

John M Hancock

List of Publications by Year in descending order

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Version: 2024-02-01

111
papers

5,960
citations

61945

43
h-index

79644

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. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194785.	0.9	1
2	ELIXIRâ€™EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021, 40, e107409.	3.5	18
3	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	3.2	70
4	Community curation of bioinformatics software and data resources. <i>Briefings in Bioinformatics</i> , 2020, 21, 1697-1705.	3.2	12
5	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. <i>Nucleic Acids Research</i> , 2020, 48, W77-W84.	6.5	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	0.8	12
7	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. <i>F1000Research</i> , 2020, 9, 1229.	0.8	5
8	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
9	BioCIDER: a Contextualisation InDEx for biological Resources discovery. <i>Bioinformatics</i> , 2017, 33, 2607-2608.	1.8	1
10	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. <i>F1000Research</i> , 2017, 6, 465.	0.8	16
11	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. <i>F1000Research</i> , 2017, 6, 465.	0.8	10
12	Developing a strategy for computational lab skills training through Software and Data Carpentry: Experiences from the ELIXIR Pilot action. <i>F1000Research</i> , 2017, 6, 1040.	0.8	8
13	ELIXIR-UK role in bioinformatics training at the national level and across ELIXIR. <i>F1000Research</i> , 2017, 6, 952.	0.8	12
14	Human Variome Project Quality Assessment Criteria for Variation Databases. <i>Human Mutation</i> , 2016, 37, 549-558.	1.1	18
15	Introduction to â€™Phenomicsâ€™, 2016, , 11-17.		2
16	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. <i>F1000Research</i> , 2016, 5, 2894.	0.8	6
17	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. <i>F1000Research</i> , 2016, 5, 2894.	0.8	6
18	Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. <i>Nature Genetics</i> , 2015, 47, 969-978.	9.4	137

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19	Editorial: biological ontologies and semantic biology. <i>Frontiers in Genetics</i> , 2014, 5, 18.	1.1	5
20	Commentary on Shimoyama et al. (2012): three ontologies to define phenotype measurement data. <i>Frontiers in Genetics</i> , 2014, 5, 93.	1.1	1
21	Analyzing gene expression data in mice with the Neuro Behavior Ontology. <i>Mammalian Genome</i> , 2014, 25, 32-40.	1.0	19
22	Circles within circles: commentary on Ghosal et al. (2013) "Circ2Traits: a comprehensive database for circular RNA potentially associated with disease and traits". <i>Frontiers in Genetics</i> , 2014, 5, 459.	1.1	16
23	Functional modelling of planar cell polarity: an approach for identifying molecular function. <i>BMC Developmental Biology</i> , 2013, 13, 20.	2.1	12
24	A comparative phenotypic and genomic analysis of C57BL/6j and C57BL/6N mouse strains. <i>Genome Biology</i> , 2013, 14, R82.	13.9	403
25	NucleoFinder: a statistical approach for the detection of nucleosome positions. <i>Bioinformatics</i> , 2013, 29, 711-716.	1.8	20
26	A tale of two drug targets: the evolutionary history of BACE1 and BACE2. <i>Frontiers in Genetics</i> , 2013, 4, 293.	1.1	17
27	Low microsatellite frequencies in neuron and brain expressed microRNAs. <i>Gene</i> , 2012, 508, 73-77.	1.0	2
28	Integration of global resources for human genetic variation and disease. <i>Human Mutation</i> , 2012, 33, 813-816.	1.1	9
29	A Gene-Phenotype Network for the Laboratory Mouse and Its Implications for Systematic Phenotyping. <i>PLoS ONE</i> , 2011, 6, e19693.	1.1	12
30	Anatomy ontologies and potential users: bridging the gap. <i>Journal of Biomedical Semantics</i> , 2011, 2, S3.	0.9	6
31	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. <i>BMC Evolutionary Biology</i> , 2011, 11, 142.	3.2	3
32	Towards BioDBcore: a community-defined information specification for biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, baq027-baq027.	1.4	30
33	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	6.5	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. <i>Experimental Cell Research</i> , 2010, 316, 1856-1870.	1.2	26
36	Mouse Resource Browser—a database of mouse databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq010-baq010.	1.4	3

