Daniel M Jordan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4942129/publications.pdf

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26	5,808	471509 17	610901 24
papers	citations	h-index	g-index

35	35	35	16641
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Predicting Functional Effect of Human Missense Mutations Using PolyPhenâ€2. Current Protocols in Human Genetics, 2013, 76, Unit7.20.	3.5	2,389
2	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	12.6	1,535
3	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. Cell, 2015, 161, 647-660.	28.9	482
4	Genome analysis reveals insights into physiology and longevity of the Brandtâ€™s bat Myotis brandtii. Nature Communications, 2013, 4, 2212.	12.8	213
5	Estimating the selective effects of heterozygous protein-truncating variants from human exome data. Nature Genetics, 2017, 49, 806-810.	21.4	157
6	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
7	Identification of cis-suppression of human disease mutations by comparative genomics. Nature, 2015, 524, 225-229.	27.8	106
8	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 2019, 10, 790.	12.8	98
9	No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002725.	8.4	97
10	Large Numbers of Genetic Variants Considered to be Pathogenic are Common in Asymptomatic Individuals. Human Mutation, 2013, 34, 1216-1220.	2.5	78
11	Development and Validation of a Computational Method for Assessment of Missense Variants in Hypertrophic Cardiomyopathy. American Journal of Human Genetics, 2011, 88, 183-192.	6.2	73
12	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	3.5	70
13	Human allelic variation: perspective from protein function, structure, and evolution. Current Opinion in Structural Biology, 2010, 20, 342-350.	5.7	63
14	Excess of Deleterious Mutations around HLA Genes Reveals Evolutionary Cost of Balancing Selection. Molecular Biology and Evolution, 2016, 33, 2555-2564.	8.9	55
15	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222.	8.8	47
16	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
17	Population-Based Penetrance of Deleterious Clinical Variants. JAMA - Journal of the American Medical Association, 2022, 327, 350.	7.4	34
18	Mitigating False-Positive Associations in Rare Disease Gene Discovery. Human Mutation, 2015, 36, 998-1003.	2.5	18

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19	Using Full Genomic Information to Predict Disease: Breaking Down the Barriers Between Complex and Mendelian Diseases. Annual Review of Genomics and Human Genetics, 2018, 19, 289-301.	6.2	9
20	Parameterization of Peptide13C Carbonyl Chemical Shielding Anisotropy in Molecular Dynamics Simulations. ChemPhysChem, 2007, 8, 1375-1385.	2.1	6
21	Reply to â€˜Selective effects of heterozygous protein-truncating variantsâ€™. Nature Genetics, 2019, 51, 3-4.	21.4	6
22	Overcoming constraints on the detection of recessive selection in human genes from population frequency data. American Journal of Human Genetics, 2022, 109, 33-49.	6.2	5
23	The Landscape of Pervasive Horizontal Pleiotropy in Human Genetic Variation is Driven by Extreme Polygenicity of Human Traits and Diseases. SSRN Electronic Journal, 0, , .	0.4	3
24	When â€œNof 2â€•is not enough: integrating statistical and functional data in gene discovery. Journal of Physical Education and Sports Management, 2017, 3, a001099.	1.2	2
25	Probing the aggregated effects of purifying selection per individual on 1,380 medical phenotypes in the UK Biobank. PLoS Genetics, 2021, 17, e1009337.	3.5	2
26	A literature review at genome scale: improving clinical variant assessment. Genetics in Medicine, 2018, 20, 936-941.	2.4	1