Electronic Supplementary Material (ESI) for Analyst.

The enhancement of enzyme cascading via tetrahedral DNA framework modification

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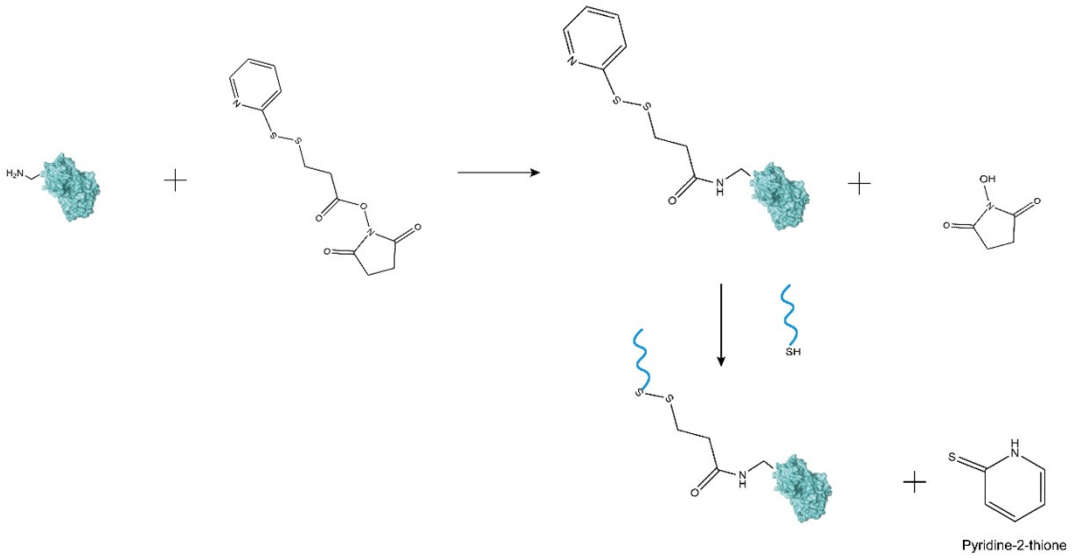

Fig. S1. DNA-enzyme conjugation by SPDP crosslinker.

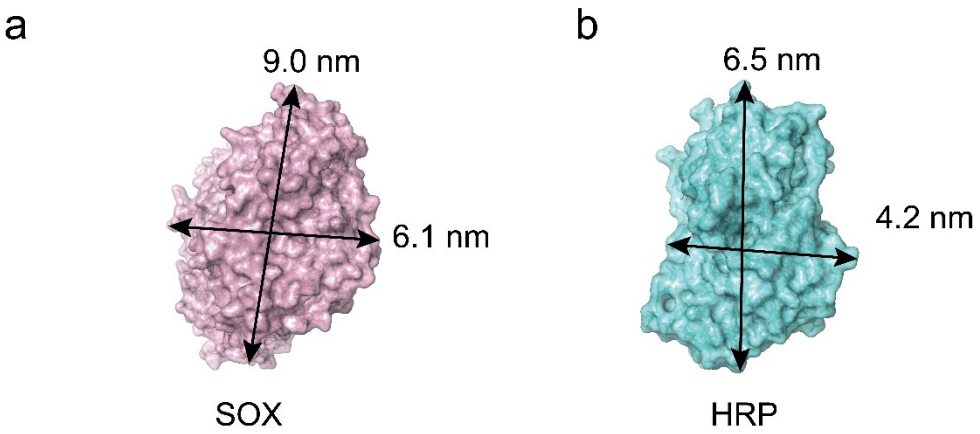

Fig. S2. The structures of enzymes. (a) Sarcosine oxidase (SOX, PDB code: 3QSE). (b) Horseradish peroxidase (HRP, PDB code: 1H5A). The structures of enzymes were visualized by PYMOL.

