Supplementary Information for

EHairpin-driven double-stem-loop programmable allosteric strategy for molecular security access control

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This PDF file includes:

Supplementary Fig. S1 – Fig. S14

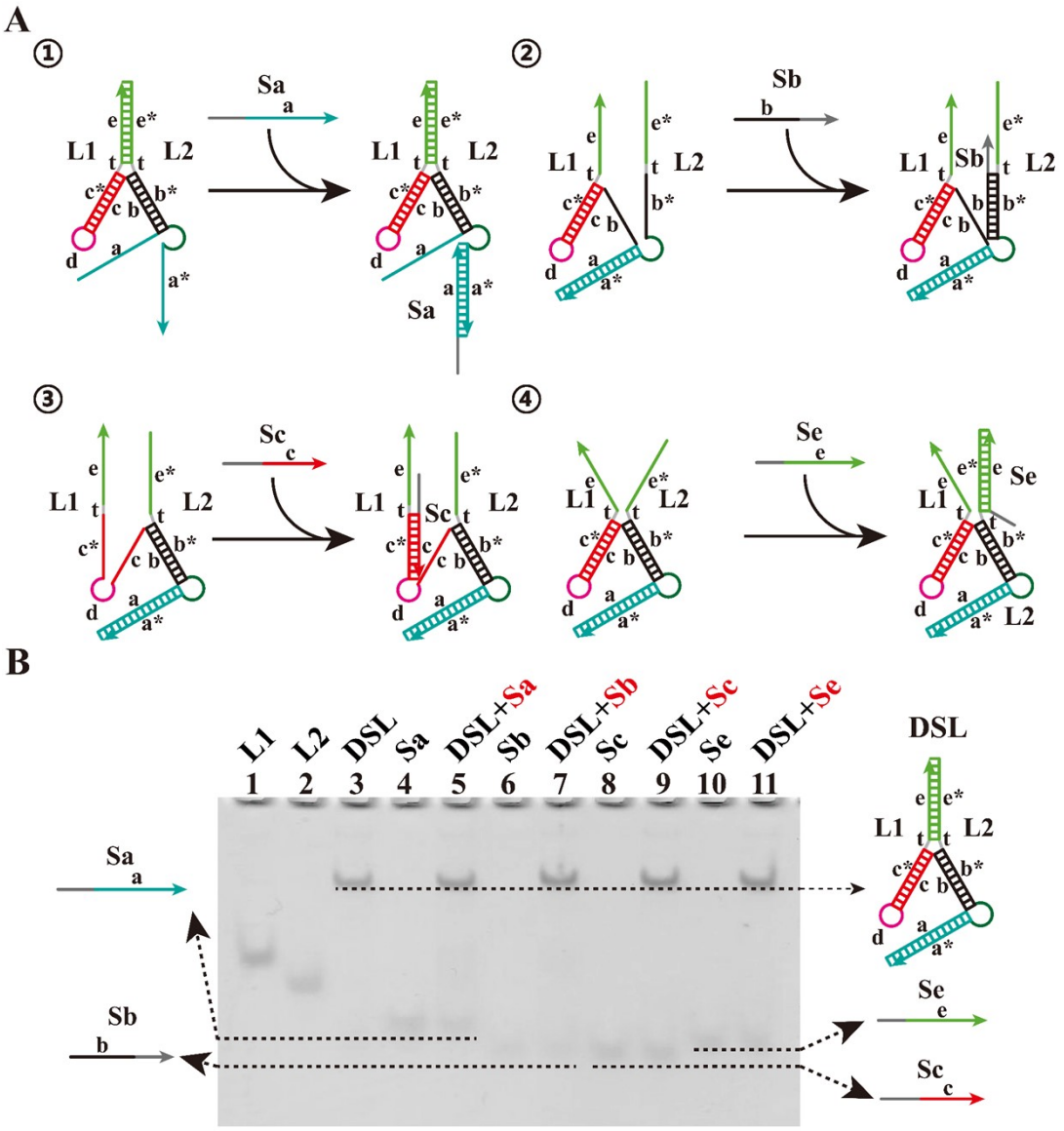

Fig. S1 Validation of double-stem-loop (DSL) structures formation. (A) Schematic diagram of the four ways to verify the formation of DSL structures respectively. ① Verify whether domain a of the DSL structure can bind to its complementary domain a* by adding single strand Sa; ② Verify whether domain b of the DSL structure can bind to its complementary domain b* by adding single strand Sb; ③ Verify whether domain c of the DSL structure can bind to its complementary domain c* by adding single strand Sc; and ④ Verify whether domain e of the DSL structure can bind to its complementary domain e* by adding single strand Se. (B) Analysis of DSL structures formation using polyacrylamide gel electrophoresis (PAGE) (12%). [L1] = [L2] = [DSL] = [Sa] = [Sb] = [Sc] = [Se] = 800 nM.

