

# Chris T A Evelo

## List of Publications by Year in descending order

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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	The FAIR Guiding Principles for scientific data management and stewardship. <i>Scientific Data</i> , 2016, 3, 160018.	5.3	8,670
2	WikiPathways: a multifaceted pathway database bridging metabolomics to other omics research. <i>Nucleic Acids Research</i> , 2018, 46, D661-D667.	14.5	708
3	WikiPathways: Pathway Editing for the People. <i>PLoS Biology</i> , 2008, 6, e184.	5.6	542
4	WikiPathways: connecting communities. <i>Nucleic Acids Research</i> , 2021, 49, D613-D621.	14.5	519
5	WikiPathways: building research communities on biological pathways. <i>Nucleic Acids Research</i> , 2012, 40, D1301-D1307.	14.5	479
6	PathVisio 3: An Extendable Pathway Analysis Toolbox. <i>PLoS Computational Biology</i> , 2015, 11, e1004085.	3.2	393
7	WikiPathways: capturing the full diversity of pathway knowledge. <i>Nucleic Acids Research</i> , 2016, 44, D488-D494.	14.5	380
8	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	21.4	362
9	Presenting and exploring biological pathways with PathVisio. <i>BMC Bioinformatics</i> , 2008, 9, 399.	2.6	305
10	The Chemistry Development Kit (CDK) v2.0: atom typing, depiction, molecular formulas, and substructure searching. <i>Journal of Cheminformatics</i> , 2017, 9, 33.	6.1	275
11	Open PHACTS: semantic interoperability for drug discovery. <i>Drug Discovery Today</i> , 2012, 17, 1188-1198.	6.4	274
12	GO-Elite: a flexible solution for pathway and ontology over-representation. <i>Bioinformatics</i> , 2012, 28, 2209-2210.	4.1	268
13	The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. <i>BMC Bioinformatics</i> , 2010, 11, 5.	2.6	180
14	Thrombospondin-2 Is Essential for Myocardial Matrix Integrity. <i>Circulation Research</i> , 2004, 95, 515-522.	4.5	179
15	<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
16	FAIR Principles: Interpretations and Implementation Considerations. <i>Data Intelligence</i> , 2020, 2, 10-29.	1.5	149
17	From Nanotechnology to Nanomedicine: Applications to Cancer Research. <i>Current Molecular Medicine</i> , 2010, 10, 640-652.	1.3	148
18	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

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19	Time-Resolved and Tissue-Specific Systems Analysis of the Pathogenesis of Insulin Resistance. PLoS ONE, 2010, 5, e8817.	2.5	126
20	CyTargetLinker: A Cytoscape App to Integrate Regulatory Interactions in Network Analysis. PLoS ONE, 2013, 8, e82160.	2.5	117
21	Four selenoproteins, protein biosynthesis, and Wnt signalling are particularly sensitive to limited selenium intake in mouse colon. Molecular Nutrition and Food Research, 2009, 53, 1561-1572.	3.3	102
22	Gene Profiling in Atherosclerosis Reveals a Key Role for Small Inducible Cytokines. Circulation, 2005, 111, 3443-3452.	1.6	100
23	Mining Biological Pathways Using WikiPathways Web Services. PLoS ONE, 2009, 4, e6447.	2.5	100
24	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
25	Impact of supervised gene signatures of early hypoxia on patient survival. Radiotherapy and Oncology, 2007, 83, 374-382.	0.6	80
26	A Combined Transcriptomics and Lipidomics Analysis of Subcutaneous, Epididymal and Mesenteric Adipose Tissue Reveals Marked Functional Differences. PLoS ONE, 2010, 5, e11525.	2.5	79
27	A Review of Pathway-Based Analysis Tools That Visualize Genetic Variants. Frontiers in Genetics, 2017, 8, 174.	2.3	67
28	Challenges of molecular nutrition research 6: the nutritional phenotype database to store, share and evaluate nutritional systems biology studies. Genes and Nutrition, 2010, 5, 189-203.	2.5	64
29	Alterations in hepatic one-carbon metabolism and related pathways following a high-fat dietary intervention. Physiological Genomics, 2011, 43, 408-416.	2.3	64
30	Hypoxia increases genome-wide bivalent epigenetic marking by specific gain of H3K27me3. Epigenetics and Chromatin, 2016, 9, 46.	3.9	63
31	Rett syndrome " biological pathways leading from MECP2 to disorder phenotypes. Orphanet Journal of Rare Diseases, 2016, 11, 158.	2.7	63
32	Effect of Vitamin E on Glutathione-Dependent Enzymes. Drug Metabolism Reviews, 2003, 35, 215-253.	3.6	59
33	WikiPathways App for Cytoscape: Making biological pathways amenable to network analysis and visualization. F1000Research, 2014, 3, 152.	1.6	57
34	Integration among databases and data sets to support productive nanotechnology: Challenges and recommendations. NanolImpact, 2018, 9, 85-101.	4.5	56
35	COVID19 Disease Map, a computational knowledge repository of virus"host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
36	Review and gap analysis: molecular pathways leading to fetal alcohol spectrum disorders. Molecular Psychiatry, 2019, 24, 10-17.	7.9	52

