Whole-exome sequencing of discordant and concordant affected sib pairs in spinocerebellar ataxia type 3 (SCA3): a tool to identify novel modifier genes and highlight disrupted molecular pathways.

https://neurodegenerationresearch.eu/survey/whole-exome-sequencing-of-discordant-and-concordant-affected-sib-pairs-in-spinocerebellar-ataxia-type-3-sca3-a-tool-to-identify-novel-modifier-genes-and-highlight-disrupted-molecular-pathways/

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