John M Hancock

List of Publications by Year
in descending order

111 papers	5,960 citations	61984 43 h-index	79698 73 g-index
172 all docs	172 docs citations	172 times ranked	8934 citing authors

#	Article	IF	Citations
1	Matching mouse models to specific human liver disease states by comparative functional genomics of mouse and human datasets. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194785.	1.9	1
2	ELIXIRâ€EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	7.8	18
3	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	6.5	70
4	Community curation of bioinformatics software and data resources. Briefings in Bioinformatics, 2020, 21, 1697-1705.	6.5	12
5	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. Nucleic Acids Research, 2020, 48, W77-W84.	14.5	71
6	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 T	1.6	12
7	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
8	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
9	BioCIDER: a Contextualisation InDEx for biological Resources discovery. Bioinformatics, 2017, 33, 2607-2608.	4.1	1
10	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. F1000Research, 2017, 6, 465.	1.6	16
11	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. F1000Research, 2017, 6, 465.	1.6	10
12	Developing a strategy for computational lab skills training through Software and Data Carpentry: Experiences from the ELIXIR Pilot action. F1000Research, 2017, 6, 1040.	1.6	8
13	ELIXIR-UK role in bioinformatics training at the national level and across ELIXIR. F1000Research, 2017, 6, 952.	1.6	12
14	Human Variome Project Quality Assessment Criteria for Variation Databases. Human Mutation, 2016, 37, 549-558.	2.5	18
15	Introduction to â€œPhenomicsâ€•, 2016, , 11-17.		2
16	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. F1000Research, 2016, 5, 2894.	1.6	6
17	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. F1000Research, 2016, 5, 2894.	1.6	6
18	Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. Nature Genetics, 2015, 47, 969-978.	21.4	137

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19	Editorial: biological ontologies and semantic biology. Frontiers in Genetics, 2014, 5, 18.	2.3	5
20	Commentary on Shimoyama et al. (2012): three ontologies to define phenotype measurement data. Frontiers in Genetics, 2014, 5, 93.	2.3	1
21	Analyzing gene expression data in mice with the Neuro Behavior Ontology. Mammalian Genome, 2014, 25, 32-40.	2.2	19
22	Circles within circles: commentary on Ghosal et al. (2013) Ã¢â‚¬Å"Circ2Traits: a comprehensive database for circular RNA potentially associated with disease and traitsÃ¢â‚¬Â Frontiers in Genetics, 2014, 5, 459.	2.3	16
23	Functional modelling of planar cell polarity: an approach for identifying molecular function. BMC Developmental Biology, 2013, 13, 20.	2.1	12
24	A comparative phenotypic and genomic analysis of C57BL/6J and C57BL/6N mouse strains. Genome Biology, 2013, 14, R82.	9.6	403
25	NucleoFinder: a statistical approach for the detection of nucleosome positions. Bioinformatics, 2013, 29, 711-716.	4.1	20
26	A tale of two drug targets: the evolutionary history of BACE1 and BACE2. Frontiers in Genetics, 2013, 4, 293.	2.3	17
27	Low microsatellite frequencies in neuron and brain expressed microRNAs. Gene, 2012, 508, 73-77.	2.2	2
28	Integration of global resources for human genetic variation and disease. Human Mutation, 2012, 33, 813-816.	2.5	9
29	A Gene-Phenotype Network for the Laboratory Mouse and Its Implications for Systematic Phenotyping. PLoS ONE, 2011, 6, e19693.	2.5	12
30	Anatomy ontologies and potential users: bridging the gap. Journal of Biomedical Semantics, 2011, 2, S3.	1.6	6
31	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. BMC Evolutionary Biology, 2011, 11, 142.	3.2	3
32	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30
33	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32
34	The Informatics of High-Throughput Mouse Phenotyping: EUMODIC and Beyond. , 2011, , 77-87.		1
35	Identification of a Z-band associated protein complex involving KY, FLNC and IGFN1. Experimental Cell Research, 2010, 316, 1856-1870.	2.6	26
36	Mouse Resource Browser--a database of mouse databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq010-baq010.	3.0	3

