

Robert J. Beynon

List of Publications by Year in descending order

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314
papers

13,276
citations

23567

58
h-index

31849

101
g-index

325
all docs

325
docs citations

325
times ranked

11358
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies. <i>Nature Communications</i> , 2022, 13, 801.	12.8	47
2	Decoding the Absolute Stoichiometric Composition and Structural Plasticity of $\hat{1}\pm$ -Carboxysomes. <i>MBio</i> , 2022, 13, e0362921.	4.1	27
3	Quantitative proteomic analysis of bronchoalveolar lavage fluid in West Highland white terriers with canine idiopathic pulmonary fibrosis. <i>BMC Veterinary Research</i> , 2022, 18, 121.	1.9	2
4	Harmonizing Labeling and Analytical Strategies to Obtain Protein Turnover Rates in Intact Adult Animals. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100252.	3.8	15
5	Monitoring recombinant protein expression in bacteria by rapid evaporative ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e8670.	1.5	8
6	The characteristic response of domestic cats to plant iridoids allows them to gain chemical defense against mosquitoes. <i>Science Advances</i> , 2021, 7, .	10.3	23
7	Probing the biogenesis pathway and dynamics of thylakoid membranes. <i>Nature Communications</i> , 2021, 12, 3475.	12.8	40
8	Lymphocytic Choriomeningitis Virus Alters the Expression of Male Mouse Scent Proteins. <i>Viruses</i> , 2021, 13, 1180.	3.3	5
9	The Impacts of Surgery and Intracerebral Electrodes in C57BL/6J Mouse Kainate Model of Epileptogenesis: Seizure Threshold, Proteomics, and Cytokine Profiles. <i>Frontiers in Neurology</i> , 2021, 12, 625017.	2.4	8
10	Construction of \hat{A} la carte QconCAT protein standards for multiplexed quantification of user-specified target proteins. <i>BMC Biology</i> , 2021, 19, 195.	3.8	8
11	Quantitative Proteomics of Enriched Esophageal and Gut Tissues from the Human Blood Fluke <i>Schistosoma mansoni</i> Pinpoints Secreted Proteins for Vaccine Development. <i>Journal of Proteome Research</i> , 2020, 19, 314-326.	3.7	17
12	A proteome-integrated, carbon source dependent genetic regulatory network in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2020, 16, 59-72.	2.8	11
13	Vulpeculin: a novel and abundant lipocalin in the urine of the common brushtail possum, <i>Trichosurus vulpecula</i> . <i>Open Biology</i> , 2020, 10, 200218.	3.6	2
14	Revealing mechanisms of mating plug function under sexual selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27465-27473.	7.1	11
15	Social status and ejaculate composition in the house mouse. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20200083.	4.0	10
16	CSF Levels of Elongation Factor Tu Is Associated With Increased Mortality in Malawian Adults With <i>Streptococcus pneumoniae</i> Meningitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 603623.	3.9	5
17	PEPPI-MS: Polyacrylamide-Gel-Based Prefractionation for Analysis of Intact Proteoforms and Protein Complexes by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 3779-3791.	3.7	49
18	The pheromone darcin drives a circuit for innate and reinforced behaviours. <i>Nature</i> , 2020, 578, 137-141.	27.8	44

