Whole-genome sequencing of 175 Mongolians uncovers architecture and gene flow throughout North and East A

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Citation Report

#	Article	IF	CITATIONS
1	Integrating Phylogeographic Analysis and Geospatial Methods to Infer Historical Dispersal Routes and Glacial Refugia of Liriodendron chinense. Forests, 2019, 10, 565.	2.1	13
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19	The genetic structure of the Turkish population reveals high levels of variation and admixture. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	42
20	Genetic insights into the paternal admixture history of Chinese Mongolians via high-resolution customized Y-SNP SNaPshot panels. Forensic Science International: Genetics, 2021, 54, 102565.	3.1	19
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