

# ConVarT: a search engine for matching human genetic v non-human species

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The 2022 <i>Nucleic Acids Research</i> database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2022, 50, D1-D10.	14.5	50
3	The conservation of human functional variants and their effects across livestock species. <i>Communications Biology</i> , 2022, 5, .	4.4	6
5	Phenotypic screening models for rapid diagnosis of genetic variants and discovery of personalized therapeutics. <i>Molecular Aspects of Medicine</i> , 2023, 91, 101153.	6.4	7
6	ConVarT: Search Engine for Missense Variants Between Humans and Other Organisms. <i>Current Protocols</i> , 2022, 2, .	2.9	2
10	mutscan—a flexible R package for efficient end-to-end analysis of multiplexed assays of variant effect data. <i>Genome Biology</i> , 2023, 24, .	8.8	1
11	<i>Caenorhabditis elegans</i> for research on cancer hallmarks. <i>DMM Disease Models and Mechanisms</i> , 2023, 16, .	2.4	3
12	Comparative Investigation of Coincident Single Nucleotide Polymorphisms Underlying Avian Influenza Viruses in Chickens and Ducks. <i>Biology</i> , 2023, 12, 969.	2.8	0
13	CiliaMiner: an integrated database for ciliopathy genes and ciliopathies. <i>Database: the Journal of Biological Databases and Curation</i> , 2023, 2023, .	3.0	0
14	Cell-type-specific gene expression and regulation in the cerebral cortex and kidney of atypical <i>Setbp1</i> <sup>S858R</sup> Schinzel Giedion Syndrome mice. <i>Journal of Cellular and Molecular Medicine</i> , 2023, 27, 3565-3577.	3.6	1
15	Matching variants for functional characterization of genetic variants. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0
16	Harnessing Computational Methods to Characterize Chemical Impacts on Biodiversity. <i>Environmental Science and Technology Letters</i> , 2024, 11, 185-194.	8.7	0