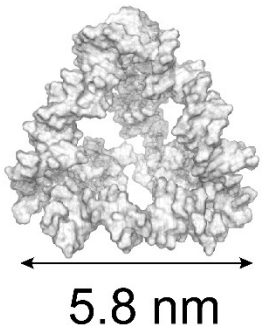

Fig. S3. Structure of tetrahedral DNA nanostructure (TDN). The TDN structure was rendered by PYMOL.

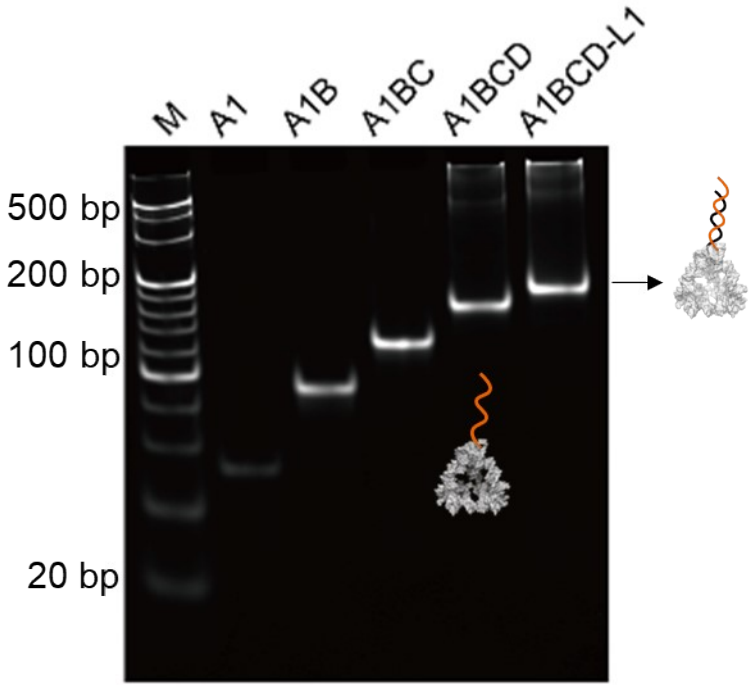

Fig. S4. Characterization of TDN1 assembly by PAGE. TDN1 (A1BCD) assembly was shown as a "staircase-like" pattern by adding all four required DNA strands. Lane A1BCD-L1 confirmed the successful hybridization of TDN1 with DNA L1. Lane M: 20 bp marker.

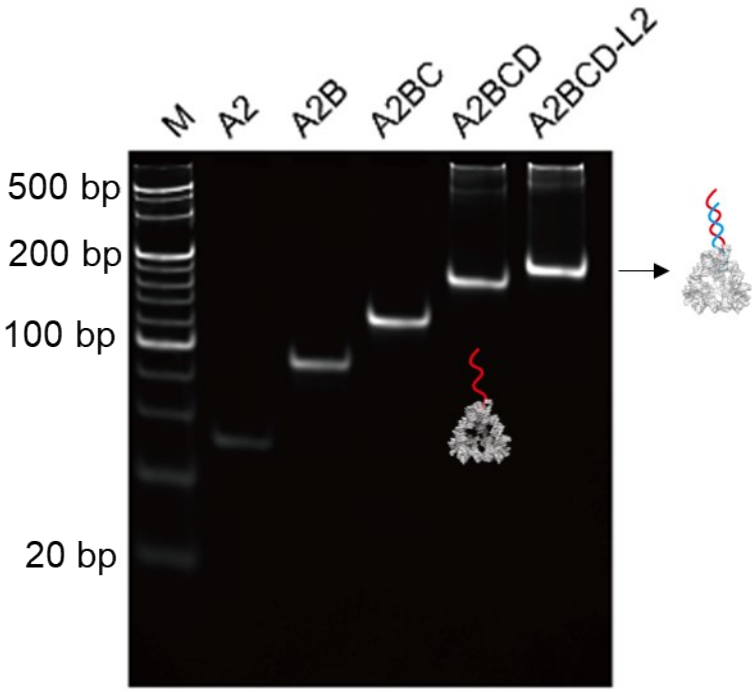

Fig. S5. Characterization of TDN2 assembly by PAGE. Lane A2BCD indicated the formation of TDN2 and lane A1BCD-L2 confirmed the successful hybridization of TDN2 with DNA L2. Lane M: 20 bp marker.

