

Simon Hubbard

List of Publications by Year in descending order

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113
papers

6,805
citations

71061

41
h-index

64755

79
g-index

129
all docs

129
docs citations

129
times ranked

11545
citing authors

#	ARTICLE	IF	CITATIONS
1	MRSD: A quantitative approach for assessing suitability of RNA-seq in the investigation of mis-splicing in Mendelian disease. <i>American Journal of Human Genetics</i> , 2022, 109, 210-222.	2.6	12
2	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies. <i>Nature Communications</i> , 2022, 13, 801.	5.8	47
3	Implementing the reuse of public DIA proteomics datasets: from the PRIDE database to Expression Atlas. <i>Scientific Data</i> , 2022, 9, .	2.4	13
4	Model Parameterization with Quantitative Proteomics: Case Study with Trehalose Metabolism in <i>Saccharomyces cerevisiae</i> . <i>Processes</i> , 2021, 9, 139.	1.3	1
5	Core Fermentation (CoFe) granules focus coordinated glycolytic mRNA localization and translation to fuel glucose fermentation. <i>IScience</i> , 2021, 24, 102069.	1.9	26
6	Integrated multi-omics reveals common properties underlying stress granule and P-body formation. <i>RNA Biology</i> , 2021, 18, 655-673.	1.5	10
7	A proteome-integrated, carbon source dependent genetic regulatory network in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2020, 16, 59-72.	1.4	11
8	Characterisation of protein isoforms encoded by the <i>Drosophila</i> Glycogen Synthase Kinase 3 gene shaggy. <i>PLoS ONE</i> , 2020, 15, e0236679.	1.1	5
9	Title is missing!. , 2020, 15, e0236679.		0
10	Title is missing!. , 2020, 15, e0236679.		0
11	Title is missing!. , 2020, 15, e0236679.		0
12	Title is missing!. , 2020, 15, e0236679.		0
13	Disease modeling of core pre-mRNA splicing factor haploinsufficiency. <i>Human Molecular Genetics</i> , 2019, 28, 3704-3723.	1.4	24
14	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.	1.7	9
15	A quantitative and temporal map of proteostasis during heat shock in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2018, 14, 37-52.	1.4	17
16	Ribosomal flavours: an acquired taste for specific mRNAs?. <i>Biochemical Society Transactions</i> , 2018, 46, 1529-1539.	1.6	8
17	Archetypal transcriptional blocks underpin yeast gene regulation in response to changes in growth conditions. <i>Scientific Reports</i> , 2018, 8, 7949.	1.6	6
18	Dynamic Acclimation to High Light in <i>Arabidopsis thaliana</i> Involves Widespread Reengineering of the Leaf Proteome. <i>Frontiers in Plant Science</i> , 2017, 8, 1239.	1.7	39

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19	Dynamic changes in eIF4F-mRNA interactions revealed by global analyses of environmental stress responses. <i>Genome Biology</i> , 2017, 18, 201.	3.8	37
20	Absolute protein quantification of the yeast chaperome under conditions of heat shock. <i>Proteomics</i> , 2016, 16, 2128-2140.	1.3	18
21	Direct and Absolute Quantification of over 1800 Yeast Proteins via Selected Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1309-1322.	2.5	80
22	Analysis of Intrinsic Peptide Detectability via Integrated Label-Free and SRM-Based Absolute Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 2945-2959.	1.8	46
23	The mzqLibrary – An open source Java library supporting the HUPO-PSI quantitative proteomics standard. <i>Proteomics</i> , 2015, 15, 3152-3162.	1.3	5
24	Quantitative proteomics and network analysis of SSA1 and SSB1 deletion mutants reveals robustness of chaperone HSP70 network in <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2015, 15, 3126-3139.	1.3	12
25	Representation of selected reaction monitoring data in the mzQuantML data standard. <i>Proteomics</i> , 2015, 15, 2592-2596.	1.3	7
26	Focus on Quantitative Proteomics. <i>Proteomics</i> , 2015, 15, 3101-3103.	1.3	2
27	Integrated multi-omics analyses reveal the pleiotropic nature of the control of gene expression by Puf3p. <i>Scientific Reports</i> , 2015, 5, 15518.	1.6	51
28	Global mRNA selection mechanisms for translation initiation. <i>Genome Biology</i> , 2015, 16, 10.	3.8	92
29	The 4E-BP Caf20p Mediates Both eIF4E-Dependent and Independent Repression of Translation. <i>PLoS Genetics</i> , 2015, 11, e1005233.	1.5	36
30	The Yeast La Related Protein Slf1p Is a Key Activator of Translation during the Oxidative Stress Response. <i>PLoS Genetics</i> , 2015, 11, e1004903.	1.5	36
31	Computational phosphoproteomics: From identification to localization. <i>Proteomics</i> , 2015, 15, 950-963.	1.3	24
32	Puf3p induces translational repression of genes linked to oxidative stress. <i>Nucleic Acids Research</i> , 2014, 42, 1026-1041.	6.5	34
33	Analysis of Chaperone Network Throughput. , 2014, , 3-23.		1
34	Quantitative analysis of chaperone network throughput in budding yeast. <i>Proteomics</i> , 2013, 13, 1276-1291.	1.3	33
35	Prediction of Missed Proteolytic Cleavages for the Selection of Surrogate Peptides for Quantitative Proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 449-456.	1.0	72
36	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014381-1-M111.014381-10.	2.5	175

