Helen Parkinson

List of Publications by Year in Descending Order

121 papers	16,667 citations	48 h-index	129 g-index
132 ext. papers	20,837 ext. citations	14.1 avg, IF	5.88 L-index

#	Paper	IF	Citations
121	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen.. *Pain*, **2022**, 163, 1139-1157	8	0
120	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy **2022**, 1, 157-173		2
119	The EurOPDX Data Portal: an open platform for patient-derived cancer xenograft data sharing and visualization.. *BMC Genomics*, **2022**, 23, 156	4.5	1
118	The European Variation Archive: a FAIR resource of genomic variation for all species. *Nucleic Acids Research*, **2021**,	20.1	10
117	The European Genome-phenome Archive in 2021. *Nucleic Acids Research*, **2021**,	20.1	5
116	Workshop proceedings: GWAS summary statistics standards and sharing. *Cell Genomics*, **2021**, 1, 100004		4
115	Sequencing-based genome-wide association studies reporting standards. *Cell Genomics*, **2021**, 1, 100005-100005		5
114	The Polygenic Score Catalog as an open database for reproducibility and systematic evaluation. *Nature Genetics*, **2021**, 53, 420-425	36.3	58
113	Improving reporting standards for polygenic scores in risk prediction studies. *Nature*, **2021**, 591, 211-219	50.4	70
112	REMBI: Recommended Metadata for Biological Images-enabling reuse of microscopy data in biology. *Nature Methods*, **2021**, 18, 1418-1422	21.6	16
111	Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. *Nucleic Acids Research*, **2021**, 49, D1311-D1320	20.1	49
110	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. *Nature Genetics*, **2021**, 53, 1290-1299	36.3	28
109	Desiderata for the development of next-generation electronic health record phenotype libraries. *GigaScience*, **2021**, 10,	7.6	4
108	Pleiotropy data resource as a primer for investigating co-morbidities/multi-morbidities and their role in disease. *Mammalian Genome*, **2021**, 1	3.2	0
107	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimer's Disease Gene Expression Data. *Journal of Alzheimer's Disease*, **2020**, 75, 1417-1435	4.3	6
106	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. *PLoS Genetics*, **2020**, 16, e1009190	6	8
105	OpenStats: A robust and scalable software package for reproducible analysis of high-throughput phenotypic data. *PLoS ONE*, **2020**, 15, e0242933	3.7	5

104	Human and mouse essentiality screens as a resource for disease gene discovery. *Nature Communications*, **2020**, 11, 655	17.4	25
103	LifeTime and improving European healthcare through cell-based interceptive medicine. *Nature*, **2020**, 587, 377-386	50.4	56
102	Soft windowing application to improve analysis of high-throughput phenotyping data. *Bioinformatics*, **2020**, 36, 1492-1500	7.2	5
101	Leveraging European infrastructures to access 1 million human genomes by 2022. *Nature Reviews Genetics*, **2019**, 20, 693-701	30.1	36
100	PDX Finder: A portal for patient-derived tumor xenograft model discovery. *Nucleic Acids Research*, **2019**, 47, D1073-D1079	20.1	42
99	BioSamples database: an updated sample metadata hub. *Nucleic Acids Research*, **2019**, 47, D1172-D1178	20.1	27
98	The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. *Nucleic Acids Research*, **2019**, 47, D1005-D1012	20.1	1422
97	Harmonising phenomics information for a better interoperability in the rare disease field. *European Journal of Medical Genetics*, **2018**, 61, 706-714	2.6	16
96	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. *Stem Cell Reports*, **2018**, 10, 1-6	8	39
95	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog. *Genome Biology*, **2018**, 19, 21	18.3	87
94	Identification of genes required for eye development by high-throughput screening of mouse knockouts. *Communications Biology*, **2018**, 1, 236	6.7	20
93	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer's Disease Data. *Genes*, **2018**, 9,	4.2	6
92	Rapid establishment of the European Bank for induced Pluripotent Stem Cells (EBiSC) - the Hot Start experience. *Stem Cell Research*, **2017**, 20, 105-114	1.6	45
91	Open Targets: a platform for therapeutic target identification and validation. *Nucleic Acids Research* , **2017**, 45, D985-D994	20.1	241
90	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. *Cancer Research*, **2017**, 77, e62-e66	10.1	65
89	Prevalence of sexual dimorphism in mammalian phenotypic traits. *Nature Communications*, **2017**, 8, 15475	17.4	130
88	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. *Nature Genetics*, **2017**, 49, 1231-1238	36.3	145
87	The human-induced pluripotent stem cell initiative-data resources for cellular genetics. *Nucleic Acids Research*, **2017**, 45, D691-D697	20.1	63