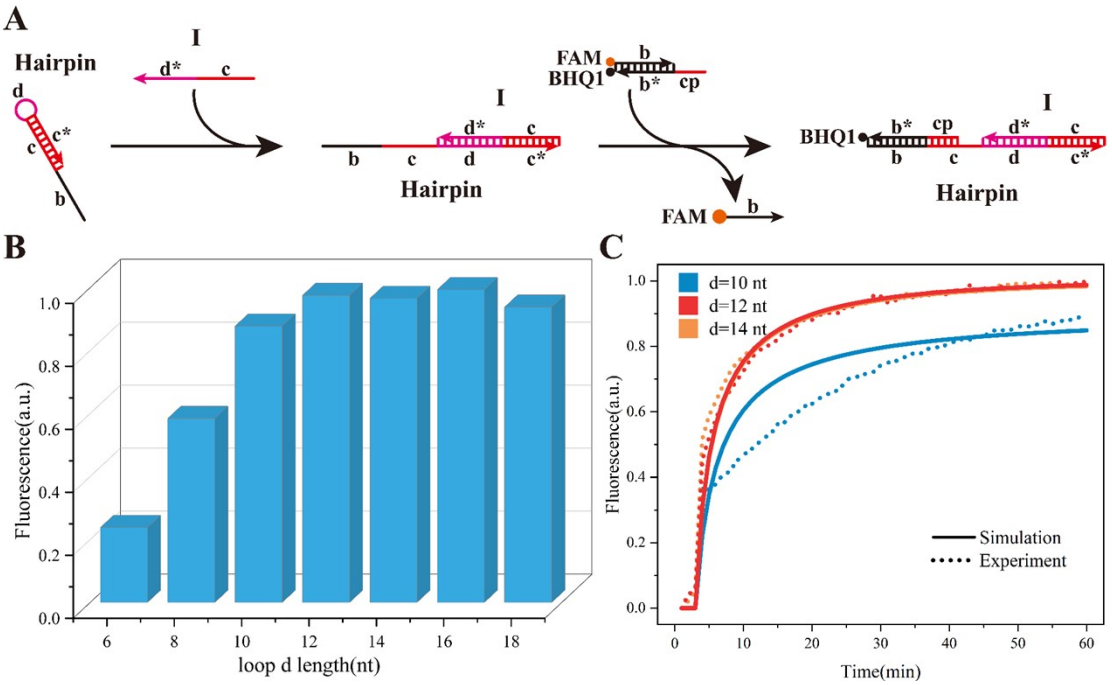

Fig. S2 Exploration of the loop domain base numbers of the hairpin structure. (A) Experimental process of the hairpin structure being opened by a single strand to occur a strand displacement reaction. (B) Comparison of fluorescence experiment results at different base numbers in the loop domain d of the hairpin structure on the opening of the hairpin structure. Seven different base numbers of domain d are listed on the x-axis. (C) Simulation and fluorescence kinetic curves for base numbers of 10, 12, and 14 nt in domain d of the hairpin structure, respectively. [Hairpin] = [I] = [FAM] = [BHQ1] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