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37	Addressing Statistical Biases in Nucleotide-Derived Protein Databases for Proteogenomic Search Strategies. <i>Journal of Proteome Research</i> , 2012, 11, 5221-5234.	1.8	83
38	A Critical Appraisal of Techniques, Software Packages, and Standards for Quantitative Proteomic Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 431-442.	1.0	50
39	FDRAnalysis: A Tool for the Integrated Analysis of Tandem Mass Spectrometry Identification Results from Multiple Search Engines. <i>Journal of Proteome Research</i> , 2011, 10, 2088-2094.	1.8	18
40	Global absolute quantification of a proteome: Challenges in the deployment of a QconCAT strategy. <i>Proteomics</i> , 2011, 11, 2957-2970.	1.3	103
41	UKPMC: a full text article resource for the life sciences. <i>Nucleic Acids Research</i> , 2011, 39, D58-D65.	6.5	40
42	CONSeQuence: Prediction of Reference Peptides for Absolute Quantitative Proteomics Using Consensus Machine Learning Approaches. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003384.	2.5	121
43	BioMart Central Portal: an open database network for the biological community. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar041-bar041.	1.4	145
44	Distributions of Ion Series in ETD and CID Spectra: Making a Comparison. <i>Methods in Molecular Biology</i> , 2011, 696, 327-337.	0.4	4
45	Investigating protein isoforms <i>via</i> proteomics: A feasibility study. <i>Proteomics</i> , 2010, 10, 1127-1140.	1.3	41
46	Identifying eIF4E-binding protein translationally-controlled transcripts reveals links to mRNAs bound by specific PUF proteins. <i>Nucleic Acids Research</i> , 2010, 38, 8039-8050.	6.5	47
47	Computational Approaches to Peptide Identification via Tandem MS. <i>Methods in Molecular Biology</i> , 2010, 604, 23-42.	0.4	5
48	An Introduction to Proteome Bioinformatics. <i>Methods in Molecular Biology</i> , 2010, 604, 1-5.	0.4	5
49	SILACAnalyzer - A Tool for Differential Quantitation of Stable Isotope Derived Data. <i>Lecture Notes in Computer Science</i> , 2010, , 45-55.	1.0	6
50	Cross Species Proteomics. <i>Methods in Molecular Biology</i> , 2010, 604, 123-135.	0.4	23
51	Recent Developments in Proteome Informatics for Mass Spectrometry Analysis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2009, 12, 194-202.	0.6	14
52	Exploiting proteomic data for genome annotation and gene model validation in <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2009, 10, 61.	1.2	35
53	Upstream sequence elements direct post-transcriptional regulation of gene expression under stress conditions in yeast. <i>BMC Genomics</i> , 2009, 10, 7.	1.2	87
54	Expression screening and annotation of a zebrafish myoblast cDNA library. <i>Gene Expression Patterns</i> , 2009, 9, 73-82.	0.3	8

