

John M Hancock

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8613113/publications.pdf>

Version: 2024-02-01

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	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	17.5	506
2	A comparative phenotypic and genomic analysis of C57BL/6J and C57BL/6N mouse strains. <i>Genome Biology</i> , 2013, 14, R82.	9.6	403
3	Complete sequences of the rRNA genes of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 1988, 5, 366-76.	8.9	299
4	PlantProm: a database of plant promoter sequences. <i>Nucleic Acids Research</i> , 2003, 31, 114-117.	14.5	240
5	Using ontologies to describe mouse phenotypes. <i>Genome Biology</i> , 2004, 6, R8.	9.6	191
6	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.	4.2	185
7	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.	8.9	168
8	EMPRESS: standardized phenotype screens for functional annotation of the mouse genome. <i>Nature Genetics</i> , 2005, 37, 1155-1155.	21.4	146
9	Post-publication sharing of data and tools. <i>Nature</i> , 2009, 461, 171-173.	27.8	142
10	Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. <i>Nature Genetics</i> , 2015, 47, 969-978.	21.4	137
11	The contribution of slippage-like processes to genome evolution. <i>Journal of Molecular Evolution</i> , 1995, 41, 1038-47.	1.8	135
12	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.	8.9	115
13	Tandem and cryptic amino acid repeats accumulate in disordered regions of proteins. <i>Genome Biology</i> , 2009, 10, R59.	9.6	104
14	Simple sequences and the expanding genome. <i>BioEssays</i> , 1996, 18, 421-425.	2.5	103
15	Molecular coevolution among cryptically simple expansion segments of eukaryotic 26S/28S rRNAs. <i>Molecular Biology and Evolution</i> , 1988, 5, 377-91.	8.9	98
16	Simple sequence repeats in proteins and their significance for network evolution. <i>Gene</i> , 2005, 345, 113-118.	2.2	91
17	Rapid restructuring of bicoid-dependent hunchback promoters within and between Dipteran species: implications for molecular coevolution. <i>Evolution & Development</i> , 2001, 3, 397-407.	2.0	87
18	Compensatory slippage™ in the evolution of ribosomal RNA genes. <i>Nucleic Acids Research</i> , 1990, 18, 5949-5954.	14.5	86

#	ARTICLE	IF	CITATIONS
19	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.	3.4	86
20	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.	1.8	83
21	Understanding Mammalian Genetic Systems: The Challenge of Phenotyping in the Mouse. <i>PLoS Genetics</i> , 2006, 2, e118.	3.5	82
22	Genome size and the accumulation of simple sequence repeats: implications of new data from genome sequencing projects. <i>Genetica</i> , 2002, 115, 93-103.	1.1	80
23	EuroPhenome: a repository for high-throughput mouse phenotyping data. <i>Nucleic Acids Research</i> , 2010, 38, D577-D585.	14.5	75
24	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.	7.1	73
25	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.	1.8	71
26	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.	14.5	71
27	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	6.5	70
28	EuroPhenome and EMPReSS: online mouse phenotyping resource. <i>Nucleic Acids Research</i> , 2007, 36, D715-D718.	14.5	68
29	A structural model of 5S RNA from <i>E. coli</i> based on intramolecular crosslinking evidence. <i>Nucleic Acids Research</i> , 1982, 10, 1257-1269.	14.5	67
30	Entity/quality-based logical definitions for the human skeletal phenome using PATO. , 2009, 2009, 7069-72.		67
31	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.	2.7	62
32	Detecting cryptically simple protein sequences using the SIMPLE algorithm. <i>Bioinformatics</i> , 2002, 18, 672-678.	4.1	61
33	[38] Detection and quantification of concerted evolution and molecular drive. <i>Methods in Enzymology</i> , 1993, 224, 525-541.	1.0	60
34	The Functional Annotation of Mammalian Genomes: The Challenge of Phenotyping. <i>Annual Review of Genetics</i> , 2009, 43, 305-333.	7.6	60
35	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.	4.1	59
36	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.	4.2	58