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37	A Data Fusion Pipeline for Generating and Enriching Adverse Outcome Pathway Descriptions. <i>Toxicological Sciences</i> , 2018, 162, 264-275.	3.1	51
38	A pathway approach to investigate the function and regulation of SREBPs. <i>Genes and Nutrition</i> , 2013, 8, 289-300.	2.5	50
39	Finding the Right Questions: Exploratory Pathway Analysis to Enhance Biological Discovery in Large Datasets. <i>PLoS Biology</i> , 2010, 8, e1000472.	5.6	49
40	Genetic variation in thioredoxin interacting protein (TXNIP) is associated with hypertriglyceridaemia and blood pressure in diabetes mellitus. <i>Diabetic Medicine</i> , 2007, 24, 498-504.	2.3	47
41	The Micronutrient Genomics Project: a community-driven knowledge base for micronutrient research. <i>Genes and Nutrition</i> , 2010, 5, 285-296.	2.5	47
42	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
43	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
44	The public road to high-quality curated biological pathways. <i>Drug Discovery Today</i> , 2008, 13, 856-862.	6.4	44
45	Reduction of colonic inflammation in HLA-B27 transgenic rats by feeding Marie MÃ©nard apples, rich in polyphenols. <i>British Journal of Nutrition</i> , 2009, 102, 1620.	2.3	43
46	Fasting induces a biphasic adaptive metabolic response in murine small intestine. <i>BMC Genomics</i> , 2007, 8, 361.	2.8	41
47	Applying linked data approaches to pharmacology: Architectural decisions and implementation. <i>Semantic Web</i> , 2014, 5, 101-113.	1.9	41
48	diXa: a data infrastructure for chemical safety assessment. <i>Bioinformatics</i> , 2015, 31, 1505-1507.	4.1	40
49	Erythrocyte antioxidant defense response against cigarette smoking in humansâ€”the glutathione S-transferase vulnerability. <i>Journal of Biochemical and Molecular Toxicology</i> , 2005, 19, 226-233.	3.0	39
50	Visualizing the regulatory role of Angiopoietin-like protein 8 (ANGPTL8) in glucose and lipid metabolic pathways. <i>Genomics</i> , 2017, 109, 408-418.	2.9	38
51	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
52	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
53	Reactome from a WikiPathways Perspective. <i>PLoS Computational Biology</i> , 2016, 12, e1004941.	3.2	35
54	Inhibition of various glutathione S-transferase isoenzymes by RRR-Î±-tocopherol. <i>Toxicology in Vitro</i> , 2003, 17, 245-251.	2.4	34