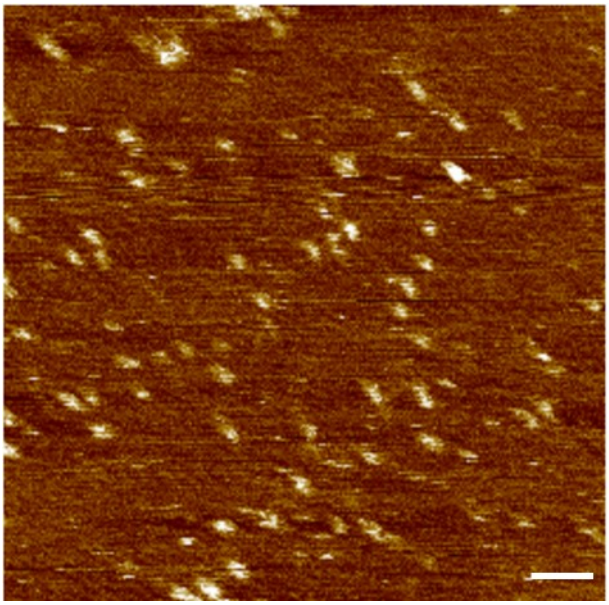

Fig. S6. The AFM image of the TDNs. Scale bar: 100 nm.

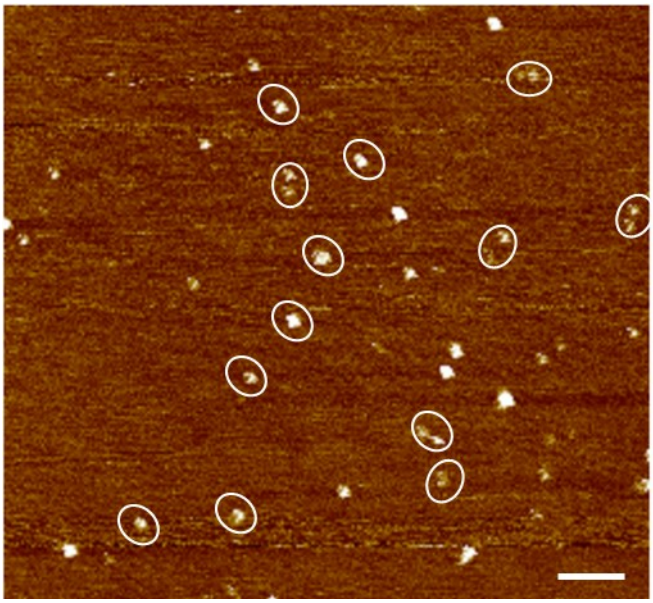

Fig. S7. The AFM image of the TDN1-SOX. Scale bar: 200 nm. White ellipses indicate the TDN1-SOX conjugations.