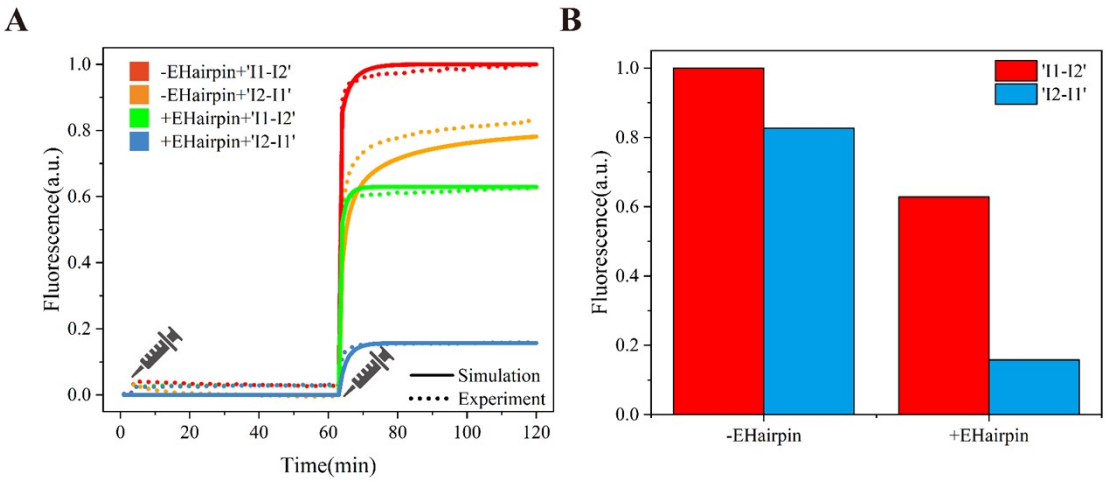

Fig. S3 Comparison of experiment results with and without the addition of EHairpin. (A) Simulation and fluorescence kinetic curves with and without the addition of EHairpin ([EHairpin] = 0×, 1×, where 1× = 200 nM). The red curves represent the experiment results of adding strand I1 first and then strand I2 when EHairpin is not added; the orange curves represent the experiment results of adding strand I2 first and then strand I1 when EHairpin is not added; the green curves represent the experiment results of adding strand I1 first and then strand I2 when EHairpin is added; and the blue curves represent the experiment results of adding strand I2 first and then strand I1 when EHairpin is added; (B) Histograms of the output fluorescence signals with and without the addition of EHairpin ([EHairpin] = 0×, 1×, where 1× = 200 nM). Red bars correspond to the experiment results of adding strand I1 first and then strand I2; blue bars correspond to the experiment results of adding strand I2 first and then strand I1. [DSL] = [Report] = [I1] = [I2] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

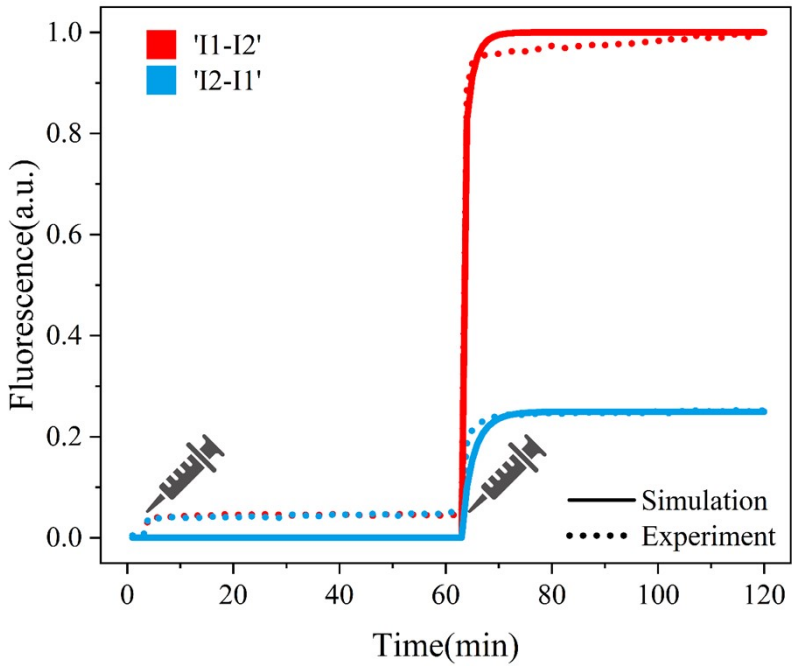

Fig. S4 Simulation and fluorescence kinetic reaction of the EHairpin-driven double-stem-loop programmable allosteric strategy. Red correlates with the experimental result of adding strand I1 at the first input and then strand I2 at the second input; blue correlates with the experimental result of adding strand I2 at the first input and then strand I1 at the second input. [DSL] = [EHairpin] = [Report] = [I1] = [I2] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