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55	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
56	From SNPs to pathways: Biological interpretation of type 2 diabetes (T2DM) genome wide association study (GWAS) results. <i>PLoS ONE</i> , 2018, 13, e0193515.	2.5	34
57	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
58	Using the Semantic Web for Rapid Integration of WikiPathways with Other Biological Online Data Resources. <i>PLoS Computational Biology</i> , 2016, 12, e1004989.	3.2	33
59	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
60	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
61	The Application of the Open Pharmacological Concepts Triple Store (Open PHACTS) to Support Drug Discovery Research. <i>PLoS ONE</i> , 2014, 9, e115460.	2.5	31
62	The systems biology format converter. <i>BMC Bioinformatics</i> , 2016, 17, 154.	2.6	30
63	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
64	Protein profiling of 3T3-L1 adipocyte differentiation and (tumor necrosis factor $\alpha$ -mediated) starvation. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 492-503.	5.4	29
65	A network biology workflow to study transcriptomics data of the diabetic liver. <i>BMC Genomics</i> , 2014, 15, 971.	2.8	29
66	Identification of novel ER- $\alpha$ target genes in breast cancer cells: Gene- and cell-selective co-regulator recruitment at target promoters determines the response to 17 $\beta$ -estradiol and tamoxifen. <i>Molecular and Cellular Endocrinology</i> , 2010, 314, 90-100.	3.2	28
67	Gene profiling of cathepsin K deficiency in atherogenesis: profibrotic but lipogenic. <i>Journal of Pathology</i> , 2006, 210, 334-343.	4.5	26
68	Biologically relevant effects of mRNA amplification on gene expression profiles. <i>BMC Bioinformatics</i> , 2006, 7, 200.	2.6	26
69	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
70	Consensus statement understanding health and malnutrition through a systems approach: the ENOUGH program for early life. <i>Genes and Nutrition</i> , 2014, 9, 378.	2.5	26
71	Pathway analysis of transcriptomic data shows immunometabolic effects of vitamin D. <i>Journal of Molecular Endocrinology</i> , 2018, 60, 95-108.	2.5	26
72	CyTargetLinker app update: A flexible solution for network extension in Cytoscape. <i>F1000Research</i> , 2018, 7, 743.	1.6	26

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73	Inhibition of human glutathione S-transferase P1-1 by tocopherols and $\hat{\pm}$ -tocopherol derivatives. BBA - Proteins and Proteomics, 2001, 1548, 23-28.	2.1	25
74	$\hat{\pm}$ -Tocopherol Inhibits Human Glutathione S-Transferase $\hat{\text{I}}\text{€}$ . Biochemical and Biophysical Research Communications, 2001, 280, 631-633.	2.1	24
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	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	23
77	Two Mechanisms for Toxic Effects of Hydroxylamines in Human Erythrocytes: Involvement of Free Radicals and Risk of Potentiation. Blood Cells, Molecules, and Diseases, 1998, 24, 280-295.	1.4	22
78	Validating nutrient-related gene expression changes from microarrays using RT2 PCR-arrays. Genes and Nutrition, 2008, 3, 153-157.	2.5	22
79	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
80	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. Archives of Toxicology, 1991, 65, 95-99.	4.2	21
81	Microarray profiling of human white adipose tissue after exogenous leptin injection. European Journal of Clinical Investigation, 2006, 36, 153-163.	3.4	21
82	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
83	Hydroxylamine Treatment Increases Glutathione-Protein and Protein-Protein Binding in Human Erythrocytes. Blood Cells, Molecules, and Diseases, 1997, 23, 323-336.	1.4	20
84	Advancing food, nutrition, and health research in Europe by connecting and building research infrastructures in a DISH-RI: Results of the EuroDISH project. Trends in Food Science and Technology, 2018, 73, 58-66.	15.1	19
85	Integrated analysis of human transcriptome data for Rett syndrome finds a network of involved genes. World Journal of Biological Psychiatry, 2020, 21, 712-725.	2.6	19
86	Tocotrienols Inhibit Human Glutathione S-Transferase P1-1. IUBMB Life, 2002, 54, 81-84.	3.4	18
87	Role of $1\hat{\pm},25$ -Dihydroxyvitamin D3 in Adipogenesis of SGBS Cells: New Insights into Human Preadipocyte Proliferation. Cellular Physiology and Biochemistry, 2018, 48, 397-408.	1.6	18
88	Comprehensive bioinformatics analysis of trabecular meshwork gene expression data to unravel the molecular pathogenesis of primary open-angle glaucoma. Acta Ophthalmologica, 2020, 98, 48-57.	1.1	18
89	ELIXIR $\hat{\text{€}}$ EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	7.8	18
90	CyTargetLinker app update: A flexible solution for network extension in Cytoscape. F1000Research, 2018, 7, 743.	1.6	18