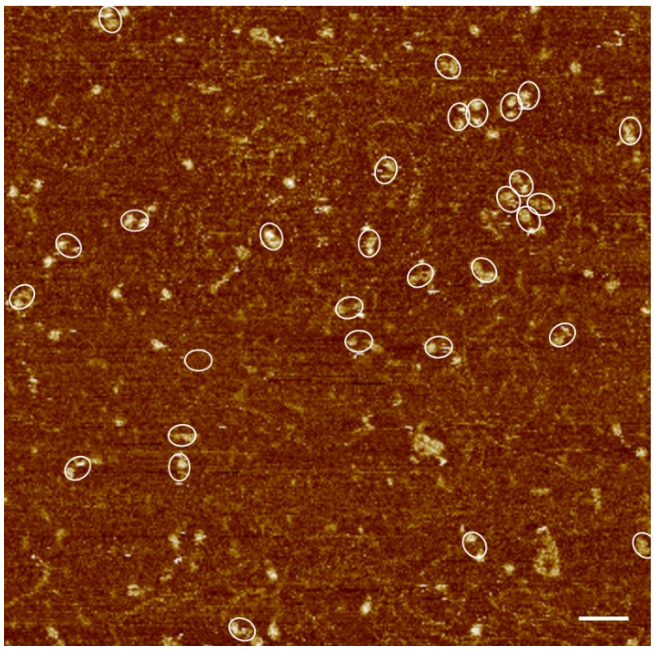

Fig. S8. The AFM image of the TDN2-HRP. Scale bar: 50 nm. White ellipses indicate the TDN2-HRP conjugations.

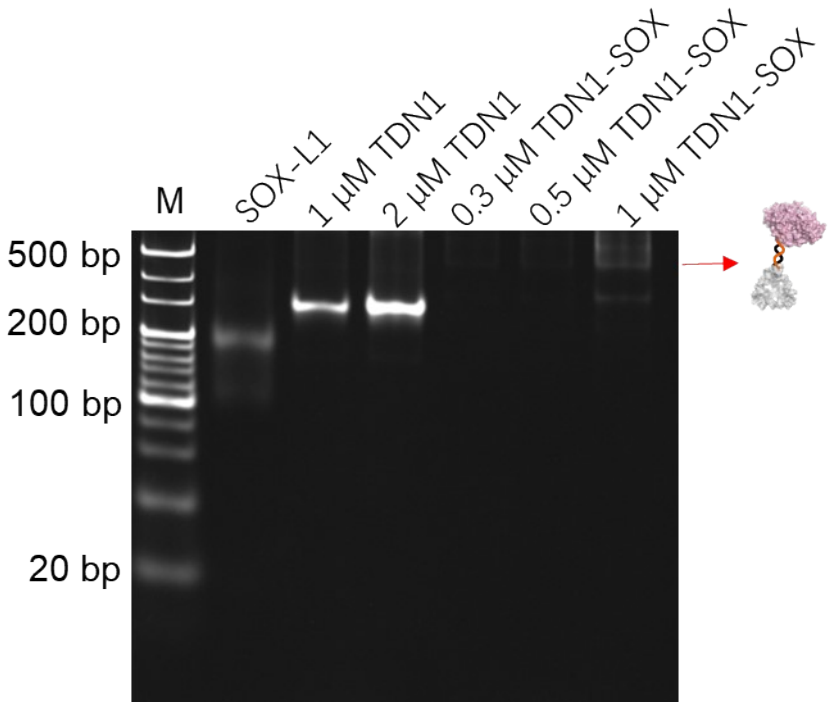

Fig. S9. Characterization of the formation of TDN1-SOX by gel electrophoresis mobility shift assay (EMSA). Lane M: 20 bp marker. Immobilization of L1-SOX on the vertex of TDN1 decreased its migration rate significantly.

