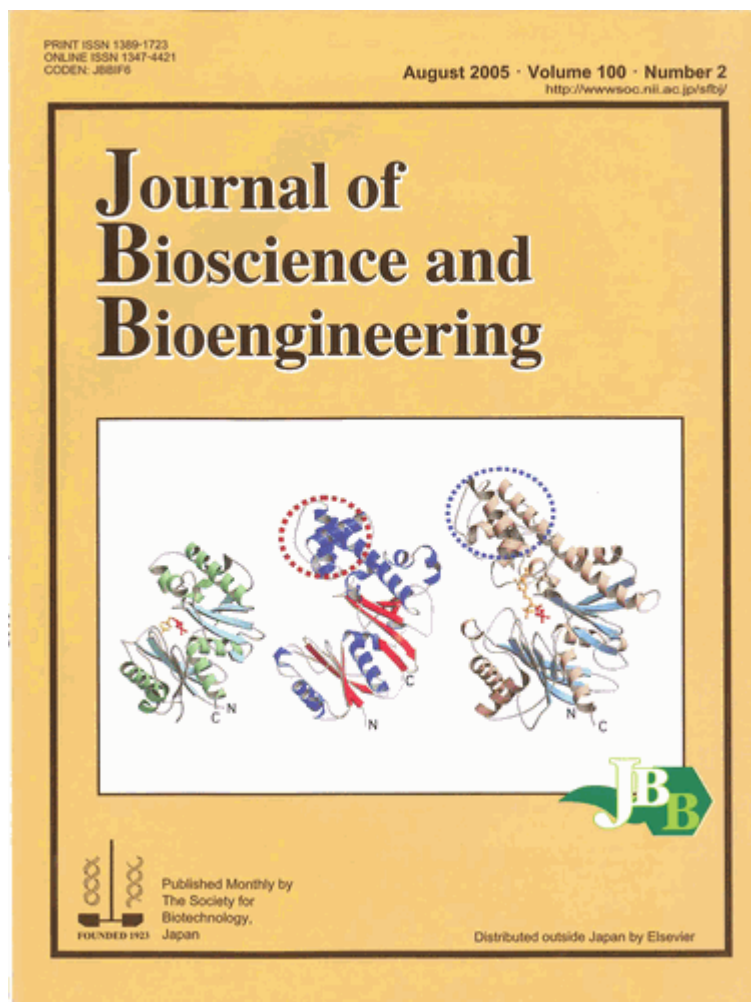


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Hypothesis on the evolution of glucose kinases.

A putative evolutionary process for glucose kinases through the acquisition of flexible subdomains, which are enclosed by dotted lines, was postulated based on the three-dimensional structures of *Arthrobacter* sp. KM1 inorganic polyphosphate/ATP-glucomannokinase (left), *Escherichia coli* ATP-specific glucokinase (middle), and human ATP-specific hexokinase (right).

The hypothesis emphasizes that glucose kinases evolved from an ancestral “polyphosphate/ATP-dependent glucokinase” into an ATP-specific hexokinase, via an ATP-specific glucokinase, thereby losing polyphosphate-utilizing capability and acquiring flexible subdomains of increasing sizes, which enable enzymes to be regulated more precisely and ingeniously.

Related article: Kawai, S., Mukai, T., Mori, S., Mikami, B., and Murata, K., “**Hypothesis: structure, evolution, and ancestor of glucose kinases in the hexokinase family**”, *J. Biosci. Bioeng.*, vol. 99, 320-330 (2005).

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