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91	Exploring pathway interactions in insulin resistant mouse liver. BMC Systems Biology, 2011, 5, 127.	3.0	17
92	An evaluation of two-channel CHIP-on-chip and DNA methylation microarray normalization strategies. BMC Genomics, 2012, 13, 42.	2.8	17
93	Molecular Pathways Involved in Prostate Carcinogenesis: Insights from Public Microarray Datasets. PLoS ONE, 2012, 7, e49831.	2.5	17
94	Up-regulation of CD36/FAT in preadipocytes in familial combined hyperlipidemia. FASEB Journal, 2005, 19, 2063-2065.	0.5	16
95	Scientific Lenses to Support Multiple Views over Linked Chemistry Data. Lecture Notes in Computer Science, 2014, , 98-113.	1.3	16
96	Bilberries potentially alleviate stress-related retinal gene expression induced by a high-fat diet in mice. Molecular Vision, 2012, 18, 2338-51.	1.1	16
97	Oxidative effects in human erythrocytes caused by some oximes and hydroxylamine. Archives of Toxicology, 1998, 72, 270-276.	4.2	15
98	<i>MECP2</i> variation in Rett syndrome-An overview of current coverage of genetic and phenotype data within existing databases. Human Mutation, 2018, 39, 914-924.	2.5	15
99	Hypochlorous acid is a potent inhibitor of GST P1-1. Chemico-Biological Interactions, 2001, 138, 77-83.	4.0	14
100	Differential valine metabolism in adipose tissue of low and high fat-oxidizing obese subjects. Proteomics - Clinical Applications, 2007, 1, 1306-1315.	1.6	14
101	The role of bioinformatics in pathway curation. Genes and Nutrition, 2008, 3, 139-142.	2.5	14
102	Pathway Enrichment Based on Text Mining and Its Validation on Carotenoid and Vitamin A Metabolism. OMICS A Journal of Integrative Biology, 2009, 13, 367-379.	2.0	14
103	Effect of supplementation with an 80:20 <i>cis</i> : <i>trans</i> 11 conjugated linoleic acid blend on the human platelet proteome. Molecular Nutrition and Food Research, 2012, 56, 1148-1159.	3.3	14
104	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
105	Sexual Dimorphism, Age, and Fat Mass Are Key Phenotypic Drivers of Proteomic Signatures. Journal of Proteome Research, 2017, 16, 4122-4133.	3.7	14
106	Identification of Biological Pathways Contributing to Marbling in Skeletal Muscle to Improve Beef Cattle Breeding. Frontiers in Genetics, 2020, 10, 1370.	2.3	14
107	Automatically visualise and analyse data on pathways using PathVisioRPC from any programming environment. BMC Bioinformatics, 2015, 16, 267.	2.6	13
108	XMetDB: an open access database for xenobiotic metabolism. Journal of Cheminformatics, 2016, 8, 47.	6.1	13

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109	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
110	The Molecular Processes in the Trabecular Meshwork After Exposure to Corticosteroids and in Corticosteroid-Induced Ocular Hypertension. , 2020, 61, 24.		13
111	Ten simple rules for creating reusable pathway models for computational analysis and visualization. <i>PLoS Computational Biology</i> , 2021, 17, e1009226.	3.2	13
112	No reduction of Î±-tocopherol quinone by glutathione in rat liver microsomes. <i>Biochemical Pharmacology</i> , 2001, 61, 715-719.	4.4	12
113	Linking microarray reporters with protein functions. <i>BMC Bioinformatics</i> , 2007, 8, 360.	2.6	12
114	Exploring the cellular network of metabolic flexibility in the adipose tissue. <i>Genes and Nutrition</i> , 2018, 13, 17.	2.5	12
115	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
116	In vitro haematotoxic effects of three methylated hydroxylamines. <i>Archives of Toxicology</i> , 1997, 71, 299-305.	4.2	11
117	Transcriptome analysis of peripheral blood mononuclear cells in human subjects following a 36Âh fast provides evidence of effects on genes regulating inflammation, apoptosis and energy metabolism. <i>Genes and Nutrition</i> , 2014, 9, 432.	2.5	11
118	Integrative network-based analysis of mRNA and microRNA expression in 1,25-dihydroxyvitamin D3-treated cancer cells. <i>Genes and Nutrition</i> , 2015, 10, 35.	2.5	11
119	A resource to explore the discovery of rare diseases and their causative genes. <i>Scientific Data</i> , 2021, 8, 124.	5.3	11
120	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
121	Gene expression in human small intestinal mucosa in vivo is mediated by iron-induced oxidative stress. <i>Physiological Genomics</i> , 2006, 25, 242-249.	2.3	10
122	Beyond Pathway Analysis: Identification of Active Subnetworks in Rett Syndrome. <i>Frontiers in Genetics</i> , 2019, 10, 59.	2.3	10
123	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
124	Integrated visualization of a multi-omics study of starvation in mouse intestine. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 1-16.	1.5	9
125	Organ-Specific Gene Expression Changes in the Fetal Liver and Placenta in Response to Maternal Folate Depletion. <i>Nutrients</i> , 2016, 8, 661.	4.1	9
126	New insights in Rett syndrome using pathway analysis for transcriptomics data. <i>Wiener Medizinische Wochenschrift</i> , 2016, 166, 346-352.	1.1	9



