Kim M Summers

List of Publications by Year
in descending order

144 papers	8,768 citations	94269 37 h-index	51492 86 g-index
159 all docs	159 docs citations	159 times ranked	14343 citing authors

#	Article	IF	Citations
1	Generation and network analysis of an RNA-seq transcriptional atlas for the rat. NAR Genomics and Bioinformatics, 2022, 4, lqac017.	1.5	4
2	A kinase-dead Csf1r mutation associated with adult-onset leukoencephalopathy has a dominant inhibitory impact on CSF1R signalling. Development (Cambridge), 2022, 149, .	1.2	9
3	Canine reference genome accuracy impacts variant calling: Lessons learned from investigating embryonic lethal variants. Animal Genetics, 2022, 53, 706-708.	0.6	1
4	The influence of X chromosome variants on trait neuroticism. Molecular Psychiatry, 2021, 26, 483-491.	4.1	17
5	Clinical and Echocardiographic Findings in an Aged Population of Cavalier King Charles Spaniels. Animals, 2021, 11, 949.	1.0	0
6	Analysis of homozygous and heterozygous Csf1r knockout in the rat as a model for understanding microglial function in brain development and the impacts of human CSF1R mutations. Neurobiology of Disease, 2021, 151, 105268.	2.1	29
7	Microdeletion of 9q22.3: A patient with minimal deletion size associated with a severe phenotype. American Journal of Medical Genetics, Part A, 2021, 185, 2070-2083.	0.7	2
8	CRISPR-Cas9 Editing of Human Histone Deubiquitinase Gene USP16 in Human Monocytic Leukemia Cell Line THP-1. Frontiers in Cell and Developmental Biology, 2021, 9, 679544.	1.8	2
9	The Mononuclear Phagocyte System of the Rat. Journal of Immunology, 2021, 206, 2251-2263.	0.4	15
10	CSF1R-dependent macrophages control postnatal somatic growth and organ maturation. PLoS Genetics, 2021, 17, e1009605.	1.5	44
11	Improving the resolution of canine genomeâ€wide association studies using genotype imputation: A study of two breeds. Animal Genetics, 2021, 52, 703-713.	0.6	5
12	Role of macrophages and phagocytes in orchestrating normal and pathologic hematopoietic niches. Experimental Hematology, 2021, 100, 12-31.e1.	0.2	8
13	Macrophages form erythropoietic niches and regulate iron homeostasis to adapt erythropoiesis in response to infections and inflammation. Experimental Hematology, 2021, 103, 1-14.	0.2	9
14	Fragmentation of tissue-resident macrophages during isolation confounds analysis of single-cell preparations from mouse hematopoietic tissues. Cell Reports, 2021, 37, 110058.	2.9	36
15	Phenotypic impacts of CSF1R deficiencies in humans and model organisms. Journal of Leukocyte Biology, 2020, 107, 205-219.	1.5	97
16	Network analysis of transcriptomic diversity amongst resident tissue macrophages and dendritic cells in the mouse mononuclear phagocyte system. PLoS Biology, 2020, 18, e3000859.	2.6	94
17	Expression of Calcification and Extracellular Matrix Genes in the Cardiovascular System of the Healthy Domestic Sheep (Ovis aries). Frontiers in Genetics, 2020, 11, 919.	1.1	9
18	Influence of the MUC1 Cell Surface Mucin on Gastric Mucosal Gene Expression Profiles in Response to Helicobacter pylori Infection in Mice. Frontiers in Cellular and Infection Microbiology, 2020, 10, 343.	1.8	6

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19	Species-Specificity of Transcriptional Regulation and the Response to Lipopolysaccharide in Mammalian Macrophages. Frontiers in Cell and Developmental Biology, 2020, 8, 661.	1.8	29
20	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. Journal of Virology, 2020, 94, .	1.5	14
21	The Transcriptional Network That Controls Growth Arrest and Macrophage Differentiation in the Human Myeloid Leukemia Cell Line THP-1. Frontiers in Cell and Developmental Biology, 2020, 8, 498.	1.8	25
22	Compound heterozygous mutations in FBN1 in a large family with Marfan syndrome. Molecular Genetics & Genomic Medicine, 2020, 8, e1116.	0.6	5