86	Comparison, alignment, and synchronization of cell line information between CLO and EFO. *BMC Bioinformatics*, **2017**, 18, 557	3.6	3
85	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). *Nucleic Acids Research*, **2017**, 45, D896-D901	20.1	1321
84	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	9.7	63
83	PhenoImageShare: an image annotation and query infrastructure. *Journal of Biomedical Semantics*, **2016**, 7, 35	2.2	12
82	The cellular microscopy phenotype ontology. *Journal of Biomedical Semantics*, **2016**, 7, 28	2.2	17
81	Gramene 2016: comparative plant genomics and pathway resources. *Nucleic Acids Research*, **2016**, 44, D1133-40	20.1	102
80	Reporting phenotypes in mouse models when considering body size as a potential confounder. *Journal of Biomedical Semantics*, **2016**, 7, 2	2.2	7
79	Linking rare and common disease: mapping clinical disease-phenotypes to ontologies in therapeutic target validation. *Journal of Biomedical Semantics*, **2016**, 7, 8	2.2	26
78	Webulous and the Webulous Google Add-On--a web service and application for ontology building from templates. *Journal of Biomedical Semantics*, **2016**, 7, 17	2.2	6
77	Tools and data services registry: a community effort to document bioinformatics resources. *Nucleic Acids Research*, **2016**, 44, D38-47	20.1	81
76	The Ontology for Biomedical Investigations. *PLoS ONE*, **2016**, 11, e0154556	3.7	143
75	Identification of Cancer Related Genes Using a Comprehensive Map of Human Gene Expression. *PLoS ONE*, **2016**, 11, e0157484	3.7	24
74	Finding our way through phenotypes. *PLoS Biology*, **2015**, 13, e1002033	9.7	144
73	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. *American Journal of Human Genetics*, **2015**, 97, 111-24	11	147
72	Precision medicine: Look to the mice. *Science*, **2015**, 349, 390	33.3	7
71	Applying the ARRIVE Guidelines to an In Vivo Database. *PLoS Biology*, **2015**, 13, e1002151	9.7	56
70	Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. *Nucleic Acids Research*, **2015**, 43, D1071-8	20.1	403
69	A mouse informatics platform for phenotypic and translational discovery. *Mammalian Genome*, **2015**, 26, 413-21	3.2	20

