

# Dynamic biomolecular computing system for artificial genetic network

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RTRACS (Reverse-transcription and TRanscription-based Autonomous Computing System) is a modular biomolecular computing system composed of DNA, RNA and enzymes, whose mechanism is based on retroviral replication [1, 2]. The modularity of RTRACS allows various simple modules to be combined together by using output RNA of a module as input for successive modules to create systems capable of sophisticated computational operations. When the output RNA of the module is assigned to mRNA, RTRACS is available for artificial genetic network with cell-free protein synthesis.

RTRACS can basically perform computation to process time-dependent input data by employing modules capable of dynamically changing output RNA depending on input RNA. However, logic gate modules previously developed [2, 3] do not operate dynamically because output RNA production continues indefinitely once the logical operation is complete. Here, we report a new AND gate module that can operate dynamically in response to input RNA data. The dynamic operation was achieved by two additional degradation reactions, one for the newly synthesized DNA strands and the other for the remaining input and output RNA strands. These degradation reactions return the AND gate module to the original state when the input RNA strands are no longer present. Since the degradation reactions are effective for all kinds of RTRACS modules, the present method can be applied to other RTRACS modules to make them succeed in operating dynamically.

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