23	Disease Severity-Associated Gene Expression in Canine Myxomatous Mitral Valve Disease Is Dominated by TGFÎ² Signaling. Frontiers in Genetics, 2020, 11, 372.	1.1	14
24	A Gene Expression Atlas of the Domestic Water Buffalo (Bubalus bubalis). Frontiers in Genetics, 2019, 10, 668.	1.1	49
25	Deletion of a Csf1r enhancer selectively impacts CSF1R expression and development of tissue macrophage populations. Nature Communications, 2019, 10, 3215.	5.8	191
26	Visualization and analysis of RNA-Seq assembly graphs. Nucleic Acids Research, 2019, 47, 7262-7275.	6.5	4
27	A comprehensive biomedical variant catalogue based on whole genome sequences of 582 dogs and eight wolves. Animal Genetics, 2019, 50, 695-704.	0.6	138
28	Evaluation of canine 2D cell cultures as models of myxomatous mitral valve degeneration. PLoS ONE, 2019, 14, e0221126.	1.1	12
29	The Effect of Race Training on the Basal Gene Expression of Alveolar Macrophages Derived From Standardbred Racehorses. Journal of Equine Veterinary Science, 2019, 75, 48-54.	0.4	3
30	Arginine to Glutamine Variant in Olfactomedin Like 3 (OLFML3) Is a Candidate for Severe Goniodysgenesis and Glaucoma in the Border Collie Dog Breed. G3: Genes, Genomes, Genetics, 2019, 9, 943-954.	0.8	11
31	Lysine demethylases KDM6A and UTY: The X and Y of histone demethylation. Molecular Genetics and Metabolism, 2019, 127, 31-44.	0.5	44
32	Analysis of the Progeny of Sibling Matings Reveals Regulatory Variation Impacting the Transcriptome of Immune Cells in Commercial Chickens. Frontiers in Genetics, 2019, 10, 1032.	1.1	18
33	Characterization of Subpopulations of Chicken Mononuclear Phagocytes That Express TIM4 and CSF1R. Journal of Immunology, 2019, 202, 1186-1199.	0.4	47
34	Functional Annotation of the Transcriptome of the Pig, Sus scrofa, Based Upon Network Analysis of an RNAseq Transcriptional Atlas. Frontiers in Genetics, 2019, 10, 1355.	1.1	42
35	Exploiting novel valve interstitial cell lines to study calcific aortic valve disease. Molecular Medicine Reports, 2018, 17, 2100-2106.	1.1	13
36	An analysis of anterior segment development in the chicken eye. Mechanisms of Development, 2018, 150, 42-49.	1.7	12

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37	Pleiotropic Impacts of Macrophage and Microglial Deficiency on Development in Rats with Targeted Mutation of the Csf1r Locus. Journal of Immunology, 2018, 201, 2683-2699.	0.4	114
38	Environmentally enriched pigs have transcriptional profiles consistent with neuroprotective effects and reduced microglial activity. Behavioural Brain Research, 2018, 350, 6-15.	1.2	11
39	Combination of novel and public RNA-seq datasets to generate an mRNA expression atlas for the domestic chicken. BMC Genomics, 2018, 19, 594.	1.2	86
40	Identification of Pathological FBN1 Variants Is Not Straightforward. Circulation Genomic and Precision Medicine, 2018, 11, e002168.	1.6	0
41	Comparative transcriptome analysis of equine alveolar macrophages. Equine Veterinary Journal, 2017, 49, 375-382.	0.9	31
42	Incidence rates and risk factor analyses for owner reported vomiting and diarrhoea in Labrador Retrievers â€“ findings from the Dogslife Cohort. Preventive Veterinary Medicine, 2017, 140, 19-29.	0.7	18
43	Myxomatous Degeneration of the Canine Mitral Valve: From Gross Changes to Molecular Events. Journal of Comparative Pathology, 2017, 156, 371-383.	0.1	19
44	Analysis of gene expression in the nervous system identifies key genes and novel candidates for health and disease. Neurogenetics, 2017, 18, 81-95.	0.7	23
45	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	9.4	456
46	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	2.4	195