68	ArrayExpress update--simplifying data submissions. *Nucleic Acids Research*, **2015**, 43, D1113-6	20.1	550
67	The Software Ontology (SWO): a resource for reproducibility in biomedical data analysis, curation and digital preservation. *Journal of Biomedical Semantics*, **2014**, 5, 25	2.2	39
66	CLO: The cell line ontology. *Journal of Biomedical Semantics*, **2014**, 5, 37	2.2	70
65	Expression Atlas update--a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. *Nucleic Acids Research*, **2014**, 42, D926-32	20.1	247
64	Toward richer metadata for microbial sequences: replacing strain-level NCBI taxonomy taxids with BioProject, BioSample and Assembly records. *Standards in Genomic Sciences*, **2014**, 9, 1275-7		26
63	The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. *Nucleic Acids Research*, **2014**, 42, D1001-6	20.1	2124
62	The EBI RDF platform: linked open data for the life sciences. *Bioinformatics*, **2014**, 30, 1338-9	7.2	160
61	The International Mouse Phenotyping Consortium Web Portal, a unified point of access for knockout mice and related phenotyping data. *Nucleic Acids Research*, **2014**, 42, D802-9	20.1	189
60	Updates to BioSamples database at European Bioinformatics Institute. *Nucleic Acids Research*, **2014** , 42, D50-2	20.1	30
59	ArrayExpress update--trends in database growth and links to data analysis tools. *Nucleic Acids Research*, **2013**, 41, D987-90	20.1	286
58	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. *Mammalian Genome*, **2012**, 23, 641-52	3.2	32
57	MageComet--web application for harmonizing existing large-scale experiment descriptions. *Bioinformatics*, **2012**, 28, 1402-3	7.2	1
56	Observ-OM and Observ-TAB: Universal syntax solutions for the integration, search, and exchange of phenotype and genotype information. *Human Mutation*, **2012**, 33, 867-73	4.7	16
55	The BioSample Database (BioSD) at the European Bioinformatics Institute. *Nucleic Acids Research*, **2012**, 40, D64-70	20.1	47
54	Gene Expression Atlas update--a value-added database of microarray and sequencing-based functional genomics experiments. *Nucleic Acids Research*, **2012**, 40, D1077-81	20.1	133
53	Data standards for Omics data: the basis of data sharing and reuse. *Methods in Molecular Biology*, **2011**, 719, 31-69	1.4	52
52	Anatomy ontologies and potential users: bridging the gap. *Journal of Biomedical Semantics*, **2011**, 2 Suppl 4, S3	2.2	5
51	OntoCAT--simple ontology search and integration in Java, R and REST/JavaScript. *BMC Bioinformatics*, **2011**, 12, 218	3.6	23

50	ArrayExpress update--an archive of microarray and high-throughput sequencing-based functional genomics experiments. *Nucleic Acids Research*, **2011**, 39, D1002-4	20.1	273
49	Contributions of the EMERALD project to assessing and improving microarray data quality. *BioTechniques*, **2011**, 50, 27-31	2.5	9
48	A global map of human gene expression. *Nature Biotechnology*, **2010**, 28, 322-4	44.5	271
47	Annotare--a tool for annotating high-throughput biomedical investigations and resulting data. *Bioinformatics*, **2010**, 26, 2470-1	7.2	12
46	Modeling sample variables with an Experimental Factor Ontology. *Bioinformatics*, **2010**, 26, 1112-8	7.2	302
45	Gene expression atlas at the European bioinformatics institute. *Nucleic Acids Research*, **2010**, 38, D690-8	20.1	167
44	Large scale comparison of global gene expression patterns in human and mouse. *Genome Biology*, **2010**, 11, R124	18.3	85
43	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. *Standards in Genomic Sciences*, **2010**, 3, 259-66		26
42	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. *BMC Bioinformatics*, **2010**, 11 Suppl 12, S12	3.6	76
41	Modeling biomedical experimental processes with OBI. *Journal of Biomedical Semantics*, **2010**, 1 Suppl 1, S7	2.2	187
40	MAGETabulator, a suite of tools to support the microarray data format MAGE-TAB. *Bioinformatics*, **2009**, 25, 279-80	7.2	12
39	ArrayExpress update--from an archive of functional genomics experiments to the atlas of gene expression. *Nucleic Acids Research*, **2009**, 37, D868-72	20.1	346
38	Importing ArrayExpress datasets into R/Bioconductor. *Bioinformatics*, **2009**, 25, 2092-4	7.2	68
37	Standards for Functional Genomics **2009**, 293-329		
36	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). *Nature Biotechnology*, **2008**, 26, 305-12	44.5	97
35	Data storage and analysis in ArrayExpress and Expression Profiler. *Current Protocols in Bioinformatics*, **2008**, Chapter 7, Unit 7.13	24.2	12
34	Mouse Phenotype Database Integration Consortium: integration [corrected] of mouse phenome data resources. *Mammalian Genome*, **2007**, 18, 157-63	3.2	41
33	The MGED Ontology: a resource for semantics-based description of microarray experiments. *Bioinformatics*, **2006**, 22, 866-73	7.2	152