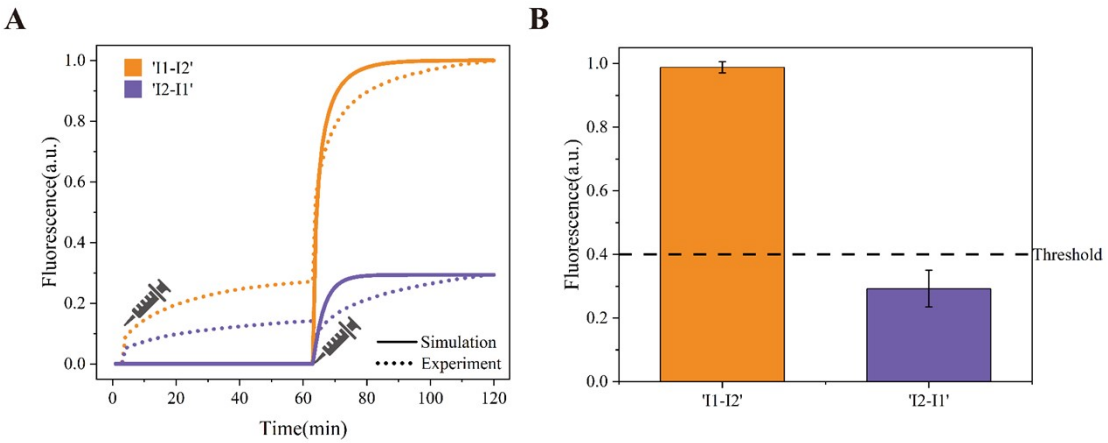

Fig. S5 Implementation of EHairpin-driven double-stem-loop programmable allosteric strategy with different base sequences. (A) Simulation and fluorescence kinetic curves. (B) Histogram of the output fluorescence signal. The orange color corresponds to the experimental result of adding strand I1 at the first input and then strand I2 at the second input; the purple color corresponds to the experiment result of adding strand I2 at the first input and then strand I1 at the second input. The black dashed line indicates a threshold of 0.4, which is used to differentiate between output results 0 and 1. [DSL] = [EHairpin] = [Report] = [I1] = [I2] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

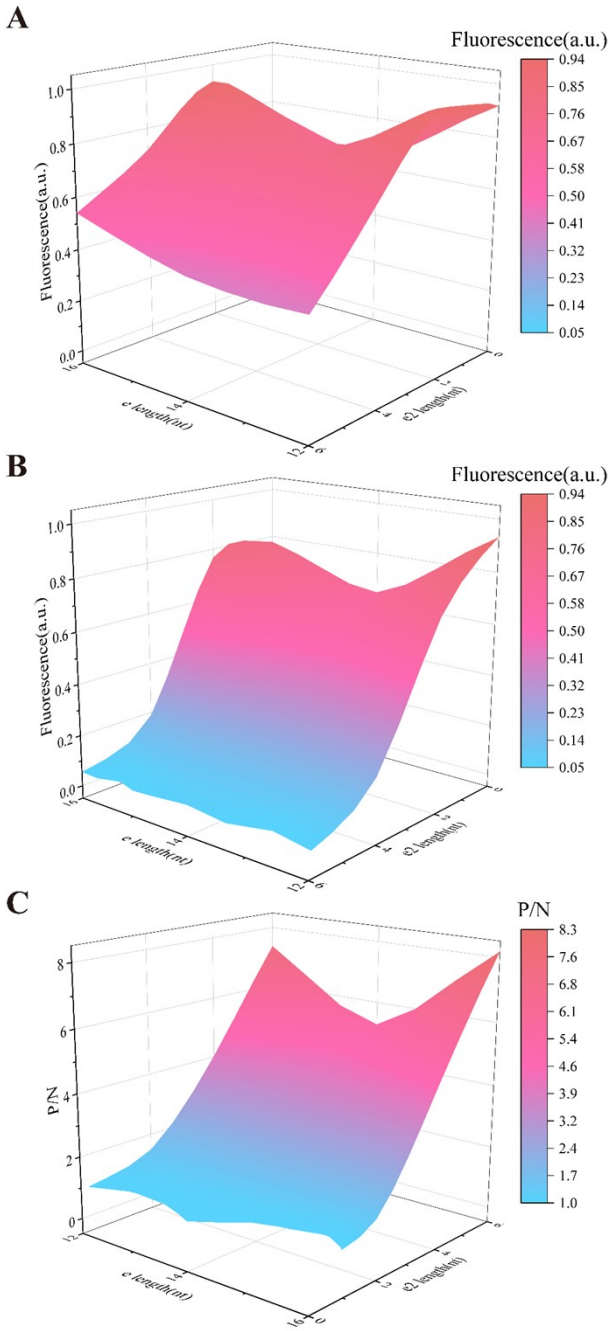

Fig. S6 Conditional optimization of EHairpin structures for the EHairpin-driven double-stem-loop programmable allosteric strategy. Fluorescence experiment results for different domain e and domain e2 base numbers, (A) indicates the fluorescence experiment results of adding strand I1 reaction first for 1 h and then strand I2 reaction for 1 h (i.e., P, color mapping: P), (B) indicates the fluorescence experiment results of adding strand I2 reaction first for 1 h and then strand I1 reaction for 1 h (i.e., N, color mapping: N), and (C) indicates the fluorescence experiment results of the corresponding signal-to-noise ratio (SNR) (i.e., P/N, color mapping: P/N). [DSL] = [EHairpin] = [Report] = [I1] = [I2] = 200 nM, and a.u. = arbitrary units.

