Genome-Wide SNP Analysis Reveals Population Structu Ryukyu Islanders in the Southern Part of the Japanese A

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Citation Report

#	Article	IF	CITATIONS
1	On the use of kernel approximate Bayesian computation to infer population history. Genes and Genetic Systems, 2015, 90, 153-162.	0.2	1
2	Human genetic diversity in the Japanese Archipelago: dual structure and beyond. Genes and Genetic Systems, 2015, 90, 147-152.	0.2	28
3	Mapping the genetic diversity of HLA haplotypes in the Japanese populations. Scientific Reports, 2015, 5, 17855.	1.6	8
4	Model-Based Verification of Hypotheses on the Origin of Modern Japanese Revisited by Bayesian Inference Based on Genome-Wide SNP Data. Molecular Biology and Evolution, 2015, 32, 1533-1543.	3.5	32
5	Unique characteristics of the Ainu population in Northern Japan. Journal of Human Genetics, 2015, 60, 565-571.	1.1	26
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9	Characterising private and shared signatures of positive selection in 37 Asian populations. European Journal of Human Genetics, 2017, 25, 499-508.	1.4	22
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17	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. Nature Communications, 2018, 9, 1631.	5 <b>.</b> 8	132
18	Fine-tuning of Approximate Bayesian Computation for human population genomics. Current Opinion in Genetics and Development, 2018, 53, 60-69.	1.5	6

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20	The geographical configuration of a language area influences linguistic diversity. PLoS ONE, 2019, 14, e0217363.	1.1	15
21	Biomedical and genetic characteristics of the Ryukyuans: demographic history, diseases and physical and physiological traits. Annals of Human Biology, 2019, 46, 354-366.	0.4	6
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