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19	Decoding the stoichiometric composition and organisation of bacterial metabolosomes. <i>Nature Communications</i> , 2020, 11, 1976.	12.8	49
20	The application of rapid evaporative ionization mass spectrometry in the analysis of <i>Drosophila</i> species—a potential new tool in entomology. <i>Open Biology</i> , 2020, 10, 200196.	3.6	7
21	Large-scale and significant expression from pseudogenes in <i>Sodalis glossinidius</i> —a facultative bacterial endosymbiont. <i>Microbial Genomics</i> , 2020, 6, .	2.0	12
22	Rapid identification of species, sex and maturity by mass spectrometric analysis of animal faeces. <i>BMC Biology</i> , 2019, 17, 66.	3.8	8
23	Molecular complexity of the major urinary protein system of the Norway rat, <i>Rattus norvegicus</i> . <i>Scientific Reports</i> , 2019, 9, 10757.	3.3	14
24	The heparin-binding proteome in normal pancreas and murine experimental acute pancreatitis. <i>PLoS ONE</i> , 2019, 14, e0217633.	2.5	27
25	The impact of postsynaptic density 95 blocking peptide (Tat-NR2B9c) and an iNOS inhibitor (1400W) on proteomic profile of the hippocampus in C57BL/6J mouse model of kainate-induced epileptogenesis. <i>Journal of Neuroscience Research</i> , 2019, 97, 1378-1392.	2.9	11
26	Glycolytic flux in <i>Saccharomyces cerevisiae</i> is dependent on RNA polymerase III and its negative regulator Maf1. <i>Biochemical Journal</i> , 2019, 476, 1053-1082.	3.7	9
27	Caught in a Trap? Proteomic Analysis of Neutrophil Extracellular Traps in Rheumatoid Arthritis and Systemic Lupus Erythematosus. <i>Frontiers in Immunology</i> , 2019, 10, 423.	4.8	136
28	Landscape of heart proteome changes in a diet-induced obesity model. <i>Scientific Reports</i> , 2019, 9, 18050.	3.3	25
29	Chemerin acts via CMKLR1 and GPR1 to stimulate migration and invasion of gastric cancer cells: putative role of decreased TIMP-1 and TIMP-2. <i>Oncotarget</i> , 2019, 10, 98-112.	1.8	29
30	Individual odour signatures that mice learn are shaped by involatile major urinary proteins (MUPs). <i>BMC Biology</i> , 2018, 16, 48.	3.8	41
31	Tumour compartment transcriptomics demonstrates the activation of inflammatory and odontogenic programmes in human adamantinomatous craniopharyngioma and identifies the MAPK/ERK pathway as a novel therapeutic target. <i>Acta Neuropathologica</i> , 2018, 135, 757-777.	7.7	106
32	Specificity of the osmotic stress response in <i>Candida albicans</i> highlighted by quantitative proteomics. <i>Scientific Reports</i> , 2018, 8, 14492.	3.3	18
33	Matrix metalloproteinase (MMP)-7 in Barrett's esophagus and esophageal adenocarcinoma: expression, metabolism, and functional significance. <i>Physiological Reports</i> , 2018, 6, e13683.	1.7	12
34	Stable Isotope Dynamic Labeling of Secretomes (SIDLS) Identifies Authentic Secretory Proteins Released by Cancer and Stromal Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1837-1849.	3.8	14
35	Characterisation of urinary WFDC12 in small nocturnal basal primates, mouse lemurs (<i>Microcebus</i>) Tj ETQq1 1 0.784314 rgBT/Overl	3.3	11
36	Direct characterization of the native structure and mechanics of cyanobacterial carboxysomes. <i>Nanoscale</i> , 2017, 9, 10662-10673.	5.6	81