47	Identification of the macrophage-specific promoter signature in FANTOM5 mouse embryo developmental time course data. Journal of Leukocyte Biology, 2017, 102, 1081-1092.	1.5	35
48	16â€...Investigating calcific aortic valve disease using novel immortalised sheep and rat valve interstitial cell lines. , 2017, , .		0
49	Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. BMC Bioinformatics, 2017, 18, 301.	1.2	40
50	8â€...Generating a genomic-wide transcriptomic atlas of the mammalian cardiovascular system. , 2017, , .		0
51	Transcriptional Regulation and Macrophage Differentiation. , 2017, , 117-139.		1
52	Comparative Transcriptomic Profiling and Gene Expression for Myxomatous Mitral Valve Disease in the Dog and Human. Veterinary Sciences, 2017, 4, 34.	0.6	16
53	A high resolution atlas of gene expression in the domestic sheep (Ovis aries). PLoS Genetics, 2017, 13, e1006997.	1.5	210
54	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. PLoS Genetics, 2017, 13, e1006641.	1.5	161

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55	Cumulative incidence and risk factors for limber tail in the Dogslife labrador retriever cohort. Veterinary Record, 2016, 179, 275-275.	0.2	6
56	Macrophage colony-stimulating factor (CSF1) controls monocyte production and maturation and the steady-state size of the liver in pigs. American Journal of Physiology - Renal Physiology, 2016, 311, G533-G547.	1.6	55
57	Transcriptional Regulation and Macrophage Differentiation. Microbiology Spectrum, 2016, 4, .	1.2	35
58	A Deletion in the Canine POMC Gene Is Associated with Weight and Appetite in Obesity-Prone Labrador Retriever Dogs. Cell Metabolism, 2016, 23, 893-900.	7.2	117
59	Expression of FBN1 during adipogenesis: Relevance to the lipodystrophy phenotype in Marfan syndrome and related conditions. Molecular Genetics and Metabolism, 2016, 119, 174-185.	0.5	29
60	Datasets of genes coexpressed with FBN1 in mouse adipose tissue and during human adipogenesis. Data in Brief, 2016, 8, 851-857.	0.5	3
61	Large animal models of cardiovascular disease. Cell Biochemistry and Function, 2016, 34, 113-132.	1.4	105
62	Microglial brain regionâ^'dependent diversity and selective regional sensitivities to aging. Nature Neuroscience, 2016, 19, 504-516.	7.1	919
63	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	6.0	517
64	Dogslife: A cohort study of Labrador Retrievers in the UK. Preventive Veterinary Medicine, 2015, 122, 426-435.	0.7	18
65	The challenges of pedigree dog health: approaches to combating inherited disease. Canine Genetics and Epidemiology, 2015, 2, 3.	2.9	56
66	Validity of Internet-Based Longitudinal Study Data: The Elephant in the Virtual Room. Journal of Medical Internet Research, 2015, 17, e96.	2.1	12
67	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	13.7	1,838
68	Transcriptional switching in macrophages associated with the peritoneal foreign body response. Immunology and Cell Biology, 2014, 92, 518-526.	1.0	40
69	Limited genetic divergence between dog breeds from geographically isolated countries. Veterinary Record, 2014, 175, 562-562.	0.2	3
70	What can cohort studies in the dog tell us?. Canine Genetics and Epidemiology, 2014, 1, 5.	2.9	6
71	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. Molecular Genetics and Metabolism, 2014, 112, 73-83.	0.5	39
72	Dogslife: A web-based longitudinal study of Labrador Retriever health in the UK. BMC Veterinary Research, 2013, 9, 13.	0.7	27

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73	Population structure and genetic heterogeneity in popular dog breeds in the UK. Veterinary Journal, 2013, 196, 92-97.	0.6	55
74	Whole exome sequencing is an efficient, sensitive and specific method of mutation detection in osteogenesis imperfecta and Marfan syndrome. BoneKEy Reports, 2013, 2, 456.	2.7	24
