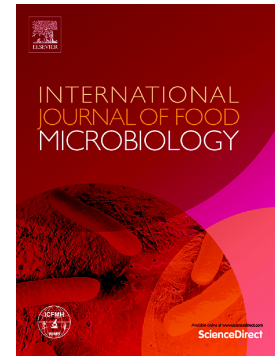


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Application of whole genome sequence data in analyzing the molecular epidemiology of Shiga toxin-producing *Escherichia coli* O157:H7/H-

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