32	Using ontologies to annotate microarray experiments. *Methods in Enzymology*, **2006**, 411, 325-39	1.7	6
31	Development of FuGO: an ontology for functional genomics investigations. *OMICS A Journal of Integrative Biology*, **2006**, 10, 199-204	3.8	45
30	Annotation of environmental OMICS data: application to the transcriptomics domain. *OMICS A Journal of Integrative Biology*, **2006**, 10, 172-8	3.8	18
29	Data storage and analysis in ArrayExpress. *Methods in Enzymology*, **2006**, 411, 370-86	1.7	33
28	ArrayExpress service for reviewers/editors of DNA microarray papers. *Nature Biotechnology*, **2006**, 24, 1321-2	44.5	20
27	Wrestling with SUMO and bio-ontologies. *Nature Biotechnology*, **2006**, 24, 21-2; author reply 23	44.5	6
26	The ArrayExpress gene expression database: a software engineering and implementation perspective. *Bioinformatics*, **2005**, 21, 1495-501	7.2	33
25	NCRI informatics initiative. *Nature Biotechnology*, **2005**, 23, 1212	44.5	1
24	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, 632-6	6.6	9
23	Pedro Ontology Services: A Framework for Rapid Ontology Markup. *Lecture Notes in Computer Science*, **2005**, 578-591	0.9	2
22	Standards for microarray data: an open letter. *Environmental Health Perspectives*, **2004**, 112, A666-7	8.4	13
21	Submission of microarray data to public repositories. *PLoS Biology*, **2004**, 2, E317	9.7	87
20	The SOFG Anatomy Entry List (SAEL): an annotation tool for functional genomics data. *Comparative and Functional Genomics*, **2004**, 5, 521-7		8
19	Standards and ontologies for functional genomics 2. *Comparative and Functional Genomics*, **2004**, 5, 618-22		4
18	The MGED ontology: a framework for describing functional genomics experiments. *Comparative and Functional Genomics*, **2003**, 4, 127-32		36
17	Standards and ontologies for functional genomics: towards unified ontologies for biology and biomedicine. *Comparative and Functional Genomics*, **2003**, 4, 116-20		2
16	ArrayExpress: a public database of gene expression data at EBI. *Comptes Rendus - Biologies*, **2003**, 326, 1075-8	1.4	58
15	ArrayExpress--a public repository for microarray gene expression data at the EBI. *Nucleic Acids Research*, **2003**, 31, 68-71	20.1	637

14	The European Bioinformatics Institute's data resources. *Nucleic Acids Research*, **2003**, 31, 43-50	20.1	38
13	Standards for microarray data. *Science*, **2002**, 298, 539	33.3	120
12	The underlying principles of scientific publication. *Bioinformatics*, **2002**, 18, 1409	7.2	27
11	A guide to microarray experiments-an open letter to the scientific journals. *Lancet, The*, **2002**, 360, 1019	40	8
10	Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. *Nature Genetics*, **2001**, 29, 365-71	36.3	3326
9	The EMBL nucleotide sequence database. *Nucleic Acids Research*, **2001**, 29, 17-21	20.1	77
8	Natural variation in a Drosophila clock gene and temperature compensation. *Science*, **1997**, 278, 2117-20	33.3	278
7	PDX Finder: A Portal for Patient-Derived tumor Xenograft Model Discovery		2
6	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog		2
5	eQTL Catalogue: a compendium of uniformly processed human gene expression and splicing QTLs		33
4	Improving reporting standards for polygenic scores in risk prediction studies		4
3	OpenStats: A Robust and Scalable Software Package for Reproducible Analysis of High-Throughput Phenotypic Data		1
2	Analyzing the heterogeneity of rule-based EHR phenotyping algorithms in CALIBER and the UK Biobank		1
1	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data		1