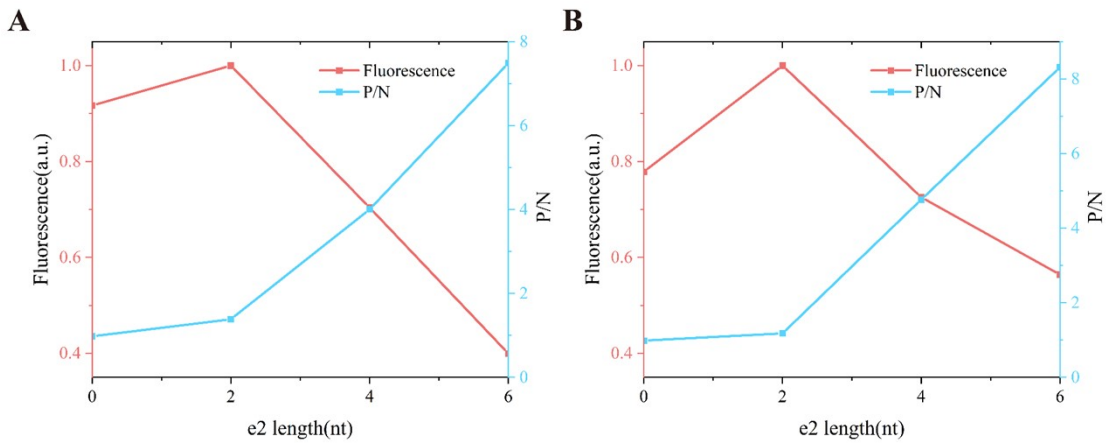

Fig. S7 Fluorescence and SNR change curves for different domain e2 base lengths of the EHairpin-driven double-stem-loop programmable allosteric strategy. The fluorescence and SNR curves in the case of domain e base length of (A) 12 nt, and (B) 16 nt both intersect when domain e2 is 4 nt. [DSL] = [EHairpin] = [Report] = [I1] = [I2] = 200 nM, and a.u. = arbitrary units.

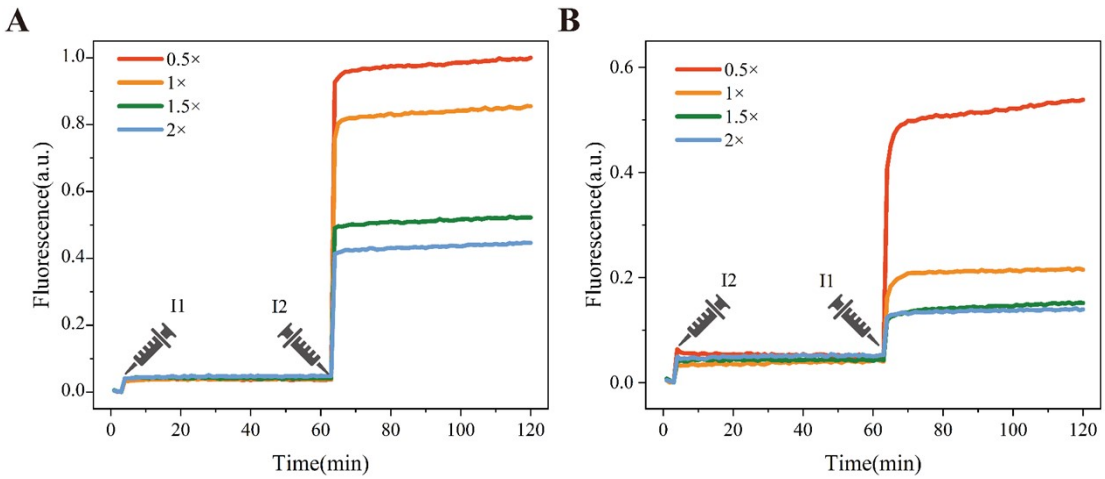

Fig. S8 Probe analysis of EHairpin concentrations for the EHairpin-driven double-stem-loop programmable allosteric strategy ([EHairpin] = 0.5×, 1×, 1.5×, 2×, where 1× = 200 nM). In the EHairpin different concentration probe experiments, (A) shows the real-time fluorescence kinetic curves of adding in the order of 'I1-I2', and (B) shows the real-time fluorescence kinetic curves of adding in the order of 'I2-I1'. The red, orange, green, and blue curves correspond to the fluorescence experiment results when the EHairpin concentration is 0.5, 1, 1.5, and 2 times, respectively. [DSL] = [Report] = [I1] = [I2] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