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55	Improving sensitivity in proteome studies by analysis of false discovery rates for multiple search engines. <i>Proteomics</i> , 2009, 9, 1220-1229.	1.3	91
56	Getting a grip on proteomics data – Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009, 9, 3928-3933.	1.3	15
57	Observations on the detection of b̂and ŷtype ions in the collisionally activated decomposition spectra of protonated peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 1508-1514.	0.7	38
58	Analysis of the trypanosome flagellar proteome using a combined electron transfer/collisionally activated dissociation strategy. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 167-175.	1.2	36
59	Predicted transcription factor binding sites as predictors of operons in <i>Escherichia coli</i> and <i>Streptomyces coelicolor</i> . <i>BMC Genomics</i> , 2008, 9, 79.	1.2	9
60	PepSeeker: Mining Information from Proteomic Data. <i>Methods in Molecular Biology</i> , 2008, 484, 319-332.	0.4	5
61	ISPIDER Central: an integrated database web-server for proteomics. <i>Nucleic Acids Research</i> , 2008, 36, W485-W490.	6.5	18
62	Comparative Genome Analysis of Filamentous Fungi Reveals Gene Family Expansions Associated with Fungal Pathogenesis. <i>PLoS ONE</i> , 2008, 3, e2300.	1.1	169
63	Comparative genome analysis across a kingdom of eukaryotic organisms: Specialization and diversification in the Fungi. <i>Genome Research</i> , 2007, 17, 1809-1822.	2.4	94
64	Human and mouse homo-oligomeric meprin A metalloendopeptidase: substrate and inhibitor specificities. <i>Biological Chemistry</i> , 2007, 388, 1163-1172.	1.2	15
65	Characterising alternate splicing and tissue specific expression in the chicken from ESTs. <i>Cytogenetic and Genome Research</i> , 2007, 117, 268-277.	0.6	5
66	A Methodology for Comparative Functional Genomics. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 112-122.	1.0	1
67	Prediction of Missed Cleavage Sites in Tryptic Peptides Aids Protein Identification in Proteomics. <i>Journal of Proteome Research</i> , 2007, 6, 399-408.	1.8	152
68	An informatic pipeline for the data capture and submission of quantitative proteomic data using iTRAQ. <i>Proteome Science</i> , 2007, 5, 4.	0.7	21
69	Capture and analysis of quantitative proteomic data. <i>Proteomics</i> , 2007, 7, 2787-2799.	1.3	54
70	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007, 25, 1127-1133.	9.4	96
71	e-Fungi: a data resource for comparative analysis of fungal genomes. <i>BMC Genomics</i> , 2007, 8, 426.	1.2	32
72	A kingdom-specific protein domain HMM library for improved annotation of fungal genomes. <i>BMC Genomics</i> , 2007, 8, 97.	1.2	12

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73	Analysis of gene expression in operons of <i>Streptomyces coelicolor</i> . <i>Genome Biology</i> , 2006, 7, R46.	13.9	34
74	PepSeeker: a database of proteome peptide identifications for investigating fragmentation patterns. <i>Nucleic Acids Research</i> , 2006, 34, D649-D654.	6.5	35
75	Differential Expression of Ion Channel Transcripts in Atrial Muscle and Sinoatrial Node in Rabbit. <i>Circulation Research</i> , 2006, 99, 1384-1393.	2.0	134
76	Global Translational Responses to Oxidative Stress Impact upon Multiple Levels of Protein Synthesis. <i>Journal of Biological Chemistry</i> , 2006, 281, 29011-29021.	1.6	357
77	Data Access and Integration in the ISPIDER Proteomics Grid. <i>Lecture Notes in Computer Science</i> , 2006, , 3-18.	1.0	14
78	Mass spectrometric data mining for protein sequences. , 2005, , .		0
79	Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. <i>Genome Research</i> , 2005, 15, 174-183.	2.4	79
80	Global Gene Expression Profiling Reveals Widespread yet Distinctive Translational Responses to Different Eukaryotic Translation Initiation Factor 2B-Targeting Stress Pathways. <i>Molecular and Cellular Biology</i> , 2005, 25, 9340-9349.	1.1	85
81	Conservation of Orientation and Sequence in Protein Domainâ€œDomain Interactions. <i>Journal of Molecular Biology</i> , 2005, 345, 1265-1279.	2.0	35
82	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	13.7	391
83	PEDRo: A database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , 2004, 5, 68.	1.2	58
84	Improved prediction for N-termini of α -helices using empirical information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 322-330.	1.5	14
85	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , 2003, 21, 247-254.	9.4	246
86	The chicken as a model for large-scale analysis of vertebrate gene function. <i>Nature Reviews Genetics</i> , 2003, 4, 87-98.	7.7	154
87	SiteSeer: visualisation and analysis of transcription factor binding sites in nucleotide sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3572-3575.	6.5	16
88	A critical assessment of the secondary structure α -helices and their termini in proteins. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 545-554.	1.0	15
89	A Comprehensive Collection of Chicken cDNAs. <i>Current Biology</i> , 2002, 12, 1965-1969.	1.8	305
90	Stable isotope labelling in vivo as an aid to protein identification in peptide mass fingerprinting. <i>Proteomics</i> , 2002, 2, 157-163.	1.3	58