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37	EuroPhenome: a repository for high-throughput mouse phenotyping data. Nucleic Acids Research, 2010, 38, D577-D585.	14.5	75
38	Finding and sharing: new approaches to registries of databases and services for the biomedical sciences. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq014-baq014.	3.0	12
39	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. Genome Biology, 2010, 11, R27.	9.6	20
40	Sustaining the Data and Bioresource Commons. Science, 2010, 330, 592-593.	12.6	52
41	MouseBook: an integrated portal of mouse resources. Nucleic Acids Research, 2010, 38, D593-D599.	14.5	18
42	Phenotype ontologies for mouse and man: bridging the semantic gap. DMM Disease Models and Mechanisms, 2010, 3, 281-289.	2.4	39
43	Entity/quality-based logical definitions for the human skeletal phenome using PATO. , 2009, 2009, 7069-72.		67
44	Phylogenetic inference under recombination using Bayesian stochastic topology selection. Bioinformatics, 2009, 25, 197-203.	4.1	17
45	Models for financial sustainability of biological databases and resources. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap017-bap017.	3.0	27
46	Practical application of ontologies to annotate and analyse large scale raw mouse phenotype data. BMC Bioinformatics, 2009, 10, S2.	2.6	39
47	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. Mammalian Genome, 2009, 20, 457-461.	2.2	21
48	Post-publication sharing of data and tools. Nature, 2009, 461, 171-173.	27.8	142
49	The Functional Annotation of Mammalian Genomes: The Challenge of Phenotyping. Annual Review of Genetics, 2009, 43, 305-333.	7.6	60
50	Tandem and cryptic amino acid repeats accumulate in disordered regions of proteins. Genome Biology, 2009, 10, R59.	9.6	104
51	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
52	The Mouse Resource Browser (MRB) - A near-complete registry of mouse resources. , 2008, , .		1
53	Digital preservation - financial sustainability of biological data and material resources. , 2008, , .		1
54	CASIMIR: Coordination and Sustainability of International Mouse Informatics Resources. , 2008, , .		7

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55	Solutions for data integration in functional genomics: a critical assessment and case study. Briefings in Bioinformatics, 2008, 9, 532-544.	6.5	23
56	Phenobabelomics--mouse phenotype data resources. Briefings in Functional Genomics & Proteomics, 2008, 6, 292-301.	3.8	13
57	ENFIN - An Integrative Structure for Systems Biology. Lecture Notes in Computer Science, 2008, , 132-143.	1.3	0
58	EuroPhenome and EMPReSS: online mouse phenotyping resource. Nucleic Acids Research, 2007, 36, D715-D718.	14.5	68
59	Integration of mouse phenome data resources. Mammalian Genome, 2007, 18, 157-163.	2.2	44
60	A kinetic core model of the glucose-stimulated insulin secretion network of pancreatic β cells. Mammalian Genome, 2007, 18, 508-520.	2.2	44
61	Phenostat: visualization and statistical tool for analysis of phenotyping data. Mammalian Genome, 2007, 18, 677-681.	2.2	2
62	Understanding Mammalian Genetic Systems: The Challenge of Phenotyping in the Mouse. PLoS Genetics, 2006, 2, e118.	3.5	82
63	The Mouse Genome. , 2006, 2, 33-45.		16
64	EMPReSS: standardized phenotype screens for functional annotation of the mouse genome. Nature Genetics, 2005, 37, 1155-1155.	21.4	146
65	Gene factories, microfunctionalization and the evolution of gene families. Trends in Genetics, 2005, 21, 591-595.	6.7	34
66	EMPReSS: European Mouse Phenotyping Resource for Standardized Screens. Bioinformatics, 2005, 21, 2930-2931.	4.1	58
67	CRAVE: a database, middleware and visualization system for phenotype ontologies. Bioinformatics, 2005, 21, 1257-1262.	4.1	11
68	Dictionary of Bioinformatics and Computational Biology. Briefings in Bioinformatics, 2005, 6, 211-212.	6.5	1
69	Simple sequence repeats in proteins and their significance for network evolution. Gene, 2005, 345, 113-118.	2.2	91
70	Organization and Evolution of a Gene-Rich Region of the Mouse Genome: A 12.7-Mb Region Deleted in the Del(13)Svea36H Mouse. Genome Research, 2004, 14, 1888-1901.	5.5	25
71	A bigger mouse? The rat genome unveiled. BioEssays, 2004, 26, 1039-1042.	2.5	9
72	Ontologies for the Description of Mouse Phenotypes. Comparative and Functional Genomics, 2004, 5, 545-551.	2.0	31