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37	Quantitative Proteomics Shows Extensive Remodeling Induced by Nitrogen Limitation in <i>Prochlorococcus marinus</i> SS120. <i>MSystems</i> , 2017, 2, .	3.8	25
38	Galectin-3 interacts with the cell-surface glycoprotein CD146 (MCAM, MUC18) and induces secretion of metastasis-promoting cytokines from vascular endothelial cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 8381-8389.	3.4	59
39	Molecular heterogeneity in major urinary proteins of <i>Mus musculus</i> subspecies: potential candidates involved in speciation. <i>Scientific Reports</i> , 2017, 7, 44992.	3.3	41
40	DOSCATs: Double standards for protein quantification. <i>Scientific Reports</i> , 2017, 7, 45570.	3.3	8
41	MEERCAT: Multiplexed Efficient Cell Free Expression of Recombinant QconCATs For Large Scale Absolute Proteome Quantification. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2169-2183.	3.8	23
42	Glareosin: a novel sexually dimorphic urinary lipocalin in the bank vole, <i>Myodes glareolus</i> . <i>Open Biology</i> , 2017, 7, 170135.	3.6	7
43	Quantitative Proteomics of Cerebrospinal Fluid in Paediatric Pneumococcal Meningitis. <i>Scientific Reports</i> , 2017, 7, 7042.	3.3	14
44	The Role of Eif6 in Skeletal Muscle Homeostasis Revealed by Endurance Training Co-expression Networks. <i>Cell Reports</i> , 2017, 21, 1507-1520.	6.4	22
45	Glucose Uptake in <i>Prochlorococcus</i> : Diversity of Kinetics and Effects on the Metabolism. <i>Frontiers in Microbiology</i> , 2017, 8, 327.	3.5	22
46	Selection on Coding and Regulatory Variation Maintains Individuality in Major Urinary Protein Scent Marks in Wild Mice. <i>PLoS Genetics</i> , 2016, 12, e1005891.	3.5	46
47	Absolute protein quantification of the yeast chaperome under conditions of heat shock. <i>Proteomics</i> , 2016, 16, 2128-2140.	2.2	18
48	Elastase levels and activity are increased in dystrophic muscle and impair myoblast cell survival, proliferation and differentiation. <i>Scientific Reports</i> , 2016, 6, 24708.	3.3	40
49	Direct and Absolute Quantification of over 1800 Yeast Proteins via Selected Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1309-1322.	3.8	80
50	Protein turnover measurement using selected reaction monitoring-mass spectrometry (SRM-MS). <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20150362.	3.4	10
51	A selected reaction monitoring-based analysis of acute phase proteins in interstitial fluids from experimental equine wounds healing by secondary intention. <i>Wound Repair and Regeneration</i> , 2016, 24, 525-532.	3.0	16
52	Cross-species proteomics in analysis of mammalian sperm proteins. <i>Journal of Proteomics</i> , 2016, 135, 38-50.	2.4	31
53	Proteome Dynamics: Tissue Variation in the Kinetics of Proteostasis in Intact Animals. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1204-1219.	3.8	33
54	In-depth proteomic profiling of the uveal melanoma secretome. <i>Oncotarget</i> , 2016, 7, 49623-49635.	1.8	45

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55	Focus on Quantitative Proteomics. <i>Proteomics</i> , 2015, 15, 3101-3103.	2.2	2
56	Sperm competition risk drives plasticity in seminal fluid composition. <i>BMC Biology</i> , 2015, 13, 87.	3.8	69
57	The male sex pheromone darcin stimulates hippocampal neurogenesis and cell proliferation in the subventricular zone in female mice. <i>Frontiers in Behavioral Neuroscience</i> , 2015, 9, 106.	2.0	28
58	Accuracy and Reproducibility in Quantification of Plasma Protein Concentrations by Mass Spectrometry without the Use of Isotopic Standards. <i>PLoS ONE</i> , 2015, 10, e0140097.	2.5	20
59	The Genetic Basis of Kin Recognition in a Cooperatively Breeding Mammal. <i>Current Biology</i> , 2015, 25, 2631-2641.	3.9	63
60	Mass spectrometry for structural analysis and quantification of the Major Urinary Proteins of the house mouse. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 146-156.	1.5	14
61	From sexual attraction to maternal aggression: When pheromones change their behavioural significance. <i>Hormones and Behavior</i> , 2015, 68, 65-76.	2.1	56
62	Mesenchymal Stem Cells Exhibit Regulated Exocytosis in Response to Chemerin and IGF. <i>PLoS ONE</i> , 2015, 10, e0141331.	2.5	11
63	Increased Expression of Chemerin in Squamous Esophageal Cancer Myofibroblasts and Role in Recruitment of Mesenchymal Stromal Cells. <i>PLoS ONE</i> , 2014, 9, e104877.	2.5	38
64	Sex pheromones are not always attractive: changes induced by learning and illness in mice. <i>Animal Behaviour</i> , 2014, 97, 265-272.	1.9	16
65	The role of proteomics in studies of protein moonlighting. <i>Biochemical Society Transactions</i> , 2014, 42, 1698-1703.	3.4	4
66	Development of a Method for Absolute Quantification of Equine Acute Phase Proteins Using Concatenated Peptide Standards and Selected Reaction Monitoring. <i>Journal of Proteome Research</i> , 2014, 13, 5635-5647.	3.7	12
67	The neuroendocrine phenotype of gastric myofibroblasts and its loss with cancer progression. <i>Carcinogenesis</i> , 2014, 35, 1798-1806.	2.8	16
68	Female attraction to male scent and associative learning: the house mouse as a mammalian model. <i>Animal Behaviour</i> , 2014, 97, 313-321.	1.9	38
69	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. <i>Proteomics</i> , 2014, 14, 2233-2241.	2.2	54
70	The major urinary protein system in the rat. <i>Biochemical Society Transactions</i> , 2014, 42, 886-892.	3.4	30
71	Comparative study of the molecular variation between "central"™ and "peripheral"™ MUPs and significance for behavioural signalling. <i>Biochemical Society Transactions</i> , 2014, 42, 866-872.	3.4	30
72	The complexity of protein semiochemistry in mammals. <i>Biochemical Society Transactions</i> , 2014, 42, 837-845.	3.4	17