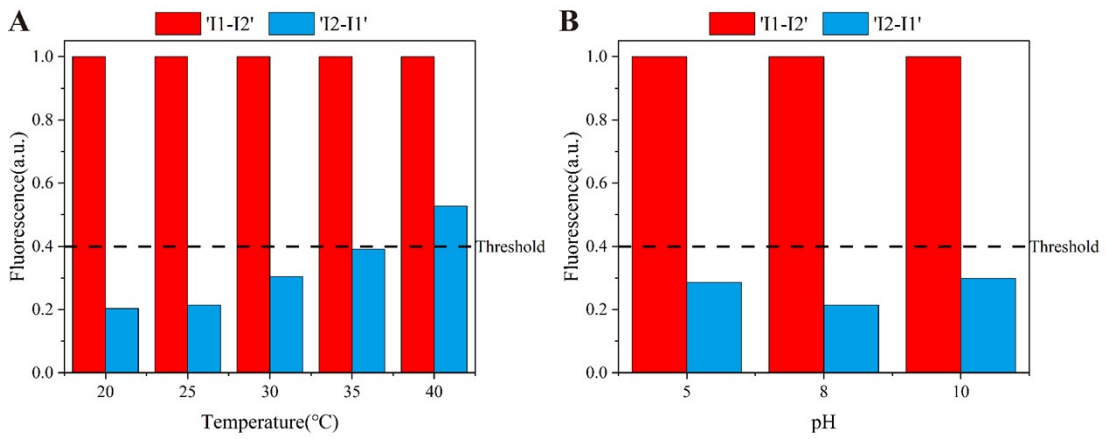

Fig. S9 Conditional exploration of the EHairpin-driven double-stem-loop programmable allosteric strategy under different temperatures and pH. (A) Histogram of the output fluorescence signals at temperatures of 20, 25, 30, 35 and 40°C. (B) Histogram of the output fluorescence signals at pH of 5, 8 and 10. Red correlates with the experimental result of adding strand I1 at the first input and then strand I2 at the second input; blue correlates with the experimental result of adding strand I2 at the first input and then strand I1 at the second input. The black dashed line indicates a threshold of 0.4, which is used to differentiate between output results 0 and 1. [DSL] = [EHairpin] = [Report] = [I1] = [I2] = 200 nM, and a.u. = arbitrary units.

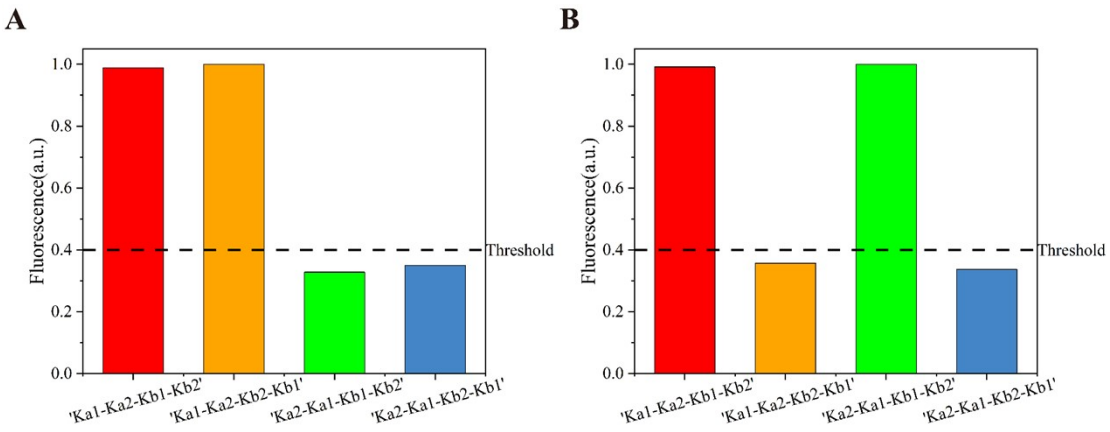

Fig. S10 Histograms of the output fluorescence signals under different input strand orders. (A) corresponds to the FAM fluorophore, and (B) corresponds to the Cy5 fluorophore. Red color corresponds to the experiment results of sequential addition of strand Ka1, Ka2, Kb1, Kb2; orange color corresponds to the experiment results of sequential addition of strand Ka1, Ka2, Kb2, Kb1; green color corresponds to the experiment results of sequential addition of strand Ka2, Ka1, Kb1, Kb2; blue color corresponds to the experiment results of sequential addition of strand Ka2, Ka1, Kb2, Kb1. The black dashed line indicates a threshold of 0.4, which is used to differentiate between output results 0 and 1. [DSL1] = [DSL2] = [EHairpin1] = [EHairpin2] = [Report1] = [Report2] = [Ka1] = [Ka2] = [Kb1] = [Kb2] = 200 nM, and a.u. = arbitrary units.