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37	EuroPhenome: a repository for high-throughput mouse phenotyping data. <i>Nucleic Acids Research</i> , 2010, 38, D577-D585.	6.5	75
38	Finding and sharing: new approaches to registries of databases and services for the biomedical sciences. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq014-baq014.	1.4	12
39	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. <i>Genome Biology</i> , 2010, 11, R27.	13.9	20
40	Sustaining the Data and Bioresource Commons. <i>Science</i> , 2010, 330, 592-593.	6.0	52
41	MouseBook: an integrated portal of mouse resources. <i>Nucleic Acids Research</i> , 2010, 38, D593-D599.	6.5	18
42	Phenotype ontologies for mouse and man: bridging the semantic gap. <i>DMM Disease Models and Mechanisms</i> , 2010, 3, 281-289.	1.2	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. <i>Bioinformatics</i> , 2009, 25, 197-203.	1.8	17
45	Models for financial sustainability of biological databases and resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap017-bap017.	1.4	27
46	Practical application of ontologies to annotate and analyse large scale raw mouse phenotype data. <i>BMC Bioinformatics</i> , 2009, 10, S2.	1.2	39
47	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. <i>Mammalian Genome</i> , 2009, 20, 457-461.	1.0	21
48	Post-publication sharing of data and tools. <i>Nature</i> , 2009, 461, 171-173.	13.7	142
49	The Functional Annotation of Mammalian Genomes: The Challenge of Phenotyping. <i>Annual Review of Genetics</i> , 2009, 43, 305-333.	3.2	60
50	Tandem and cryptic amino acid repeats accumulate in disordered regions of proteins. <i>Genome Biology</i> , 2009, 10, R59.	13.9	104
51	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	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.	3.2	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.	1.0	0
58	EuroPhenome and EMPReSS: online mouse phenotyping resource. Nucleic Acids Research, 2007, 36, D715-D718.	6.5	68
59	Integration of mouse phenome data resources. Mammalian Genome, 2007, 18, 157-163.	1.0	44
60	A kinetic core model of the glucose-stimulated insulin secretion network of pancreatic β^2 cells. Mammalian Genome, 2007, 18, 508-520.	1.0	44
61	Phenostat: visualization and statistical tool for analysis of phenotyping data. Mammalian Genome, 2007, 18, 677-681.	1.0	2
62	Understanding Mammalian Genetic Systems: The Challenge of Phenotyping in the Mouse. PLoS Genetics, 2006, 2, e118.	1.5	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.	9.4	146
65	Gene factories, microfunctionalization and the evolution of gene families. Trends in Genetics, 2005, 21, 591-595.	2.9	34
66	EMPreSS: European Mouse Phenotyping Resource for Standardized Screens. Bioinformatics, 2005, 21, 2930-2931.	1.8	58
67	CRAVE: a database, middleware and visualization system for phenotype ontologies. Bioinformatics, 2005, 21, 1257-1262.	1.8	11
68	Dictionary of Bioinformatics and Computational Biology. Briefings in Bioinformatics, 2005, 6, 211-212.	3.2	1
69	Simple sequence repeats in proteins and their significance for network evolution. Gene, 2005, 345, 113-118.	1.0	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.	2.4	25
71	A bigger mouse? The rat genome unveiled. BioEssays, 2004, 26, 1039-1042.	1.2	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. <i>Genome Biology</i> , 2004, 6, R8.	13.9	191
74	A phylogenetic approach to assessing the significance of missense mutations in disease genes. <i>Human Mutation</i> , 2003, 22, 51-58.	1.1	19
75	PlantProm: a database of plant promoter sequences. <i>Nucleic Acids Research</i> , 2003, 31, 114-117.	6.5	240
76	Detecting cryptically simple protein sequences using the SIMPLE algorithm. <i>Bioinformatics</i> , 2002, 18, 672-678.	1.8	61
77	Genome size and the accumulation of simple sequence repeats: implications of new data from genome sequencing projects. <i>Genetica</i> , 2002, 115, 93-103.	0.5	80
78	Rapid restructuring of bicoid-dependent hunchback promoters within and between Dipteran species: implications for molecular coevolution. <i>Evolution & Development</i> , 2001, 3, 397-407.	1.1	87
79	A Relationship Between Lengths of Microsatellites and Nearby Substitution Rates in Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2001, 18, 2119-2123.	3.5	38
80	Extreme Length and Length Variation in the First Ribosomal Internal Transcribed Spacer of Ladybird Beetles (Coleoptera: Coccinellidae). <i>Molecular Biology and Evolution</i> , 2001, 18, 648-660.	3.5	115
81	The Comparative Genomics of Polyglutamine Repeats: Extreme Difference in the Codon Organization of Repeat-Encoding Regions Between Mammals and Drosophila. <i>Journal of Molecular Evolution</i> , 2001, 52, 249-259.	0.8	41
82	A Role for Selection in Regulating the Evolutionary Emergence of Disease-Causing and Other Coding CAG Repeats in Humans and Mice. <i>Molecular Biology and Evolution</i> , 2001, 18, 1014-1023.	3.5	58
83	How Slippage-Derived Sequences Are Incorporated into rRNA Variable-Region Secondary Structure: Implications for Phylogeny Reconstruction. <i>Molecular Phylogenetics and Evolution</i> , 2000, 14, 366-374.	1.2	62
84	High sequence turnover in the regulatory regions of the developmental gene hunchback in insects. <i>Molecular Biology and Evolution</i> , 1999, 16, 253-265.	3.5	48
85	A Common Binding Site on the Microsomal Triglyceride Transfer Protein for Apolipoprotein B and Protein Disulfide Isomerase. <i>Journal of Biological Chemistry</i> , 1999, 274, 3159-3164.	1.6	86
86	Amino Acid Reiterations in Yeast Are Overrepresented in Particular Classes of Proteins and Show Evidence of a Slippage-Like Mutational Process. <i>Journal of Molecular Evolution</i> , 1999, 49, 789-797.	0.8	83
87	Analysis of the Primary Sequence and Secondary Structure of the Unusually Long SSU rRNA of the Soil Bug, <i>Armadillidium vulgare</i> . <i>Journal of Molecular Evolution</i> , 1999, 49, 798-805.	0.8	27
88	The structure of vitellogenin provides a molecular model for the assembly and secretion of atherogenic lipoproteins 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 391-408.	2.0	185
89	Conservation of polyglutamine tract size between mice and humans depends on codon interruption. <i>Molecular Biology and Evolution</i> , 1999, 16, 1641-1644.	3.5	50
90	Modelling the secondary structures of slippage-prone hypervariable RNA regions: the example of the tiger beetle 18S rRNA variable region V4. <i>Nucleic Acids Research</i> , 1998, 26, 1689-1699.	6.5	20

