Helen Parkinson

List of Publications by Year
in descending order

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117 papers	23,324 citations	39113 52 h-index	21239 119 g-index
132 all docs	132 docs citations	132 times ranked	43558 citing authors

#	Article	IF	Citations
1	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. Pain, 2022, 163, 1139-1157.	2.0	4
2	The European Variation Archive: a FAIR resource of genomic variation for all species. Nucleic Acids Research, 2022, 50, D1216-D1220.	6.5	50
3	The European Genome-phenome Archive in 2021. Nucleic Acids Research, 2022, 50, D980-D987.	6.5	55
4	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
5	The EurOPDX Data Portal: an open platform for patient-derived cancer xenograft data sharing and visualization. BMC Genomics, 2022, 23, 156.	1.2	10
6	Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. Nucleic Acids Research, 2021, 49, D1311-D1320.	6.5	295
7	The Polygenic Score Catalog as an open database for reproducibility and systematic evaluation. Nature Genetics, 2021, 53, 420-425.	9.4	293
8	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
9	REMBI: Recommended Metadata for Biological Imagesâ€"enabling reuse of microscopy data in biology. Nature Methods, 2021, 18, 1418-1422.	9.0	63
10	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. Nature Genetics, 2021, 53, 1290-1299.	9.4	193
11	Desiderata for the development of next-generation electronic health record phenotype libraries. GigaScience, 2021, 10, .	3.3	17
12	Pleiotropy data resource as a primer for investigating co-morbidities/multi-morbidities and their role in disease. Mammalian Genome, 2021, , 1.	1.0	2
13	Workshop proceedings: GWAS summary statistics standards and sharing. Cell Genomics, 2021, 1, 100004.	3.0	22
14	Sequencing-based genome-wide association studies reporting standards. Cell Genomics, 2021, 1, 100005.	3.0	17
15	Soft windowing application to improve analysis of high-throughput phenotyping data. Bioinformatics, 2020, 36, 1492-1500.	1.8	9
16	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
17	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimerâ€™s Disease Gene Expression Data. Journal of Alzheimer's Disease, 2020, 75, 1417-1435.	1.2	18
18	Human and mouse essentiality screens as a resource for disease gene discovery. Nature Communications, 2020, 11, 655.	5.8	64

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19	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. PLoS Genetics, 2020, 16, e1009190.	1.5	19
20	OpenStats: A robust and scalable software package for reproducible analysis of high-throughput phenotypic data. PLoS ONE, 2020, 15, e0242933.	1.1	12
21	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
22	PDX Finder: A portal for patient-derived tumor xenograft model discovery. Nucleic Acids Research, 2019, 47, D1073-D1079.	6.5	75
23	BioSamples database: an updated sample metadata hub. Nucleic Acids Research, 2019, 47, D1172-D1178.	6.5	46
24	The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. Nucleic Acids Research, 2019, 47, D1005-D1012.	6.5	3,179
25	Harmonising phenomics information for a better interoperability in the rare disease field. European Journal of Medical Genetics, 2018, 61, 706-714.	0.7	29
26	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. Stem Cell Reports, 2018, 10, 1-6.	2.3	53
27	Identification of genes required for eye development by high-throughput screening of mouse knockouts. Communications Biology, 2018, 1, 236.	2.0	37
28	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimerâ€™s Disease Data. Genes, 2018, 9, 593.	1.0	15
29	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog. Genome Biology, 2018, 19, 21.	3.8	159
30	Rapid establishment of the European Bank for induced Pluripotent Stem Cells (EBiSC) - the Hot Start experience. Stem Cell Research, 2017, 20, 105-114.	0.3	51
31	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	6.5	355
32	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. Cancer Research, 2017, 77, e62-e66.	0.4	92
33	Prevalence of sexual dimorphism in mammalian phenotypic traits. Nature Communications, 2017, 8, 15475.	5.8	200
34	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
35	The human-induced pluripotent stem cell initiativeâ€”data resources for cellular genetics. Nucleic Acids Research, 2017, 45, D691-D697.	6.5	81
36	Comparison, alignment, and synchronization of cell line information between CLO and EFO. BMC Bioinformatics, 2017, 18, 557.	1.2	4