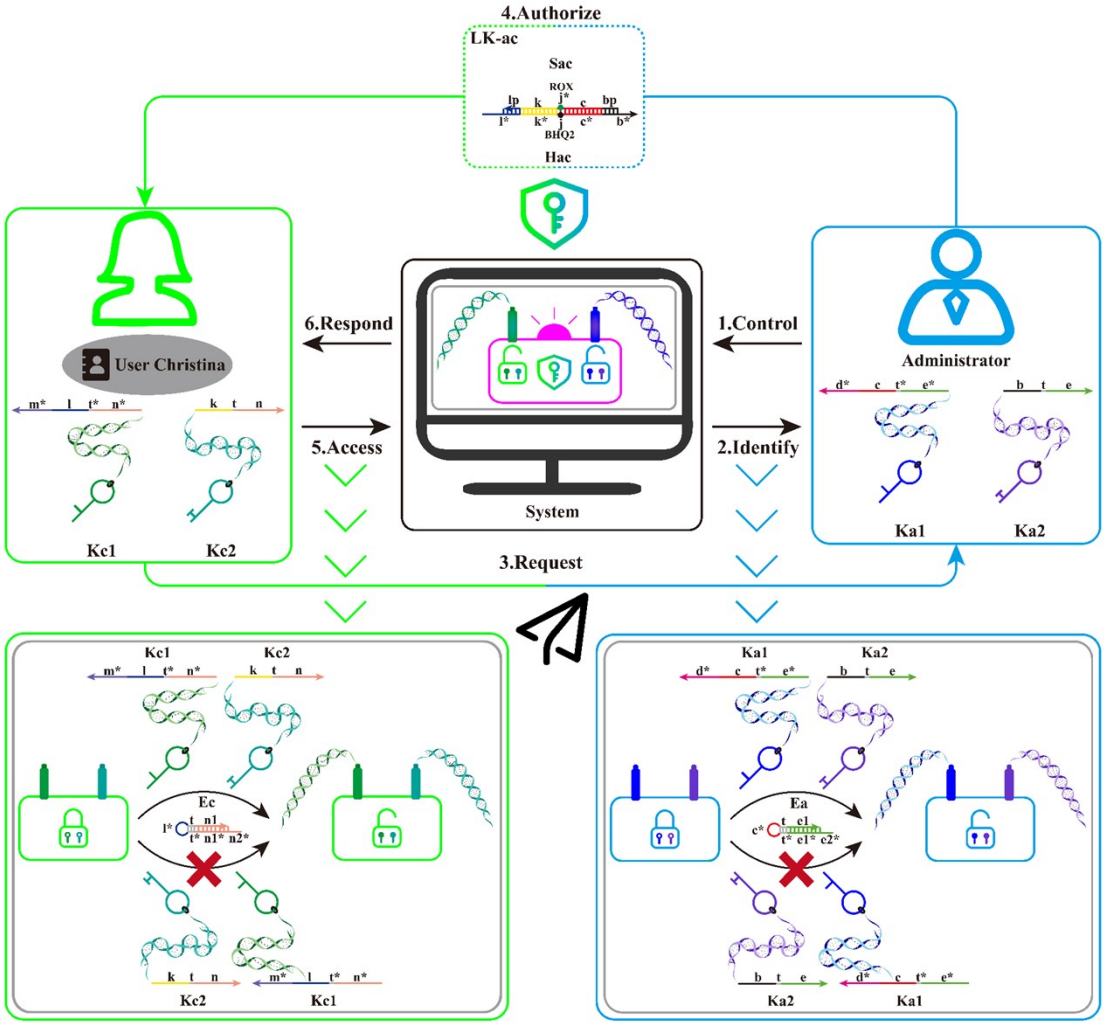

Fig. S11 Detailed workflow for user Christina to access the system. This workflow is divided into six steps: control, authentication, request, authorization, access, and response. Domain e consists of domain e1 and domain e2; domain n consists of domain n1 and domain n2.