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73	The Structure, Stability and Pheromone Binding of the Male Mouse Protein Sex Pheromone Darcin. PLoS ONE, 2014, 9, e108415.	2.5	24
74	An <i>in vivo</i> control map for the eukaryotic mRNA translation machinery. Molecular Systems Biology, 2013, 9, 635.	7.2	89
75	Quantitative analysis of chaperone network throughput in budding yeast. Proteomics, 2013, 13, 1276-1291.	2.2	33
76	Rodent Urinary Proteins: Genetic Identity Signals and Pheromones. , 2013, , 117-133.		13
77	The Application of Proteomics to the Discovery and Quantification of Proteins in Scent Signals. , 2013, , 433-447.		0
78	Absolute Quantification of Selected Proteins in the Human Osteoarthritic Secretome. International Journal of Molecular Sciences, 2013, 14, 20658-20681.	4.1	40
79	Heterogenous Turnover of Sperm and Seminal Vesicle Proteins in the Mouse Revealed by Dynamic Metabolic Labeling. Molecular and Cellular Proteomics, 2012, 11, M111.014993.	3.8	37
80	Proteome Dynamics: Revisiting Turnover with a Global Perspective. Molecular and Cellular Proteomics, 2012, 11, 1551-1565.	3.8	106
81	Pheromonal Induction of Spatial Learning in Mice. Science, 2012, 338, 1462-1465.	12.6	141
82	A Software Toolkit and Interface for Performing Stable Isotope Labeling and Top3 Quantification Using Progenesis LC-MS. OMICS A Journal of Integrative Biology, 2012, 16, 489-495.	2.0	47
83	Quantotypic Properties of QconCAT Peptides Targeting Bovine Host Response to <i>Streptococcus uberis</i> . Journal of Proteome Research, 2012, 11, 1832-1843.	3.7	39
84	QconCATs: design and expression of concatenated protein standards for multiplexed protein quantification. Analytical and Bioanalytical Chemistry, 2012, 404, 977-989.	3.7	57
85	Absolute Multiplexed Protein Quantification Using QconCAT Technology. Methods in Molecular Biology, 2012, 893, 267-293.	0.9	31
86	Protein turnover: Measurement of proteome dynamics by whole animal metabolic labelling with stable isotope labelled amino acids. Proteomics, 2012, 12, 1194-1206.	2.2	71
87	Tissue-dependent changes in oxidative damage with male reproductive effort in house mice. Functional Ecology, 2012, 26, 423-433.	3.6	57
88	Proteomic characterisation and quantification of an in-vitro early equine osteoarthritis model. Osteoarthritis and Cartilage, 2012, 20, S261-S262.	1.3	1
89	Protein Turnover Methods in Single-Celled Organisms: Dynamic SILAC. Methods in Molecular Biology, 2011, 759, 179-195.	0.9	13
90	Elevated Glucose Represses Liver Glucokinase and Induces Its Regulatory Protein to Safeguard Hepatic Phosphate Homeostasis. Diabetes, 2011, 60, 3110-3120.	0.6	53

