President

Polymer-immobilized chiral catalysts for the synthesis of optically active compounds

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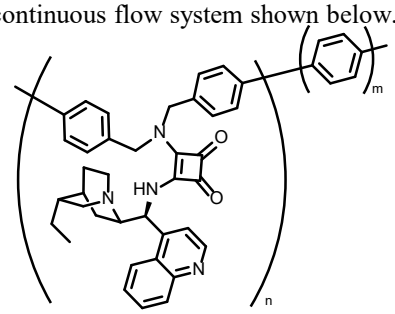
Research Outline

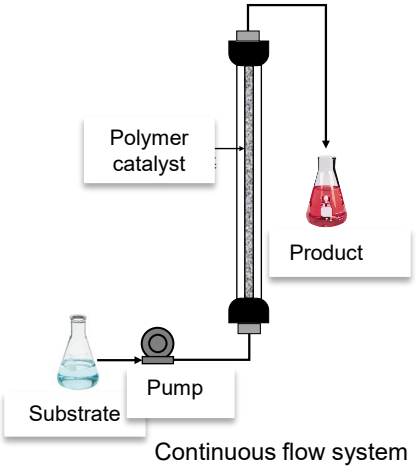
Chiral polymers as organocatalysts in asymmetric synthesis

Various efficient asymmetric catalysts have been designed based on cinchona alkaloids, an important class of which are their sulfonamide derivatives. We have developed several syntheses of polymeric cinchona-based catalysts including quaternary ammonium salts, sulfonamides, and squaramide derivatives. These chiral polymers showed excellent catalytic activities with high level of stereoselectivities in various kinds of asymmetric reactions.

We recently developed novel polymer catalysts derived from cinchona squaramides using Yamamoto coupling polymerization. These chiral polymers catalysed asymmetric Michael type reaction to give the chiral product in high yield with excellent enantioselectivity. Because of the insolubility of the polymer catalysts in usual organic solvents, the reaction proceeded in heterogeneous system. These catalysts can be used in continuous flow system shown below.



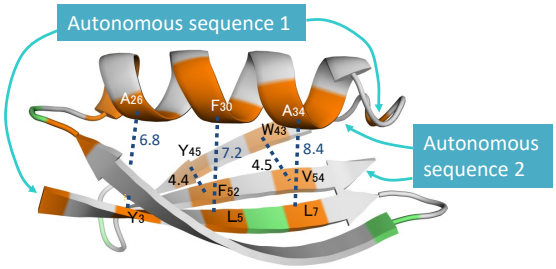
Polymer catalyst



Continuous flow system

Protein folding structures based on probability theory

Globular proteins are comprised of intrinsic continuous folding structure (FS) units. Decoding, rather than predicting, the initiation mechanism of protein folding from amino acid sequences is a stringent requirement for protein folding researchers. We proposed 44 kinds of folding elements, which covered all the amino acids in the protein chains, and defined all folding structure units. Folding structure formation based on probability theory is the general solution for the initiation mechanism of Anfinsen's tenet of protein folding.



Two autonomous sequences found in the Immunoglobulin-binding B1 Domain of Protein G (GB1)

Identification of autonomous sequences of a protein is the most attractive to elucidate the folding mechanism of the protein. The autonomous sequences fold into respective independent cooperative tertiary structure units, semifolds. As an X-ray structure of any protein can be dissected into intrinsic continuous FS units, we have every confidence to identify autonomous sequences of the protein based on the X-ray structure. The most significant feature of the semifold is that it can be verified as a small set of intrinsic continuous FS units forming hydrophobic core network within the semifold.