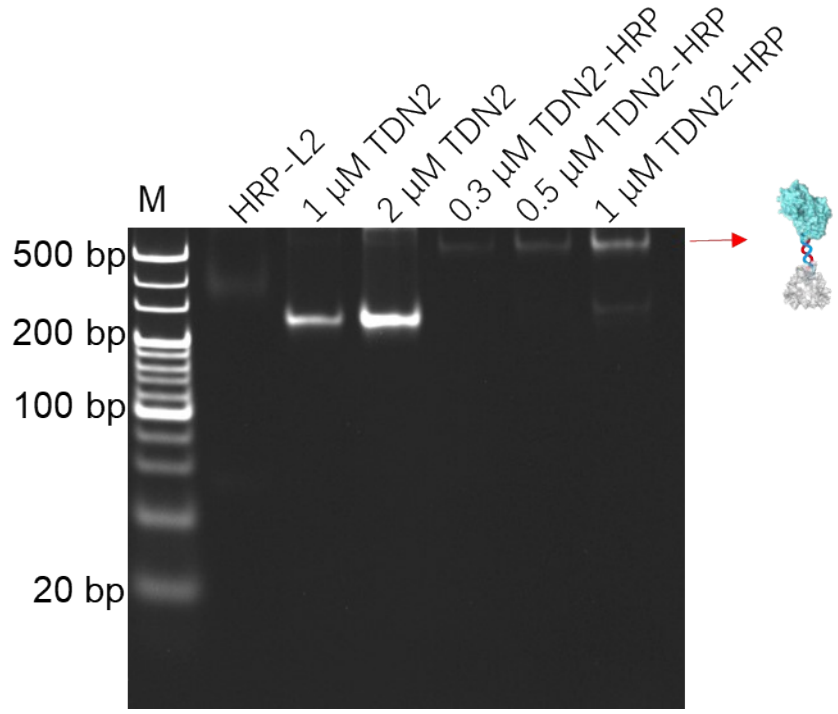

Fig. S10. Characterization of the formation of TDN2-HRP by gel electrophoresis mobility shift assay (EMSA). Lane M: 20 bp marker. Immobilization of L2-HRP on the vertex of TDN2 decreased its migration rate significantly.

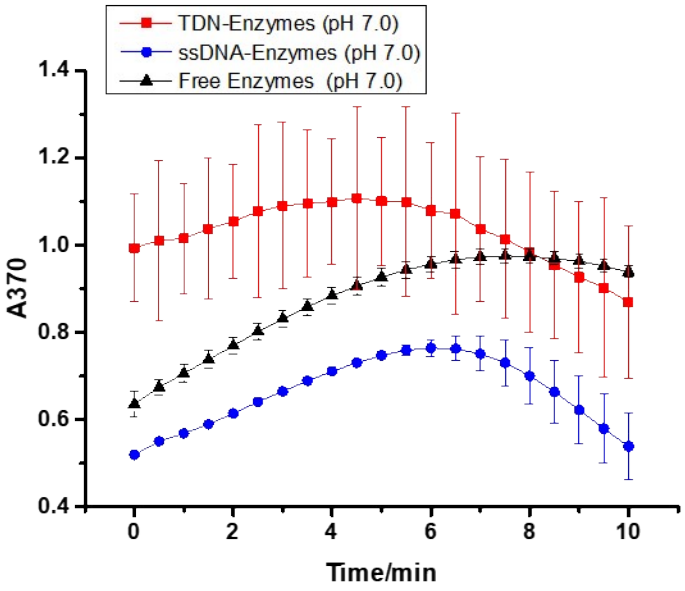

Fig. S11. The kinetics curves of the TDN-enzymes, ssDNA-enzymes and free enzymes (pH 7.0).

Table S1 DNA sequence used in this work:

name	**DNA(5'→3'）**
A	ACATTCCTAAGTCTGAAACATTACAGCTTGCTACACGAGAAGAGCCGCCATAGTAAAAAAAAAAA
A1(A-L3)	ACATTCCTAAGTCTGAAACATTACAGCTTGCTACACGAGAAGAGCCGCCATAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
A2(A-L4)	ACATTCCTAAGTCTGAAACATTACAGCTTGCTACACGAGAAGAGCCGCCATAGTAAAAAAAAAAAAAACCACCACCACCACCACCA
B	SH-TATCACCAGGCAGTTGACAGTGTAGCAAGCTGTAATAGATGCGAGGGTCCAATAC
C	SH-TCAACTGCCTGGTGATAAAACGACACTACGTGGGAATCTACTATGGCGGCTCTTC
D	SH-TTCAGACTTAGGAATGTGCTTCCCACGTAGTGTCGTTTGTATTGGACCCTCGCAT
L1	TTTTTTTTTTTTTTTTTTT-SH
L2	TTGGTGGTGGTGGTGGTGGT-SH
L3	AAAAAAAAAAAAAAAAAAAAA
L4	AACCACCACCACCACCACCA
L3'	SH-AAAAAAAAAAAAAAAAAAAAA
L4'	SH-AACCACCACCACCACCACCA