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37	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). Nucleic Acids Research, 2017, 45, D896-D901.	6.5	1,932
38	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414.	2.6	97
39	The Ontology for Biomedical Investigations. PLoS ONE, 2016, 11, e0154556.	1.1	217
40	Identification of Cancer Related Genes Using a Comprehensive Map of Human Gene Expression. PLoS ONE, 2016, 11, e0157484.	1.1	36
41	PhenoImageShare: an image annotation and query infrastructure. Journal of Biomedical Semantics, 2016, 7, 35.	0.9	12
42	The cellular microscopy phenotype ontology. Journal of Biomedical Semantics, 2016, 7, 28.	0.9	24
43	Gramene 2016: comparative plant genomics and pathway resources. Nucleic Acids Research, 2016, 44, D1133-D1140.	6.5	138
44	Reporting phenotypes in mouse models when considering body size as a potential confounder. Journal of Biomedical Semantics, 2016, 7, 2.	0.9	9
45	Linking rare and common disease: mapping clinical disease-phenotypes to ontologies in therapeutic target validation. Journal of Biomedical Semantics, 2016, 7, 8.	0.9	28
46	Webulous and the Webulous Google Add-On - a web service and application for ontology building from templates. Journal of Biomedical Semantics, 2016, 7, 17.	0.9	6
47	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	6.5	113
48	Ten Simple Rules for Selecting a Bio-ontology. PLoS Computational Biology, 2016, 12, e1004743.	1.5	29
49	ArrayExpress updateâ€"simplifying data submissions. Nucleic Acids Research, 2015, 43, D1113-D1116.	6.5	688
50	Finding Our Way through Phenotypes. PLoS Biology, 2015, 13, e1002033.	2.6	178
51	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American Journal of Human Genetics, 2015, 97, 111-124.	2.6	203
52	Precision medicine: Look to the mice. Science, 2015, 349, 390-390.	6.0	11
53	Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biology, 2015, 13, e1002151.	2.6	75
54	Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. Nucleic Acids Research, 2015, 43, D1071-D1078.	6.5	498

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55	A mouse informatics platform for phenotypic and translational discovery. Mammalian Genome, 2015, 26, 413-421.	1.0	27
56	The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. Nucleic Acids Research, 2014, 42, D1001-D1006.	6.5	2,608
57	The EBI RDF platform: linked open data for the life sciences. Bioinformatics, 2014, 30, 1338-1339.	1.8	190
58	The International Mouse Phenotyping Consortium Web Portal, a unified point of access for knockout mice and related phenotyping data. Nucleic Acids Research, 2014, 42, D802-D809.	6.5	252
59	Updates to BioSamples database at European Bioinformatics Institute. Nucleic Acids Research, 2014, 42, D50-D52.	6.5	32
60	The Software Ontology (SWO): a resource for reproducibility in biomedical data analysis, curation and digital preservation. Journal of Biomedical Semantics, 2014, 5, 25.	0.9	56
61	CLO: The cell line ontology. Journal of Biomedical Semantics, 2014, 5, 37.	0.9	89
62	Expression Atlas updateâ€"a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. Nucleic Acids Research, 2014, 42, D926-D932.	6.5	293
63	Toward richer metadata for microbial sequences: replacing strain-level NCBI taxonomy taxids with BioProject, BioSample and Assembly records. Standards in Genomic Sciences, 2014, 9, 1275-1277.	1.5	38
64	The BioSample Database (BioSD) at the European Bioinformatics Institute. Nucleic Acids Research, 2012, 40, D64-D70.	6.5	50
65	ArrayExpress updateâ€"trends in database growth and links to data analysis tools. Nucleic Acids Research, 2012, 41, D987-D990.	6.5	340
66	Gene Expression Atlas update--a value-added database of microarray and sequencing-based functional genomics experiments. Nucleic Acids Research, 2012, 40, D1077-D1081.	6.5	143
67	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. Mammalian Genome, 2012, 23, 641-652.	1.0	37
68	MageComet--web application for harmonizing existing large-scale experiment descriptions. Bioinformatics, 2012, 28, 1402-1403.	1.8	1
69	Observ-OM and Observ-TAB: Universal syntax solutions for the integration, search, and exchange of phenotype and genotype information. Human Mutation, 2012, 33, 867-873.	1.1	18
70	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. Methods in Molecular Biology, 2011, 719, 31-69.	0.4	73
71	Anatomy ontologies and potential users: bridging the gap. Journal of Biomedical Semantics, 2011, 2, S3.	0.9	6
72	OntoCAT -- simple ontology search and integration in Java, R and REST/JavaScript. BMC Bioinformatics, 2011, 12, 218.	1.2	30

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73	ArrayExpress update--an archive of microarray and high-throughput sequencing-based functional genomics experiments. Nucleic Acids Research, 2011, 39, D1002-D1004.	6.5	285
74	Contributions of the EMERALD project to assessing and improving microarray data quality. BioTechniques, 2011, 50, 27-31.	0.8	11
75	Meeting Report from the Second â€œMinimum Information for Biological and Biomedical Investigationsâ€• (MIBBI) workshop. Standards in Genomic Sciences, 2010, 3, 259-266.	1.5	32
76	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. BMC Bioinformatics, 2010, 11, S12.	1.2	102
77	Modeling biomedical experimental processes with OBI. Journal of Biomedical Semantics, 2010, 1, S7.	0.9	207
78	A global map of human gene expression. Nature Biotechnology, 2010, 28, 322-324.	9.4	315
79	Annotareâ€”a tool for annotating high-throughput biomedical investigations and resulting data. Bioinformatics, 2010, 26, 2470-2471.	1.8	14
80	Modeling sample variables with an Experimental Factor Ontology. Bioinformatics, 2010, 26, 1112-1118.	1.8	438
81	Gene Expression Atlas at the European Bioinformatics Institute. Nucleic Acids Research, 2010, 38, D690-D698.	6.5	216
82	Large scale comparison of global gene expression patterns in human and mouse. Genome Biology, 2010, 11, R124.	13.9	107
83	MAGETabulator, a suite of tools to support the microarray data format MAGE-TAB. Bioinformatics, 2009, 25, 279-280.	1.8	14
84	ArrayExpress update--from an archive of functional genomics experiments to the atlas of gene expression. Nucleic Acids Research, 2009, 37, D868-D872.	6.5	380
85	Importing ArrayExpress datasets into R/Bioconductor. Bioinformatics, 2009, 25, 2092-2094.	1.8	100
86	Standards for Functional Genomics. , 2009, , 293-329.		0
87	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). Nature Biotechnology, 2008, 26, 305-312.	9.4	111
88	Data Storage and Analysis in ArrayExpress and Expression Profiler. Current Protocols in Bioinformatics, 2008, 23, Unit 7.13.	25.8	12
89	Integration of mouse phenome data resources. Mammalian Genome, 2007, 18, 157-163.	1.0	44
90	Standard Annotation of Environmental OMICS Data: Application to the Transcriptomics Domain. OMICS A Journal of Integrative Biology, 2006, 10, 172-178.	1.0	21