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91	Comparative bioinformatic analysis of complete proteomes and protein parameters for cross-species identification in proteomics. <i>Proteomics</i> , 2002, 2, 1392-1405.	1.3	68
92	Sequence Search Algorithms for Single Pass Sequence Identification: Does One Size Fit All?. <i>Comparative and Functional Genomics</i> , 2001, 2, 4-9.	2.0	5
93	A combination of chemical derivatisation and improved bioinformatic tools optimises protein identification for proteomics. <i>Electrophoresis</i> , 2001, 22, 552-559.	1.3	61
94	Bioinformatic assessment of mass spectrometric chemical derivatisation techniques for proteome database searching. <i>Proteomics</i> , 2001, 1, 1368-1377.	1.3	25
95	Effect of polymorphisms on ligand binding by mouse major urinary proteins. <i>Protein Science</i> , 2001, 10, 411-417.	3.1	59
96	Marked Differences between Metalloproteases Meprin A and B in Substrate and Peptide Bond Specificity. <i>Journal of Biological Chemistry</i> , 2001, 276, 13248-13255.	1.6	103
97	Mice, Mups and Myths: Structure-Function Relationships of the Major Urinary Proteins. , 2001, , 149-156.		10
98	Conceptual modelling of genomic information. <i>Bioinformatics</i> , 2000, 16, 548-557.	1.8	96
99	Proteolysis of Native Proteins. <i>Journal of Biological Chemistry</i> , 1999, 274, 1108-1115.	1.6	21
100	Ligands of Urinary Lipocalins from the Mouse: Uptake of Environmentally Derived Chemicals. <i>Journal of Chemical Ecology</i> , 1998, 24, 1127-1140.	0.9	24
101	The structural aspects of limited proteolysis of native proteins. <i>BBA - Proteins and Proteomics</i> , 1998, 1382, 191-206.	2.1	351
102	Assessment of conformational parameters as predictors of limited proteolytic sites in native protein structures. <i>Protein Engineering, Design and Selection</i> , 1998, 11, 349-359.	1.0	109
103	A Functional Role for Protein Cavities in Domain:Domain Motions. <i>Journal of Molecular Biology</i> , 1996, 261, 289-300.	2.0	49
104	Limited proteolysis of native proteins: The interaction between avidin and proteinase K. <i>Protein Science</i> , 1995, 4, 1337-1345.	3.1	52
105	Comparison of atomic solvation parametric sets: Applicability and limitations in protein folding and binding. <i>Protein Science</i> , 1995, 4, 2499-2509.	3.1	84
106	Evidence on close packing and cavities in proteins. <i>Current Opinion in Biotechnology</i> , 1995, 6, 375-381.	3.3	31
107	Detection of internal cavities in globular proteins. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 1011-1015.	1.0	34
108	Modeling studies of the change in conformation required for cleavage of limited proteolytic sites. <i>Protein Science</i> , 1994, 3, 757-768.	3.1	186

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109	Cavities and packing at protein interfaces. <i>Protein Science</i> , 1994, 3, 2194-2206.	3.1	141
110	Intramolecular cavities in globular proteins. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 613-626.	1.0	167
111	Substrate recognition by proteinases. <i>Faraday Discussions</i> , 1992, 93, 13.	1.6	19
112	Molecular recognition. <i>Journal of Molecular Biology</i> , 1991, 220, 507-530.	2.0	358
113	Cytosolic aspartate aminotransferase moonlights as a ribosome-binding modulator of Gcn2 activity during oxidative stress. <i>ELife</i> , 0, 11, .	2.8	5