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Identification of potential allosteric communication pathways between functional sites of the bacterial ribosome by graph and elastic network models

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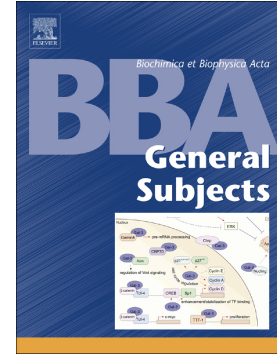
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