In the present study, formaldehyde dismutase from *Methylobacterium* sp. FD1 was partially purified and analyzed by nanoLC–MS/MS; it was then cloned from the genomic DNA of FD1 by PCR. The open reading frame of the formaldehyde dismutase gene of FD1 was estimated to be 1203 bp in length. The molecular weight and pI of formaldehyde dismutase (401 aa), as deduced from the FD1 gene, were calculated at 42,877.32 and 6.56, respectively. NAD(H)-binding residues and zinc-binding residues were found in the amino acid sequence of the deduced formaldehyde dismutase of FD1 by BLAST search. The resting *Escherichia coli* cells that were transformed with the FD1 formaldehyde dismutase gene degraded high concentrations of formaldehyde and produced formic acid and methanol that were molar equivalents of one-half of the degraded formaldehyde. The lyophilized cells of the recombinant *E. coli* also degraded high concentrations of formaldehyde.

Degradation of formaldehyde by resting and lyophilized cells of *E. coli* transformed with the formaldehyde dismutase gene of *Methylobacterium* sp. FD1.