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127	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
128	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. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1600713.	3.3	8
129	Biological Pathways Leading From ANGPTL8 to Diabetes Mellitus – A Co-expression Network Based Analysis. <i>Frontiers in Physiology</i> , 2018, 9, 1841.	2.8	8
130	Stratifying cellular metabolism during weight loss: an interplay of metabolism, metabolic flexibility and inflammation. <i>Scientific Reports</i> , 2020, 10, 1651.	3.3	8
131	The Dutch Techcentre for Life Sciences: Enabling data-intensive life science research in the Netherlands. <i>F1000Research</i> , 2015, 4, 33.	1.6	8
132	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
133	Only the glutathione dependent antioxidant enzymes are inhibited by haematotoxic hydroxylamines. <i>Human and Experimental Toxicology</i> , 1998, 17, 554-559.	2.2	7
134	EFMviz: A COBRA Toolbox Extension to Visualize Elementary Flux Modes in Genome-Scale Metabolic Models. <i>Metabolites</i> , 2020, 10, 66.	2.9	7
135	The need for standardisation in life science research - an approach to excellence and trust.. <i>F1000Research</i> , 2020, 9, 1398.	1.6	7
136	Explicit interaction information from WikiPathways in RDF facilitates drug discovery in the Open PHACTS Discovery Platform. <i>F1000Research</i> , 2018, 7, 75.	1.6	7
137	The Dutch Techcentre for Life Sciences: Enabling data-intensive life science research in the Netherlands. <i>F1000Research</i> , 2015, 4, 33.	1.6	7
138	Bioinformatic interrogation of expression array data to identify nutritionally regulated genes potentially modulated by DNA methylation. <i>Genes and Nutrition</i> , 2008, 3, 167-171.	2.5	6
139	Connecting the Human Variome Project to nutrigenomics. <i>Genes and Nutrition</i> , 2010, 5, 275-283.	2.5	6
140	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
141	Explicit interaction information from WikiPathways in RDF facilitates drug discovery in the Open PHACTS Discovery Platform. <i>F1000Research</i> , 2018, 7, 75.	1.6	6
142	Integrated visualization of a multi-omics study of starvation in mouse intestine. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 235.	1.5	6
143	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
144	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. <i>Genes and Nutrition</i> , 2008, 3, 185-191.	2.5	5

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145	Overlap of vitamin A and vitamin D target genes with CAKUT-related processes. <i>F1000Research</i> , 2021, 10, 395.	1.6	5
146	WikiPathways App for Cytoscape: Making biological pathways amenable to network analysis and visualization. <i>F1000Research</i> , 0, 3, 152.	1.6	5
147	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
148	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
149	Answering biological questions: querying a systems biology database for nutrigenomics. <i>Genes and Nutrition</i> , 2011, 6, 81-87.	2.5	4
150	Profiling Cellular Processes in Adipose Tissue during Weight Loss Using Time Series Gene Expression. <i>Genes</i> , 2018, 9, 525.	2.4	4
151	Comparison of metabolic states using genome-scale metabolic models. <i>PLoS Computational Biology</i> , 2021, 17, e1009522.	3.2	4
152	A Community-Driven, Openly Accessible Molecular Pathway Integrating Knowledge on Malignant Pleural Mesothelioma. <i>Frontiers in Oncology</i> , 2022, 12, 849640.	2.8	4
153	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
154	ELIXIR and Toxicology: a community in development. <i>F1000Research</i> , 0, 10, 1129.	1.6	3
155	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
156	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
157	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
158	Assessing the Contribution of Relative Macrophage Frequencies to Subcutaneous Adipose Tissue. <i>Frontiers in Nutrition</i> , 2021, 8, 675935.	3.7	2
159	Ten simple rules to make your publication look better. <i>PLoS Computational Biology</i> , 2021, 17, e1008938.	3.2	2
160	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
161	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
162	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

#	ARTICLE	IF	CITATIONS
163	Community curation on WikiPathways: How we assist knowledge collection. Nature Precedings, 2009, , .	0.1	1
164	Nature Europe site should highlight most productive countries. Nature, 2010, 465, 685-685.	27.8	1
165	Measuring impact in online resources with the CI-number (the CitedIn Number for online impact). Nature Precedings, 2011, , .	0.1	1
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