75	Structure and function of the mammalian fibrillin gene family: Implications for human connective tissue diseases. Molecular Genetics and Metabolism, 2012, 107, 635-647.	0.5	89
76	A gene expression atlas of the domestic pig. BMC Biology, 2012, 10, 90.	1.7	199
77	Recent developments in the diagnosis of Marfan syndrome and related disorders. Medical Journal of Australia, 2012, 197, 494-497.	0.8	13
78	Genome-wide analysis of mitral valve disease in Cavalier King Charles Spaniels. Veterinary Journal, 2012, 193, 283-286.	0.6	23
79	Expression of mesenchyme-specific gene signatures by follicular dendritic cells: insights from the meta-analysis of microarray data from multiple mouse cell populations. Immunology, 2011, 133, 482-498.	2.0	50
80	Mutations at KCNQ1 and an unknown locus cause long QT syndrome in a large Australian family: Implications for genetic testing. American Journal of Medical Genetics, Part A, 2010, 152A, 613-621.	0.7	4
81	Co-expression of FBN1 with mesenchyme-specific genes in mouse cell lines: implications for phenotypic variability in Marfan syndrome. European Journal of Human Genetics, 2010, 18, 1209-1215.	1.4	39
82	â€˜Dogslifeâ€™ research study. Veterinary Record, 2010, 167, 146-146.	0.2	0
83	Functional clustering and lineage markers: Insights into cellular differentiation and gene function from large-scale microarray studies of purified primary cell populations. Genomics, 2010, 95, 328-338.	1.3	112
84	Molecular genetics of long QT syndrome. Molecular Genetics and Metabolism, 2010, 101, 1-8.	0.5	75
85	Experimental and bioinformatic characterisation of the promoter region of the Marfan syndrome gene, FBN1. Genomics, 2009, 94, 233-240.	1.3	20
86	Identifying susceptibility to inflammatory bowel diseases: A candidate gene approach, genomeâ€wide association studies, or both?. Journal of Gastroenterology and Hepatology (Australia), 2008, 23, 6-7.	1.4	1
87	Anterior segment mesenchymal dysgenesis in a large Australian family is associated with the recurrent 17 bp duplication in PITX3. Molecular Vision, 2008, 14, 2010-5.	1.1	33
88	Familial muscular ventricular septal defects and aneurysms of the muscular interventricular septum. Cardiology in the Young, 2007, 17, 523-527.	0.4	7
89	Challenges in the diagnosis of Marfan syndrome. Medical Journal of Australia, 2006, 184, 627-631.	0.8	33
90	Histopathology and fibrillin-1 distribution in severe early onset Marfan syndrome. American Journal of Medical Genetics, Part A, 2005, 139A, 2-8.	0.7	20

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91	The Value of Screening in Siblings of Patients with Abdominal Aortic Aneurysm. European Journal of Vascular and Endovascular Surgery, 2003, 26, 396-400.	0.8	51
92	An integrated approach to management of Marfan syndrome caused by an FBN1 exon 18 mutation in an Australian Aboriginal family. Clinical Genetics, 2003, 65, 66-69.	1.0	14
93	Abnormal Extracellular Matrix Protein Transport Associated With Increased Apoptosis of Vascular Smooth Muscle Cells in Marfan Syndrome and Bicuspid Aortic Valve Thoracic Aortic Aneurysm. Circulation, 2003, 108, 329II–334.	1.6	224
94	The murine chaperonin 10 gene family contains an intronless, putative gene for early pregnancy factor, Cpn10-rs1. Mammalian Genome, 2001, 12, 133-140.	1.0	9
95	Production of a recombinant form of early pregnancy factor that can prolong allogeneic skin graft survival time in rats. Immunology and Cell Biology, 2000, 78, 603-607.	1.0	28
96	Autosomal dominant cataracts and Peters anomaly in a large Australian family. Clinical Genetics, 1999, 55, 240-247.	1.0	21
97	Mapping and characterization of the eukaryotic early pregnancy factor/chaperonin 10 gene family. Somatic Cell and Molecular Genetics, 1998, 24, 315-326.	0.7	5
