supervised gene signatures of early hypoxia on patient survival. Radiotherapy and Oncology, 2007, 83, 374-382.	0.6	80
137	Differential valine metabolism in adipose tissue of low and high fat oxidizing obese subjects. Proteomics - Clinical Applications, 2007, 1, 1306-1315.	1.6	14
138	Genetic variation in thioredoxin interacting protein (TXNIP) is associated with hypertriglyceridaemia and blood pressure in diabetes mellitus. Diabetic Medicine, 2007, 24, 498-504.	2.3	47
139	Linking microarray reporters with protein functions. BMC Bioinformatics, 2007, 8, 360.	2.6	12
140	Fasting induces a biphasic adaptive metabolic response in murine small intestine. BMC Genomics, 2007, 8, 361.	2.8	41
141	Gene expression in human small intestinal mucosa in vivo is mediated by iron-induced oxidative stress. Physiological Genomics, 2006, 25, 242-249.	2.3	10
142	Gene profiling of cathepsin K deficiency in atherogenesis: profibrotic but lipogenic. Journal of Pathology, 2006, 210, 334-343.	4.5	26
143	Microarray profiling of human white adipose tissue after exogenous leptin injection. European Journal of Clinical Investigation, 2006, 36, 153-163.	3.4	21
144	Biologically relevant effects of mRNA amplification on gene expression profiles. BMC Bioinformatics, 2006, 7, 200.	2.6	26

#	ARTICLE	IF	CITATIONS
145	Erythrocyte antioxidant defense response against cigarette smoking in humans—the glutathione S-transferase vulnerability. <i>Journal of Biochemical and Molecular Toxicology</i> , 2005, 19, 226-233.	3.0	39
146	Protein profiling of 3T3-L1 adipocyte differentiation and (tumor necrosis factor α -mediated) starvation. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 492-503.	5.4	29
147	Gene Profiling in Atherosclerosis Reveals a Key Role for Small Inducible Cytokines. <i>Circulation</i> , 2005, 111, 3443-3452.	1.6	100
148	Up-regulation of CD36/FAT in preadipocytes in familial combined hyperlipidemia. <i>FASEB Journal</i> , 2005, 19, 2063-2065.	0.5	16
149	A systematic review of large scale and heterogeneous gene array data in heart failure. <i>Journal of Molecular and Cellular Cardiology</i> , 2005, 38, 425-432.	1.9	45
150	Thrombospondin-2 Is Essential for Myocardial Matrix Integrity. <i>Circulation Research</i> , 2004, 95, 515-522.	4.5	179
151	Role of the RhoA/Rho Kinase System in Flow-Related Remodeling of Rat Mesenteric Small Arteries in Vivo. <i>Journal of Vascular Research</i> , 2004, 41, 277-290.	1.4	46
152	Effect of Vitamin E on Glutathione-Dependent Enzymes. <i>Drug Metabolism Reviews</i> , 2003, 35, 215-253.	3.6	59
153	Inhibition of various glutathione S-transferase isoenzymes by RRR- α -tocopherol. <i>Toxicology in Vitro</i> , 2003, 17, 245-251.	2.4	34
154	Tocotrienols Inhibit Human Glutathione S-Transferase P1-1. <i>IUBMB Life</i> , 2002, 54, 81-84.	3.4	18
155	α -Tocopherol Inhibits Human Glutathione S-Transferase γ . <i>Biochemical and Biophysical Research Communications</i> , 2001, 280, 631-633.	2.1	24
156	Inhibition of human glutathione S-transferase P1-1 by tocopherols and α -tocopherol derivatives. <i>BBA - Proteins and Proteomics</i> , 2001, 1548, 23-28.	2.1	25
157	No reduction of α -tocopherol quinone by glutathione in rat liver microsomes. <i>Biochemical Pharmacology</i> , 2001, 61, 715-719.	4.4	12
158	Hypochlorous acid is a potent inhibitor of GST P1-1. <i>Chemico-Biological Interactions</i> , 2001, 138, 77-83.	4.0	14
159	A Study on the Interaction between Hydroxylamine Analogues and Oxyhemoglobin in Intact Erythrocytes. <i>Blood Cells, Molecules, and Diseases</i> , 2000, 26, 373-386.	1.4	5
160	Oxidative effects in human erythrocytes caused by some oximes and hydroxylamine. <i>Archives of Toxicology</i> , 1998, 72, 270-276.	4.2	15
161	Two Mechanisms for Toxic Effects of Hydroxylamines in Human Erythrocytes: Involvement of Free Radicals and Risk of Potentiation. <i>Blood Cells, Molecules, and Diseases</i> , 1998, 24, 280-295.	1.4	22
162	Only the glutathione dependent antioxidant enzymes are inhibited by haematotoxic hydroxylamines. <i>Human and Experimental Toxicology</i> , 1998, 17, 554-559.	2.2	7

#	ARTICLE	IF	CITATIONS
163	Hydroxylamine Treatment Increases Glutathione-Protein and Protein-Protein Binding in Human Erythrocytes. <i>Blood Cells, Molecules, and Diseases</i> , 1997, 23, 323-336.	1.4	20
164	In vitro haematotoxic effects of three methylated hydroxylamines. <i>Archives of Toxicology</i> , 1997, 71, 299-305.	4.2	11
165	The Use of Biokinetics and in Vitro Methods in Toxicological Risk Evaluation. <i>ATLA Alternatives To Laboratory Animals</i> , 1996, 24, 473-497.	1.0	30
166	Development of a software package for computer simulations: The use of a sorted event list for reduction of calculation times. <i>Computers in Biology and Medicine</i> , 1993, 23, 273-281.	7.0	1
167	Glutathione depletion in human erythrocytes as an indicator for microsomal activation of cyclophosphamide and 3-hydroxyacetanilide. <i>Toxicology</i> , 1993, 84, 157-170.	4.2	3
168	Influence of oxygen supply on liver condition and elimination of dimethylacetamide in the isolated perfused rat liver. <i>Toxicology in Vitro</i> , 1992, 6, 357-365.	2.4	7
169	Genetic deficiency of human class mu glutathione S-transferase isoenzymes in relation to the urinary excretion of the mercapturic acids of Z- and E-1,3-dichloropropene. <i>Archives of Toxicology</i> , 1991, 65, 95-99.	4.2	21
170	Separation of human haemoglobin alkylated at Î²93 cysteine from its native form by fast protein liquid chromatography. <i>Biomedical Applications</i> , 1988, 427, 335-340.	1.7	1
171	WikiPathways App for Cytoscape: Making biological pathways amenable to network analysis and visualization. <i>F1000Research</i> , 0, 3, 152.	1.6	5
172	Providing gene-to-variant and variant-to-gene database identifier mappings to use with BridgeDb mapping services.. <i>F1000Research</i> , 0, 7, 1390.	1.6	1
173	ELIXIR and Toxicology: a community in development. <i>F1000Research</i> , 0, 10, 1129.	1.6	3
174	Overlap of vitamin A and vitamin D target genes with CAKUT-related processes. <i>F1000Research</i> , 0, 10, 395.	1.6	1
175	Using a data triangle to understand molecular nutrition. <i>Nature Precedings</i> , 0, , .	0.1	0
176	Exposing WikiPathways as Linked Open Data. <i>Nature Precedings</i> , 0, , .	0.1	0