

# Harendra Guturu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7899709/publications.pdf>

Version: 2024-02-01

18  
papers

1,649  
citations

759233

12  
h-index

888059

17  
g-index

24  
all docs

24  
docs citations

24  
times ranked

5047  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease. <i>Nature Genetics</i> , 2022, 54, 382-392.	21.4	97
2	Morphogenesis is transcriptionally coupled to neurogenesis during peripheral olfactory organ development. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	6
3	AMELIE speeds Mendelian diagnosis by matching patient phenotype and genotype to primary literature. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	60
4	Phrank measures phenotype sets similarity to greatly improve Mendelian diagnostic disease prioritization. <i>Genetics in Medicine</i> , 2019, 21, 464-470.	2.4	33
5	Biallelic loss of <i>WNT5A</i> mutations in an infant with severe and atypical manifestations of Robinow syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 1030-1036.	1.2	15
6	Independent erosion of conserved transcription factor binding sites points to shared hindlimb, vision and external testes loss in different mammals. <i>Nucleic Acids Research</i> , 2018, 46, 9299-9308.	14.5	15
7	An MTF1 binding site disrupted by a homozygous variant in the promoter of <i>ATP7B</i> likely causes Wilson Disease. <i>European Journal of Human Genetics</i> , 2018, 26, 1810-1818.	2.8	15
8	Mutations of <i>AKT3</i> are associated with a wide spectrum of developmental disorders including extreme megalencephaly. <i>Brain</i> , 2017, 140, 2610-2622.	7.6	102
9	Systematic reanalysis of clinical exome data yields additional diagnoses: implications for providers. <i>Genetics in Medicine</i> , 2017, 19, 209-214.	2.4	261
10	M-CAP eliminates a majority of variants of uncertain significance in clinical exomes at high sensitivity. <i>Nature Genetics</i> , 2016, 48, 1581-1586.	21.4	654
11	Erosion of Conserved Binding Sites in Personal Genomes Points to Medical Histories. <i>PLoS Computational Biology</i> , 2016, 12, e1004711.	3.2	7
12	NetworkPainter: dynamic intracellular pathway animation in Cytobank. <i>BMC Bioinformatics</i> , 2015, 16, 172.	2.6	3
13	Microbiota modulate transcription in the intestinal epithelium without remodeling the accessible chromatin landscape. <i>Genome Research</i> , 2014, 24, 1504-1516.	5.5	119
14	Structure-aided prediction of mammalian transcription factor complexes in conserved non-coding elements. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130029.	4.0	30
15	PRISM offers a comprehensive genomic approach to transcription factor function prediction. <i>Genome Research</i> , 2013, 23, 889-904.	5.5	32
16	The Enhancer Landscape during Early Neocortical Development Reveals Patterns of Dense Regulation and Co-option. <i>PLoS Genetics</i> , 2013, 9, e1003728.	3.5	33
17	Computational methods to detect conserved non-genic elements in phylogenetically isolated genomes: application to zebrafish. <i>Nucleic Acids Research</i> , 2013, 41, e151-e151.	14.5	84
18	System identification of hunchback protein patterning in early drosophila embryogenesis. , 2009, , .		2