#	ARTICLE	IF	CITATIONS
37	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.	8.9	58
38	EMPreSS: European Mouse Phenotyping Resource for Standardized Screens. <i>Bioinformatics</i> , 2005, 21, 2930-2931.	4.1	58
39	Sustaining the Data and Bioresource Commons. <i>Science</i> , 2010, 330, 592-593.	12.6	52
40	Conservation of polyglutamine tract size between mice and humans depends on codon interruption. <i>Molecular Biology and Evolution</i> , 1999, 16, 1641-1644.	8.9	50
41	High sequence turnover in the regulatory regions of the developmental gene hunchback in insects. <i>Molecular Biology and Evolution</i> , 1999, 16, 253-265.	8.9	48
42	Simple sequences in a "minimal" genome. <i>Nature Genetics</i> , 1996, 14, 14-15.	21.4	46
43	Integration of mouse phenome data resources. <i>Mammalian Genome</i> , 2007, 18, 157-163.	2.2	44
44	A kinetic core model of the glucose-stimulated insulin secretion network of pancreatic β^2 cells. <i>Mammalian Genome</i> , 2007, 18, 508-520.	2.2	44
45	The Comparative Genomics of Polyglutamine Repeats: Extreme Difference in the Codon Organization of Repeat-Encoding Regions Between Mammals and <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2001, 52, 249-259.	1.8	41
46	Practical application of ontologies to annotate and analyse large scale raw mouse phenotype data. <i>BMC Bioinformatics</i> , 2009, 10, S2.	2.6	39
47	Phenotype ontologies for mouse and man: bridging the semantic gap. <i>DMM Disease Models and Mechanisms</i> , 2010, 3, 281-289.	2.4	39
48	Phylogenetic analysis of slippage-like sequence variation in the V4 rRNA expansion segment in tiger beetles (<i>Cicindelidae</i>). <i>Molecular Biology and Evolution</i> , 1997, 14, 6-19.	8.9	38
49	A Relationship Between Lengths of Microsatellites and Nearby Substitution Rates in Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2001, 18, 2119-2123.	8.9	38
50	Evolution of sequence repetition and gene duplications in the TATA-binding protein TBP (TFIID). <i>Nucleic Acids Research</i> , 1993, 21, 2823-2830.	14.5	37
51	Gene factories, microfunctionalization and the evolution of gene families. <i>Trends in Genetics</i> , 2005, 21, 591-595.	6.7	34
52	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	14.5	32
53	Ontologies for the Description of Mouse Phenotypes. <i>Comparative and Functional Genomics</i> , 2004, 5, 545-551.	2.0	31
54	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

#	ARTICLE	IF	CITATIONS
55	The contribution of DNA slippage to eukaryotic nuclear 18S rRNA evolution. <i>Journal of Molecular Evolution</i> , 1995, 40, 629-639.	1.8	29
56	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.	1.8	27
57	Models for financial sustainability of biological databases and resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap017-bap017.	3.0	27
58	Identification of a Z-band associated protein complex involving KY, FLNC and IGFN1. <i>Experimental Cell Research</i> , 2010, 316, 1856-1870.	2.6	26
59	Organization and Evolution of a Gene-Rich Region of the Mouse Genome: A 12.7-Mb Region Deleted in the <i>Del(13)Svea36H</i> Mouse. <i>Genome Research</i> , 2004, 14, 1888-1901.	5.5	25
60	Solutions for data integration in functional genomics: a critical assessment and case study. <i>Briefings in Bioinformatics</i> , 2008, 9, 532-544.	6.5	23
61	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.	14.5	22
62	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. <i>Mammalian Genome</i> , 2009, 20, 457-461.	2.2	21
63	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.	14.5	20
64	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. <i>Genome Biology</i> , 2010, 11, R27.	9.6	20
65	NucleoFinder: a statistical approach for the detection of nucleosome positions. <i>Bioinformatics</i> , 2013, 29, 711-716.	4.1	20
66	A phylogenetic approach to assessing the significance of missense mutations in disease genes. <i>Human Mutation</i> , 2003, 22, 51-58.	2.5	19
67	Analyzing gene expression data in mice with the Neuro Behavior Ontology. <i>Mammalian Genome</i> , 2014, 25, 32-40.	2.2	19
68	MouseBook: an integrated portal of mouse resources. <i>Nucleic Acids Research</i> , 2010, 38, D593-D599.	14.5	18
69	Human Variome Project Quality Assessment Criteria for Variation Databases. <i>Human Mutation</i> , 2016, 37, 549-558.	2.5	18
70	ELIXIR–EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021, 40, e107409.	7.8	18
71	Phylogenetic inference under recombination using Bayesian stochastic topology selection. <i>Bioinformatics</i> , 2009, 25, 197-203.	4.1	17
72	A tale of two drug targets: the evolutionary history of BACE1 and BACE2. <i>Frontiers in Genetics</i> , 2013, 4, 293.	2.3	17