98	ASSOCIATION OF THE BRAIN NATRIURETIC PEPTIDE GENE WITH BLOOD PRESSURE AND HEART WEIGHT IN THE RAT. Clinical and Experimental Pharmacology and Physiology, 1997, 24, 442-444.	0.9	6
99	ASSOCIATION ANALYSIS OF SIX CANDIDATE GENES IN A SAMPLE OF AUSTRALIAN HYPERTENSIVE PATIENTS. Clinical and Experimental Pharmacology and Physiology, 1997, 24, 454-456.	0.9	2
100	The Human Early Pregnancy Factor/Chaperonin 10 Gene Family. Biochemical and Molecular Medicine, 1996, 58, 52-58.	1.5	23
101	Relationship between genotype and phenotype in monogenic diseases: Relevance to polygenic diseases. , 1996, 7, 283-293.		41
102	GENETIC VARIANTS OF PROTEINS FROM THE RENIN ANGIOTENSIN SYSTEM ARE ASSOCIATED WITH PRESSURE LOAD CARDIAC HYPERTROPHY. Clinical and Experimental Pharmacology and Physiology, 1996, 23, 587-590.	0.9	14
103	ANALYSIS OF LINKAGE OF THE ACE LOCUS WITH MEASURES OF CARDIAC HYPERTROPHY IN THE SPONTANEOUSLY HYPERTENSIVE RAT. Clinical and Experimental Pharmacology and Physiology, 1996, 23, 597-599.	0.9	5
104	?1-ANTITRYPSIN DEFICIENCY ALLELES AND BLOOD PRESSURE IN AN AUSTRALIAN POPULATION. Clinical and Experimental Pharmacology and Physiology, 1996, 23, 600-601.	0.9	8
105	Cosegregation of Genes on Chromosome 5 with Heart Weight and Blood Pressure in Genetic Hypertension. Clinical and Experimental Hypertension, 1996, 18, 1073-1087.	0.5	12
106	Angiotensin I Converting Enzyme Gene Cosegregates with Blood Pressure and Heart Weight in F2 Progeny Derived from Spontaneously Hypertensive and Normotensive Wistar-Kyoto Rats. Clinical and Experimental Hypertension, 1996, 18, 753-771.	0.5	25
107	Relationship between genotype and phenotype in monogenic diseases: Relevance to polygenic diseases. Human Mutation, 1996, 7, 283-293.	1.1	3
108	ANGIOTENSIN-CONVERTING ENZYME AND ANGIOTENSINOGEN GENES IN PATTERNS OF LEFT VENTRICULAR HYPERTROPHY AND IN DIASTOLIC DYSFUNCTION. Clinical and Experimental Pharmacology and Physiology, 1995, 22, 438-440.	0.9	20

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109	RENIN AND ANGIOTENSIN-CONVERTING ENZYME GENOTYPES IN PATIENTS WITH ESSENTIAL HYPERTENSION AND LEFT VENTRICULAR HYPERTROPHY. Clinical and Experimental Pharmacology and Physiology, 1994, 21, 207-210.	0.9	25
110	Differentiation Between Heterozygotes and Homozygotes in Genetic Hemochromatosis by Means of a Histological Hepatic Iron Index: A Study of 192 Cases. Hepatology, 1993, 17, 30-34.	3.6	147
111	Concordance of iron storage in siblings with genetic hemochromatosis: Evidence for a predominantly genetic effect on iron storage. Hepatology, 1993, 17, 833-837.	3.6	35
112	ANGIOTENSIN-CONVERTING ENZYME AND REGULATION OF BLOOD PRESSURE IN A LARGE AUSTRALIAN FAMILY. Clinical and Experimental Pharmacology and Physiology, 1993, 20, 320-323.	0.9	13
113	Concordance of iron storage in siblings with genetic hemochromatosis: Evidence for a predominantly genetic effect on iron storage,. Hepatology, 1993, 17, 833-837.	3.6	4
114	Differentiation between heterozygotes and homozygotes in genetic hemochromatosis by means of a histological hepatic iron index: A study of 192 cases. Hepatology, 1993, 17, 30-34.	3.6	6
115	Physical and genetic mapping of the telomeric major histocompatibility complex region in man and relevance to the primary hemochromatosis gene (HFE). Genomics, 1992, 14, 232-240.	1.3	29
116	Allotype distribution of human T cell receptor ? and ? chain genes in Caucasians, Asians and Australian Aborigines: Relevance to chronic hepatitis B. Human Genetics, 1992, 89, 59-63.	1.8	6
117	POLYMORPHISMS OF CANDIDATE GENES IN ESSENTIAL HYPERTENSION. Clinical and Experimental Pharmacology and Physiology, 1992, 19, 315-318.	0.9	14
118	Is determination of the hepatic iron index of diagnostic value in patients with thalassemia minor and chronic alcoholic liver disease?. Hepatology, 1991, 14, 959-960.	3.6	2