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91	The importance of the digest: Proteolysis and absolute quantification in proteomics. <i>Methods</i> , 2011, 54, 351-360.	3.8	134
92	The scent of senescence: sexual signalling and female preference in house mice. <i>Journal of Evolutionary Biology</i> , 2011, 24, 2398-2409.	1.7	52
93	Disruption of Wnt Planar Cell Polarity Signaling by Aberrant Accumulation of the MetAP-2 Substrate Rab37. <i>Chemistry and Biology</i> , 2011, 18, 1300-1311.	6.0	23
94	Global absolute quantification of a proteome: Challenges in the deployment of a QconCAT strategy. <i>Proteomics</i> , 2011, 11, 2957-2970.	2.2	103
95	Abundance of tegument surface proteins in the human blood fluke <i>Schistosoma mansoni</i> determined by QconCAT proteomics. <i>Journal of Proteomics</i> , 2011, 74, 1519-1533.	2.4	69
96	Absolute Quantification of the Glycolytic Pathway in Yeast. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.007633.	3.8	70
97	Diauxic shift-dependent relocalization of decapping activators Dhh1 and Pat1 to polysomal complexes. <i>Nucleic Acids Research</i> , 2011, 39, 7764-7774.	14.5	22
98	Positional Proteomics at the N-Terminus as a Means of Proteome Simplification. <i>Methods in Molecular Biology</i> , 2011, 753, 229-242.	0.9	2
99	Asymmetric Proteome Equalization of the Skeletal Muscle Proteome Using a Combinatorial Hexapeptide Library. <i>PLoS ONE</i> , 2011, 6, e28902.	2.5	25
100	Parallel FPGA Search Engine for Protein Identification. <i>Embedded Multi-core Systems</i> , 2010, , 313-335.	0.1	1
101	Acetone Precipitation of Proteins and the Modification of Peptides. <i>Journal of Proteome Research</i> , 2010, 9, 444-450.	3.7	67
102	A High-Performance Reconfigurable Computing Solution for Peptide Mass Fingerprinting. <i>Methods in Molecular Biology</i> , 2010, 604, 163-185.	0.9	0
103	¹ H, ¹⁵ N and ¹³ C resonance assignment of darcin, a mouse major urinary protein. <i>Biomolecular NMR Assignments</i> , 2010, 4, 239-241.	0.8	5
104	Teladorsagia circumcincta: Activation-associated secreted proteins in excretory/secretory products of fourth stage larvae are targets of early IgA responses in infected sheep. <i>Experimental Parasitology</i> , 2010, 125, 329-337.	1.2	29
105	Darcin: a male pheromone that stimulates female memory and sexual attraction to an individual male's odour. <i>BMC Biology</i> , 2010, 8, 75.	3.8	281
106	Making progress in genetic kin recognition among vertebrates. <i>Journal of Biology</i> , 2010, 9, 13.	2.7	26
107	Roborovskina, a Lipocalin in the Urine of the Roborovski Hamster, <i>Phodopus roborovskii</i> . <i>Chemical Senses</i> , 2010, 35, 675-684.	2.0	11
108	Quantitative Analysis of HGF and EGF-Dependent Phosphotyrosine Signaling Networks. <i>Journal of Proteome Research</i> , 2010, 9, 2734-2742.	3.7	48