#	ARTICLE	IF	CITATIONS
73	The Mouse Genome. , 2006, 2, 33-45.		16
74	Circles within circles: commentary on Ghosal et al. (2013) "Circ2Traits: a comprehensive database for circular RNA potentially associated with disease and traits" Frontiers in Genetics, 2014, 5, 459.	2.3	16
75	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. F1000Research, 2017, 6, 465.	1.6	16
76	Phenobabelomics--mouse phenotype data resources. Briefings in Functional Genomics & Proteomics, 2008, 6, 292-301.	3.8	13
77	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
78	A Gene-Phenotype Network for the Laboratory Mouse and Its Implications for Systematic Phenotyping. PLoS ONE, 2011, 6, e19693.	2.5	12
79	Functional modelling of planar cell polarity: an approach for identifying molecular function. BMC Developmental Biology, 2013, 13, 20.	2.1	12
80	Community curation of bioinformatics software and data resources. Briefings in Bioinformatics, 2020, 21, 1697-1705.	6.5	12
81	ELIXIR-UK role in bioinformatics training at the national level and across ELIXIR. F1000Research, 2017, 6, 952.	1.6	12
82	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
83	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS	1.6	12
84	CRAVE: a database, middleware and visualization system for phenotype ontologies. Bioinformatics, 2005, 21, 1257-1262.	4.1	11
85	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. F1000Research, 2017, 6, 465.	1.6	10
86	A bigger mouse? The rat genome unveiled. BioEssays, 2004, 26, 1039-1042.	2.5	9
87	Integration of global resources for human genetic variation and disease. Human Mutation, 2012, 33, 813-816.	2.5	9
88	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
89	CASIMIR: Coordination and Sustainability of International Mouse Informatics Resources. , 2008, , .		7
90	Anatomy ontologies and potential users: bridging the gap. Journal of Biomedical Semantics, 2011, 2, S3.	1.6	6

#	ARTICLE	IF	CITATIONS
91	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. F1000Research, 2016, 5, 2894.	1.6	6
92	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. F1000Research, 2016, 5, 2894.	1.6	6
93	Editorial: biological ontologies and semantic biology. Frontiers in Genetics, 2014, 5, 18.	2.3	5
94	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
95	Mouse Resource Browser—a database of mouse databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq010-baq010.	3.0	3
96	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. BMC Evolutionary Biology, 2011, 11, 142.	3.2	3
97	ELIXIR and Toxicology: a community in development. F1000Research, 0, 10, 1129.	1.6	3
98	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
99	Phenostat: visualization and statistical tool for analysis of phenotyping data. Mammalian Genome, 2007, 18, 677-681.	2.2	2
100	Low microsatellite frequencies in neuron and brain expressed microRNAs. Gene, 2012, 508, 73-77.	2.2	2
101	Introduction to "Phenomics", 2016, , 11-17.		2
102	Dictionary of Bioinformatics and Computational Biology. Briefings in Bioinformatics, 2005, 6, 211-212.	6.5	1
103	The Mouse Resource Browser (MRB) - A near-complete registry of mouse resources. , 2008, ,		1
104	Digital preservation - financial sustainability of biological data and material resources. , 2008, ,		1
105	Developing a Mammalian Behaviour Ontology. Nature Precedings, 0, ,	0.1	1
106	Commentary on Shimoyama et al. (2012): three ontologies to define phenotype measurement data. Frontiers in Genetics, 2014, 5, 93.	2.3	1
107	BioCIDER: a Contextualisation InDEX for biological Resources discovery. Bioinformatics, 2017, 33, 2607-2608.	4.1	1
108	The Informatics of High-Throughput Mouse Phenotyping: EUMODIC and Beyond. , 2011, , 77-87.		1

#	ARTICLE	IF	CITATIONS
109	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.	1.9	1
110	How important are repetitive regions within developmentally relevant genes?. <i>Genetical Research</i> , 1997, 70, 79-89.	0.9	0
111	ENFIN - An Integrative Structure for Systems Biology. <i>Lecture Notes in Computer Science</i> , 2008, , 132-143.	1.3	0