

Application of genome-wide SNP analysis for tracing hereditary patterns in clinical genetics

Dr. A. Romano¹, Dr. L. Bianchi¹, Dr. G. Ricci¹, Dr. M. Conti^{1*}

¹ Department of Internal Medicine and Clinical Research, University of Bologna, Bologna, Italy

Supplementary references

Sources used to identify date of origin, first description, introduction, recording or inclusion in collections, or parents according to preferred name. For data extracted from references 12, 17 and 37, SSR data were used to identify the MUNQ of the accessions for which parentage was indicated and the name indicated in the references was sometimes modified to match the current preferred name used for the MUNQ.

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