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109	Cross Species Proteomics. <i>Methods in Molecular Biology</i> , 2010, 604, 123-135.	0.9	23
110	Exploiting proteomic data for genome annotation and gene model validation in <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2009, 10, 61.	2.8	35
111	Proteomic analysis of excretory/secretory products released by <i>Trichostrongylus axei</i> larvae early post-infection. <i>Parasite Immunology</i> , 2009, 31, 10-19.	1.5	54
112	Rigorous determination of the stoichiometry of protein phosphorylation using mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 2211-2220.	2.8	40
113	Limited variation in the major urinary proteins of laboratory mice. <i>Physiology and Behavior</i> , 2009, 96, 253-261.	2.1	125
114	Peptide Mass Fingerprinting Using Field-Programmable Gate Arrays. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2009, 3, 142-149.	4.0	3
115	Turnover of the Human Proteome: Determination of Protein Intracellular Stability by Dynamic SILAC. <i>Journal of Proteome Research</i> , 2009, 8, 104-112.	3.7	294
116	Observation of heterogeneous gene products by FT-ICR MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 103-110.	2.8	7
117	Protein Quantification by Selective Isolation and Fragmentation of Isotopic Pairs Using FT-ICR MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 973-977.	2.8	9
118	Biomarkers for ragwort poisoning in horses: identification of protein targets. <i>BMC Veterinary Research</i> , 2008, 4, 30.	1.9	16
119	Proteomics and naturally occurring animal diseases: Opportunities for animal and human medicine. <i>Proteomics - Clinical Applications</i> , 2008, 2, 135-141.	1.6	21
120	QCAL™ a novel standard for assessing instrument conditions for proteome analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1275-1280.	2.8	41
121	The Direct Assessment of Genetic Heterozygosity through Scent in the Mouse. <i>Current Biology</i> , 2008, 18, 619-623.	3.9	83
122	Dynamic instability of the Major Urinary Protein gene family revealed by genomic and phenotypic comparisons between C57 and 129 strain mice. <i>Genome Biology</i> , 2008, 9, R91.	9.6	100
123	Pharmacological and nutritional treatment for McArdle disease (Glycogen Storage Disease type V). , 2008, , CD003458.		12
124	Asparagine Deamidation and the Role of Higher Order Protein Structure. <i>Journal of Proteome Research</i> , 2008, 7, 921-927.	3.7	34
125	High-performance hardware implementation of a parallel database search engine for real-time peptide mass fingerprinting. <i>Bioinformatics</i> , 2008, 24, 1498-1502.	4.1	18
126	Comparative Proteomics Reveals Evidence for Evolutionary Diversification of Rodent Seminal Fluid and Its Functional Significance in Sperm Competition. <i>Molecular Biology and Evolution</i> , 2008, 26, 189-198.	8.9	96

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127	Reconfigurable computing solution for Peptide Mass Fingerprinting. , 2008, , .		1
128	The Effect of Familiarity on Mate Choice. , 2008, , 271-280.		19
129	Scent, Mate Choice and Genetic Heterozygosity. , 2008, , 291-301.		6
130	Urinary Lipocalins in Rodenta:is there a Generic Model?. , 2008, , 37-49.		9
131	Chemical communication in societies of rodents. , 2008, , 97-118.		3
132	Hardware acceleration of processing of mass spectrometric data for proteomics. <i>Bioinformatics</i> , 2007, 23, 724-731.	4.1	25
133	Avian proteomics: advances, challenges and new technologies. <i>Cytogenetic and Genome Research</i> , 2007, 117, 358-369.	1.1	15
134	Absolute Multiplexed Quantitative Analysis of Protein Expression during Muscle Development Using QconCAT. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1416-1427.	3.8	141
135	Anabolic effects of a non-myotoxic dose of the β_2 -adrenergic receptor agonist clenbuterol on rat plantaris muscle. <i>Muscle and Nerve</i> , 2007, 35, 217-223.	2.2	32
136	Formation of 3-nitrotyrosines in carbonic anhydrase III is a sensitive marker of oxidative stress in skeletal muscle. <i>Proteomics - Clinical Applications</i> , 2007, 1, 362-372.	1.6	36
137	Global cooling: Cold acclimation and the expression of soluble proteins in carp skeletal muscle. <i>Proteomics</i> , 2007, 7, 2667-2681.	2.2	48
138	The Genetic Basis of Individual-Recognition Signals in the Mouse. <i>Current Biology</i> , 2007, 17, 1771-1777.	3.9	186
139	The Genetic Basis of Inbreeding Avoidance in House Mice. <i>Current Biology</i> , 2007, 17, 2061-2066.	3.9	169
140	The importance of exposure to other male scents in determining competitive behaviour among inbred male mice. <i>Applied Animal Behaviour Science</i> , 2007, 104, 130-142.	1.9	14
141	Evidence for multiple circulating factors in preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , 2007, 196, 266.e1-266.e6.	1.3	11
142	Characterization and Comparison of Major Urinary Proteins from the House Mouse, <i>Mus musculus domesticus</i> , and the Aboriginal Mouse, <i>Mus macedonicus</i> . <i>Journal of Chemical Ecology</i> , 2007, 33, 613-630.	1.8	33
143	Characterization of Cauxin in the Urine of Domestic and Big Cats. <i>Journal of Chemical Ecology</i> , 2007, 33, 1997-2009.	1.8	44
144	Pharmacological and nutritional treatment trials in McArdle disease. <i>Acta Myologica</i> , 2007, 26, 58-60.	1.5	6