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73	Using ontologies to describe mouse phenotypes. Genome Biology, 2004, 6, R8.	9.6	191
74	A phylogenetic approach to assessing the significance of missense mutations in disease genes. Human Mutation, 2003, 22, 51-58.	2.5	19
75	PlantProm: a database of plant promoter sequences. Nucleic Acids Research, 2003, 31, 114-117.	14.5	240
76	Detecting cryptically simple protein sequences using the SIMPLE algorithm. Bioinformatics, 2002, 18, 672-678.	4.1	61
77	Genome size and the accumulation of simple sequence repeats: implications of new data from genome sequencing projects. Genetica, 2002, 115, 93-103.	1.1	80
78	Rapid restructuring of bicoid-dependent hunchback promoters within and between Dipteran species: implications for molecular coevolution. Evolution & Development, 2001, 3, 397-407.	2.0	87
79	A Relationship Between Lengths of Microsatellites and Nearby Substitution Rates in Mammalian Genomes. Molecular Biology and Evolution, 2001, 18, 2119-2123.	8.9	38
80	Extreme Length and Length Variation in the First Ribosomal Internal Transcribed Spacer of Ladybird Beetles (Coleoptera: Coccinellidae). Molecular Biology and Evolution, 2001, 18, 648-660.	8.9	115
81	The Comparative Genomics of Polyglutamine Repeats: Extreme Difference in the Codon Organization of Repeat-Encoding Regions Between Mammals and Drosophila. Journal of Molecular Evolution, 2001, 52, 249-259.	1.8	41
82	A Role for Selection in Regulating the Evolutionary Emergence of Disease-Causing and Other Coding CAG Repeats in Humans and Mice. Molecular Biology and Evolution, 2001, 18, 1014-1023.	8.9	58
83	How Slippage-Derived Sequences Are Incorporated into rRNA Variable-Region Secondary Structure: Implications for Phylogeny Reconstruction. Molecular Phylogenetics and Evolution, 2000, 14, 366-374.	2.7	62
84	High sequence turnover in the regulatory regions of the developmental gene hunchback in insects. Molecular Biology and Evolution, 1999, 16, 253-265.	8.9	48
85	A Common Binding Site on the Microsomal Triglyceride Transfer Protein for Apolipoprotein B and Protein Disulfide Isomerase. Journal of Biological Chemistry, 1999, 274, 3159-3164.	3.4	86
86	Amino Acid Reiterations in Yeast Are Overrepresented in Particular Classes of Proteins and Show Evidence of a Slippage-Like Mutational Process. Journal of Molecular Evolution, 1999, 49, 789-797.	1.8	83
87	Analysis of the Primary Sequence and Secondary Structure of the Unusually Long SSU rRNA of the Soil Bug, Armadillidium vulgare. Journal of Molecular Evolution, 1999, 49, 798-805.	1.8	27
88	The structure of vitellogenin provides a molecular model for the assembly and secretion of atherogenic lipoproteins 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 285, 391-408.	4.2	185
89	Conservation of polyglutamine tract size between mice and humans depends on codon interruption. Molecular Biology and Evolution, 1999, 16, 1641-1644.	8.9	50
90	Modelling the secondary structures of slippage-prone hypervariable RNA regions: the example of the tiger beetle 18S rRNA variable region V4. Nucleic Acids Research, 1998, 26, 1689-1699.	14.5	20