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91	[20] Data Storage and Analysis in ArrayExpress. Methods in Enzymology, 2006, 411, 370-386.	0.4	37
92	MIAME/Plant - adding value to plant microarrray experiments. Plant Methods, 2006, 2, 1.	1.9	61
93	ArrayExpress service for reviewers/editors of DNA microarray papers. Nature Biotechnology, 2006, 24, 1321-1322.	9.4	22
94	Wrestling with SUMO and bio-ontologies. Nature Biotechnology, 2006, 24, 21-21.	9.4	8
95	A simple spreadsheet-based, MIAME-supportive format for microarray data: MAGE-TAB. BMC Bioinformatics, 2006, 7, 489.	1.2	185
96	The MGED Ontology: a resource for semantics-based description of microarray experiments. Bioinformatics, 2006, 22, 866-873.	1.8	190
97	[17] Using Ontologies to Annotate Microarray Experiments. Methods in Enzymology, 2006, 411, 325-339.	0.4	9
98	Development of FuGO: An Ontology for Functional Genomics Investigations. OMICS A Journal of Integrative Biology, 2006, 10, 199-204.	1.0	56
99	NCRI Informatics Initiative. Nature Biotechnology, 2005, 23, 1212-1212.	9.4	1
100	Plant-Based Microarray Data at the European Bioinformatics Institute. Introducing AtMIAMExpress, a Submission Tool for Arabidopsis Gene Expression Data to ArrayExpress. Plant Physiology, 2005, 139, 632-636.	2.3	10
101	The ArrayExpress gene expression database: a software engineering and implementation perspective. Bioinformatics, 2005, 21, 1495-1501.	1.8	39
102	Pedro Ontology Services: A Framework for Rapid Ontology Markup. Lecture Notes in Computer Science, 2005, , 578-591.	1.0	4
103	Microarray Data Standards: An Open Letter. Environmental Health Perspectives, 2004, 112, A666-7.	2.8	23
104	Submission of Microarray Data to Public Repositories. PLoS Biology, 2004, 2, e317.	2.6	102
105	The SOFG Anatomy Entry List (SAEL): An Annotation Tool for Functional Genomics Data. Comparative and Functional Genomics, 2004, 5, 521-527.	2.0	9
106	Standards and Ontologies for Functional Genomics 2. Comparative and Functional Genomics, 2004, 5, 618-622.	2.0	6
107	The MGED Ontology: A Framework for Describing Functional Genomics Experiments. Comparative and Functional Genomics, 2003, 4, 127-132.	2.0	49
108	Standards and Ontologies for Functional Genomics: Towards Unified Ontologies for Biology and Biomedicine. Comparative and Functional Genomics, 2003, 4, 116-120.	2.0	4

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109	ArrayExpress: a public database of gene expression data at EBI. Comptes Rendus - Biologies, 2003, 326, 1075-1078.	0.1	69
110	ArrayExpress--a public repository for microarray gene expression data at the EBI. Nucleic Acids Research, 2003, 31, 68-71.	6.5	727
111	The European Bioinformatics Institute's data resources. Nucleic Acids Research, 2003, 31, 43-50.	6.5	56
112	Standards for Microarray Data. Science, 2002, 298, 539b-539.	6.0	147
113	An open letter to the scientific journals. Bioinformatics, 2002, 18, 1409-1409.	1.8	40
114	A guide to microarray experiments-an open letter to the scientific journals. Lancet, The, 2002, 360, 1019.	6.3	11
115	Minimum information about a microarray experiment (MIAME)â€"toward standards for microarray data. Nature Genetics, 2001, 29, 365-371.	9.4	3,750
116	The EMBL nucleotide sequence database. Nucleic Acids Research, 2001, 29, 17-21.	6.5	85
117	Natural Variation in a Drosophila Clock Gene and Temperature Compensation. Science, 1997, 278, 2117-2120.	6.0	322