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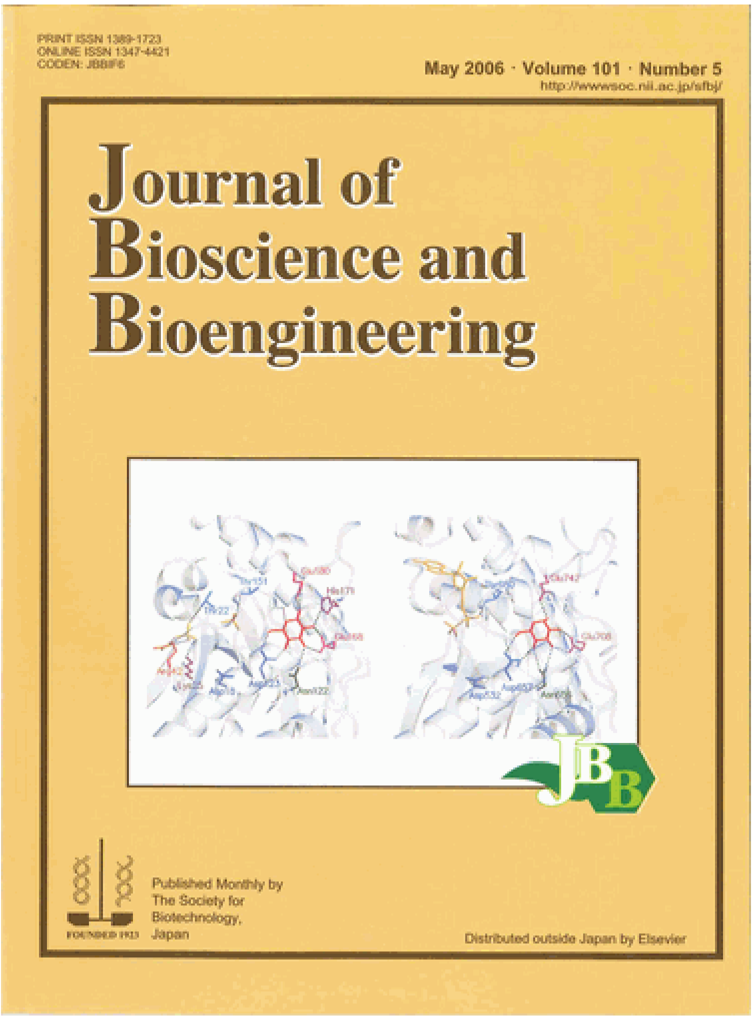

Binding sites of inorganic polyphosphate/ATP-glucomannokinase (GMK) for glucose (red), Pi-A (orange), and Pi-B (yellow) (left), and C-terminal half of human hexokinase I (C-HK I) for glucose (red) and ADP (orange) (right). Hydrogen bonds are indicated by dotted lines. In C-HK I, interactions of amino acid residues with the β-phosphoryl group are not indicated, since this group was not located at the proper site. These pictures suggest that Pi-A in GMK represents the binding site for phosphoryl group of ATP and inorganic polyphosphate.

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

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