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91	Phylogenetic analysis of slippage-like sequence variation in the V4 rRNA expansion segment in tiger beetles (Cicindelidae). Molecular Biology and Evolution, 1997, 14, 6-19.	8.9	38
92	How important are repetitive regions within developmentally relevant genes?. Genetical Research, 1997, 70, 79-89.	0.9	0
93	Codon repeats in genes associated with human diseases: fewer repeats in the genes of nonhuman primates and nucleotide substitutions concentrated at the sites of reiteration.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 417-421.	7.1	73
94	Simple sequences and the expanding genome. BioEssays, 1996, 18, 421-425.	2.5	103
95	Simple sequences in a â€˜minimal â€™ genome. Nature Genetics, 1996, 14, 14-15.	21.4	46
96	The contribution of DNA slippage to eukaryotic nuclear 18S rRNA evolution. Journal of Molecular Evolution, 1995, 40, 629-639.	1.8	29
97	The contribution of slippage-like processes to genome evolution. Journal of Molecular Evolution, 1995, 41, 1038-47.	1.8	135
98	SIMPLE34: an improved and enhanced implementation for VAX and Sun computers of the SIMPLE algorithm for analysis of clustered repetitive motifs in nucleotide sequences. Bioinformatics, 1994, 10, 67-70.	4.1	59
99	Polycytosine regions contained in DNA hairpin loops interact via a four-stranded, parallel structure similar to the i-motif. Nucleic Acids Research, 1994, 22, 4653-4659.	14.5	22
100	Generation of VNTRs and heteroplasmy by sequence turnover in the mitochondrial control region of two elephant seal species. Journal of Molecular Evolution, 1993, 37, 190-197.	1.8	71
101	[38] Detection and quantification of concerted evolution and molecular drive. Methods in Enzymology, 1993, 224, 525-541.	1.0	60
102	Evolution of sequence repetition and gene duplications in the TATA-binding protein TBP (TFIID). Nucleic Acids Research, 1993, 21, 2823-2830.	14.5	37
103	Secondary structure constraints on the evolution of Drosophila 28 S ribosomal RNA expansion segments. Journal of Molecular Biology, 1991, 219, 381-390.	4.2	58
104	â€˜Compensatory slippageâ€™ in the evolution of ribosomal RNA genes. Nucleic Acids Research, 1990, 18, 5949-5954.	14.5	86
105	Molecular coevolution among cryptically simple expansion segments of eukaryotic 26S/28S rRNAs.. Molecular Biology and Evolution, 1988, 5, 377-91.	8.9	98
106	Complete sequences of the rRNA genes of Drosophila melanogaster.. Molecular Biology and Evolution, 1988, 5, 366-76.	8.9	299
107	Evolution of the secondary structures and compensatory mutations of the ribosomal RNAs of Drosophila melanogaster.. Molecular Biology and Evolution, 1988, 5, 393-414.	8.9	168
108	Specificity and biological significance of microtubule-associated protein-DNA interactions in chick. Biochimica Et Biophysica Acta - Molecular Cell Research, 1987, 927, 163-169.	4.1	2

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109	A structural model of 5S RNA from E. coil based on intramolecular crosslinking evidence. Nucleic Acids Research, 1982, 10, 1257-1269.	14.5	67
110	Developing a Mammalian Behaviour Ontology. Nature Precedings, 0, , .	0.1	1
111	ELIXIR and Toxicology: a community in development. F1000Research, 0, 10, 1129.	1.6	3