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91	Phylogenetic analysis of slippage-like sequence variation in the V4 rRNA expansion segment in tiger beetles (Cicindelidae). <i>Molecular Biology and Evolution</i> , 1997, 14, 6-19.	3.5	38
92	How important are repetitive regions within developmentally relevant genes?. <i>Genetical Research</i> , 1997, 70, 79-89.	0.3	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.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 417-421.	3.3	73
94	Simple sequences and the expanding genome. <i>BioEssays</i> , 1996, 18, 421-425.	1.2	103
95	Simple sequences in a "minimal" genome. <i>Nature Genetics</i> , 1996, 14, 14-15.	9.4	46
96	The contribution of DNA slippage to eukaryotic nuclear 18S rRNA evolution. <i>Journal of Molecular Evolution</i> , 1995, 40, 629-639.	0.8	29
97	The contribution of slippage-like processes to genome evolution. <i>Journal of Molecular Evolution</i> , 1995, 41, 1038-47.	0.8	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. <i>Bioinformatics</i> , 1994, 10, 67-70.	1.8	59
99	Polycytosine regions contained in DNA hairpin loops interact via a four-stranded, parallel structure similar to the i-motif. <i>Nucleic Acids Research</i> , 1994, 22, 4653-4659.	6.5	22
100	Generation of VNTRs and heteroplasmy by sequence turnover in the mitochondrial control region of two elephant seal species. <i>Journal of Molecular Evolution</i> , 1993, 37, 190-197.	0.8	71
101	[38] Detection and quantification of concerted evolution and molecular drive. <i>Methods in Enzymology</i> , 1993, 224, 525-541.	0.4	60
102	Evolution of sequence repetition and gene duplications in the TATA-binding protein TBP (TFIID). <i>Nucleic Acids Research</i> , 1993, 21, 2823-2830.	6.5	37
103	Secondary structure constraints on the evolution of <i>Drosophila</i> 28 S ribosomal RNA expansion segments. <i>Journal of Molecular Biology</i> , 1991, 219, 381-390.	2.0	58
104	"Compensatory slippage" in the evolution of ribosomal RNA genes. <i>Nucleic Acids Research</i> , 1990, 18, 5949-5954.	6.5	86
105	Molecular coevolution among cryptically simple expansion segments of eukaryotic 26S/28S rRNAs.. <i>Molecular Biology and Evolution</i> , 1988, 5, 377-91.	3.5	98
106	Complete sequences of the rRNA genes of <i>Drosophila melanogaster</i> .. <i>Molecular Biology and Evolution</i> , 1988, 5, 366-76.	3.5	299
107	Evolution of the secondary structures and compensatory mutations of the ribosomal RNAs of <i>Drosophila melanogaster</i> .. <i>Molecular Biology and Evolution</i> , 1988, 5, 393-414.	3.5	168
108	Specificity and biological significance of microtubule-associated protein-DNA interactions in chick. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 1987, 927, 163-169.	1.9	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.	6.5	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.	0.8	3