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145	Protein turnover on the scale of the proteome. <i>Expert Review of Proteomics</i> , 2006, 3, 97-110.	3.0	77
146	A proteomics study of the response of North Ronaldsay sheep to copper challenge. <i>BMC Veterinary Research</i> , 2006, 2, 36.	1.9	15
147	Multiplexed absolute quantification for proteomics using concatenated signature peptides encoded by QconCAT genes. <i>Nature Protocols</i> , 2006, 1, 1029-1043.	12.0	357
148	Positional proteomics: preparation of amino-terminal peptides as a strategy for proteome simplification and characterization. <i>Nature Protocols</i> , 2006, 1, 1790-1798.	12.0	82
149	Activation of the Endosome-Associated Ubiquitin Isopeptidase AMSH by STAM, a Component of the Multivesicular Body-Sorting Machinery. <i>Current Biology</i> , 2006, 16, 160-165.	3.9	190
150	Strategies for Measuring Dynamics: The Temporal Component of Proteomics. <i>Methods of Biochemical Analysis</i> , 2005, 49, 15-25.	0.2	7
151	The signalling of competitive ability by male house mice. , 2005, , 77-88.		2
152	Multiplexed absolute quantification in proteomics using artificial QCAT proteins of concatenated signature peptides. <i>Nature Methods</i> , 2005, 2, 587-589.	19.0	456
153	Positional proteomics: selective recovery and analysis of N-terminal proteolytic peptides. <i>Nature Methods</i> , 2005, 2, 955-957.	19.0	150
154	The Greater Susceptibility of North Ronaldsay Sheep Compared with Cambridge Sheep to Copper-induced Oxidative Stress, Mitochondrial Damage and Hepatic Stellate Cell Activation. <i>Journal of Comparative Pathology</i> , 2005, 133, 114-127.	0.4	35
155	Metabolomics as a diagnostic tool for hepatology: validation in a naturally occurring canine model. <i>Metabolomics</i> , 2005, 1, 215-225.	3.0	33
156	Proteome dynamics in complex organisms: Using stable isotopes to monitor individual protein turnover rates. <i>Proteomics</i> , 2005, 5, 522-533.	2.2	158
157	The role of the major histocompatibility complex in scent communication. , 2005, , 173-182.		0
158	A simple tool for drawing proteolytic peptide maps. <i>Bioinformatics</i> , 2005, 21, 674-675.	4.1	16
159	The Subunit Structure and Dynamics of the 20S Proteasome in Chicken Skeletal Muscle. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1370-1381.	3.8	45
160	The dynamics of the proteome: Strategies for measuring protein turnover on a proteome-wide scale. <i>Briefings in Functional Genomics & Proteomics</i> , 2005, 3, 382-390.	3.8	28
161	MHC odours are not required or sufficient for recognition of individual scent owners. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 715-724.	2.6	69
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