119	Polymorphism in a ferritin H gene from chromosome 6p. Human Genetics, 1991, 86, 557-61.	1.8	5
120	Fine mapping of a human chromosome 6 ferritin heavy chain pseudogene: relevance to haemochromatosis. Human Genetics, 1991, 88, 175-8.	1.8	4
121	Expression of hemochromatosis in homozygous subjects. Gastroenterology, 1990, 98, 1625-1632.	0.6	108
122	Albumin ? vitamin D-binding protein haplotypes in Asian-Pacific populations. Human Genetics, 1990, 85, 89-97.	1.8	7
123	Identification of homozygous hemochromatosis subjects by measurement of hepatic iron index. Hepatology, 1990, 12, 20-25.	3.6	148
124	Genetic heterogeneity in Wilson's disease. Journal of Gastroenterology and Hepatology (Australia), 1990, 5, 697-699.	1.4	0
125	Applications of molecular genetics to gastrointestinal and liver diseases. I. Technical approaches. Journal of Gastroenterology and Hepatology (Australia), 1989, 4, 183-193.	1.4	2
126	Applications of molecular genetics to gastrointestinal and liver diseases. II. Clinical relevance. Journal of Gastroenterology and Hepatology (Australia), 1989, 4, 273-281.	1.4	0

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127	Molecular dissection of a contiguous gene syndrome: frequent submicroscopic deletions, evolutionarily conserved sequences, and a hypomethylated "island" in the Miller-Dieker chromosome region.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 5136-5140.	3.3	53
128	Multilocus analysis of the fragile X syndrome. Human Genetics, 1988, 78, 201-205.	1.8	57
129	Highly polymorphic locus D15S24 (CMW-1) maps to 15pter-q13. [HGM9 provisional no. D15S24]. Nucleic Acids Research, 1988, 16, 8740-8740.	6.5	32
130	Genetic distance analysis using DNA polymorphisms in the Î±-globin gene cluster. Annals of Human Biology, 1987, 14, 393-404.	0.4	1
131	Regional mapping panel for human chromosome 17: Application to neurofibromatosis type 1. Genomics, 1987, 1, 374-381.	1.3	126
132	DNA polymorphisms in human population studies: A review. Annals of Human Biology, 1987, 14, 203-217.	0.4	5
133	Alpha-thalassemia in Papua New Guinea. Human Genetics, 1986, 74, 432-437.	1.8	41
134	A SINGLE Î±-GLOBIN GENE DELETION IN AUSTRALIAN ABORIGINES. The Australian Journal of Experimental Biology and Medical Science, 1986, 64, 297-306.	0.7	11
135	?ï¿½- and ?ï¿½- Thalassemia in a Thai family: unusually mild homozygous ?ï¿½-thalassemia without ?-globin gene deletion. Human Genetics, 1985, 69, 375-377.	1.8	0
136	Regulation of the production of granulocyte-macrophage colony-stimulating factor by macrophage-like tumour cell lines. FEBS Letters, 1985, 180, 271-274.	1.3	3
137	Platelet monoamine oxidase: Specific activity and turnover number in schizophrenics and their families. Clinica Chimica Acta, 1985, 152, 289-296.	0.5	5
138	Urinary hormone levels: a population study of associations between steroid and catecholamine excretion rates. Annals of Human Biology, 1983, 10, 99-110.	0.4	12
139	Platelet monoamine oxidase: specific activity and turnover number in headache. Clinica Chimica Acta, 1982, 121, 139-146.	0.5	26
140	Biology of Eye Pigmentation in Insects. Advances in Insect Physiology, 1982, , 119-166.	1.1	95
141	Functions of the white and topaz loci of Lucilia cuprina in the production of the eye pigment xanthommatin. Biochemical Genetics, 1980, 18, 643-653.	0.8	10
142	Pteridines in wild type and eye colour mutants of the Australian sheep blowfly, Lucilia cuprina. Insect Biochemistry, 1980, 10, 151-154.	1.8	15
143	Xanthommatin biosynthesis in wild-type and mutant strains of the Australian sheep blowfly Lucilia cuprina. Biochemical Genetics, 1978, 16, 1153-1163.	0.8	23
144	Developmental patterns of 3-hydroxykynurenine accumulation in white and various other eye color mutants of Drosophila melanogaster. Biochemical Genetics, 1977, 15, 1049-1059.	0.8	66