## Gudmundur A Thorisson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/303829/publications.pdf

Version: 2024-02-01

27 papers

13,513 citations

430874 18 h-index 642732 23 g-index

27 all docs

27 docs citations

times ranked

27

20144 citing authors

#	Article	IF	CITATIONS
1	A haplotype map of the human genome. Nature, 2005, 437, 1299-1320.	27.8	5,440
2	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
3	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
4	BioMart – biological queries made easy. BMC Genomics, 2009, 10, 22.	2.8	738
5	The International HapMap Project Web site: Figure 1 Genome Research, 2005, 15, 1592-1593.	5.5	497
6	The SNP Consortium website: past, present and future. Nucleic Acids Research, 2003, 31, 124-127.	14.5	150
7	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	14.5	107
8	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. BMC Bioinformatics, 2010, 11, S12.	2.6	102
9	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. Nature Communications, 2018, 9, 4447.	12.8	95
10	Genotype–phenotype databases: challenges and solutions for the post-genomic era. Nature Reviews Genetics, 2009, 10, 9-18.	16.3	87
11	The role of a bioresource research impact factor as an incentive to share human bioresources. Nature Genetics, 2011, 43, 503-504.	21.4	66
12	HGVbaseG2P: a central genetic association database. Nucleic Acids Research, 2009, 37, D797-D802.	14.5	60
13	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. BMC Medical Genetics, 2017, 18, 129.	2.1	47
14	Quantifying the use of bioresources for promoting their sharing in scientific research. GigaScience, 2013, 2, 7.	6.4	38
15	An informatics project and online "Knowledge Centre―supporting modern genotype-to-phenotype research. Human Mutation, 2011, 32, 543-550.	2.5	35
16	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. BMC Medical Genetics, 2017, 18, 103.	2.1	28
17	Accreditation and attribution in data sharing. Nature Biotechnology, 2009, 27, 984-985.	17.5	21
18	The phenotype and genotype experiment object model (PaGE-OM): a robust data structure for information related to DNA variation. Human Mutation, 2009, 30, 968-977.	2.5	18

#	Article	IF	Citations
19	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.	2.5	18
20	VarioML framework for comprehensive variation data representation and exchange. BMC Bioinformatics, 2012, 13, 254.	2.6	17
21	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
22	Semantically enabling a genome-wide association study database. Journal of Biomedical Semantics, 2012, 3, 9.	1.6	8
23	ODIN: the ORCID and DataCite interoperability network. International Journal of Knowledge and Learning, 2014, 9, 305.	0.2	3
24	Identity in research infrastructure and scientific communication: Report from the 1st IRISC workshop, Helsinki Sep 12-13, 2011. Nature Precedings, 0, , .	0.1	1
25	The BRIF (Bioresource Research Impact Factor) as a tool for improving bioresource sharing in biomedical research. Nature Precedings, 2011, , .	0.1	0
26	Identity in research infrastructure and scientific communication: Report from the 1st IRISC workshop, Helsinki Sep 12-13, 2011. Nature Precedings, 2011, , .	0.1	0
27	Applying ontologies and exploring nanopublishing in a genome-wide association study database. , 2012,		0