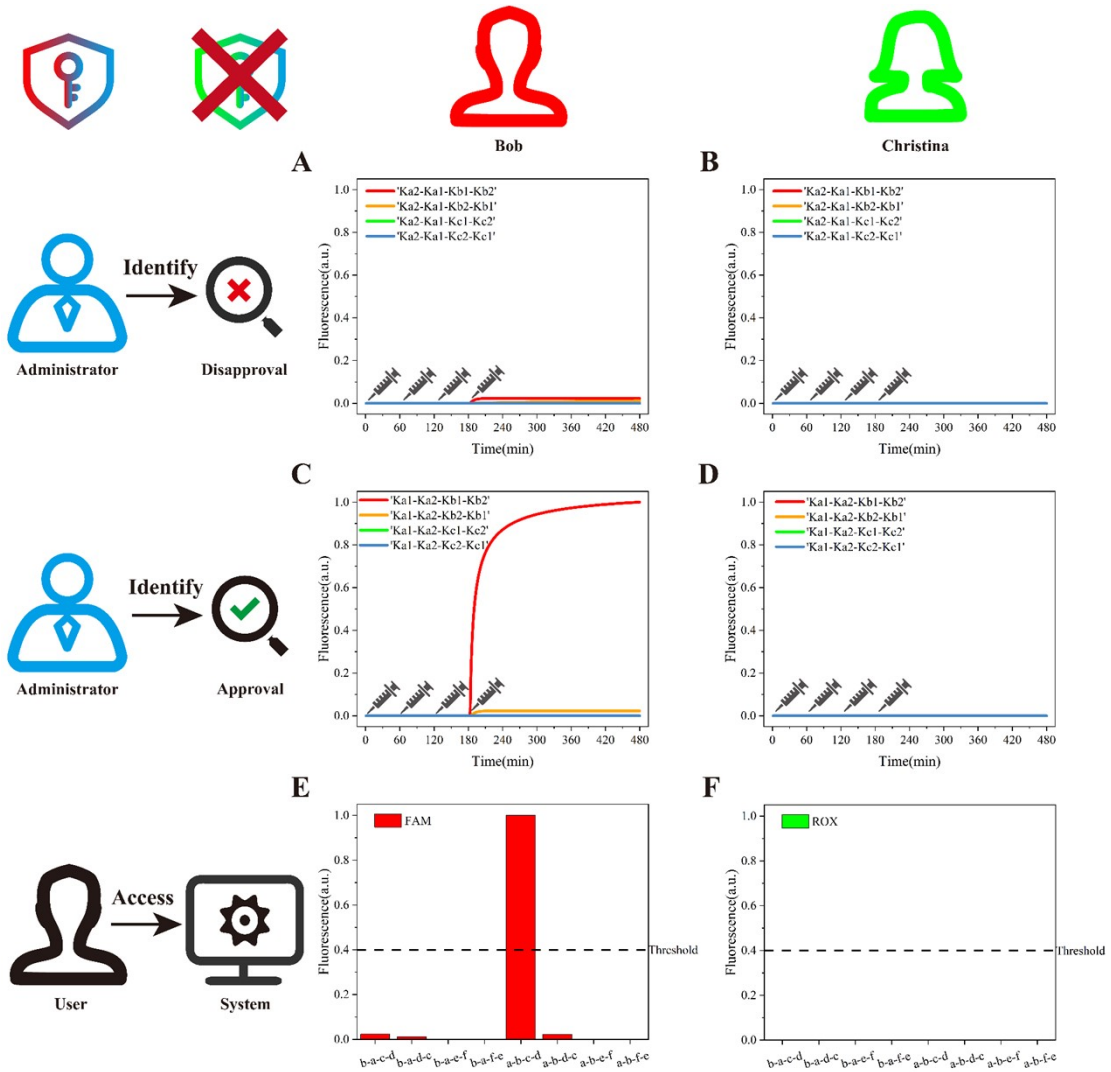

Fig. S12 Fluorescence analysis of different users accessing the system in the presence of authorization key only for Bob. Fluorescence kinetic curves of (A) user Bob, and (B) user Christina accessing the system when administrator authentication had failed in the presence of authorization key only for Bob. Fluorescence kinetic curves of (C) user Bob, and (D) user Christiana accessing the system when administrator authentication had been successful in the presence of authorization key only for Bob. Histograms of the output signals after (E) user Bob, and (F) user Christina access the system with authorization key only for Bob. In (E) and (F), a represents strand Ka1, b represents strand Ka2, c represents strand Kb1, d represents strand Kb2, e represents strand Kc1 and f represents strand Kc2. The black dashed line indicates a threshold of 0.4, which is used to differentiate between output results 0 and 1. [DSL1] = [DSL2] = [DSL3] = [EHairpin1] = [EHairpin2] = [EHairpin3] = [LK-ab] = [LK-ac] = [Ka1] = [Ka2] = [Kb1] = [Kb2] = [Kc1] = [Kc2] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

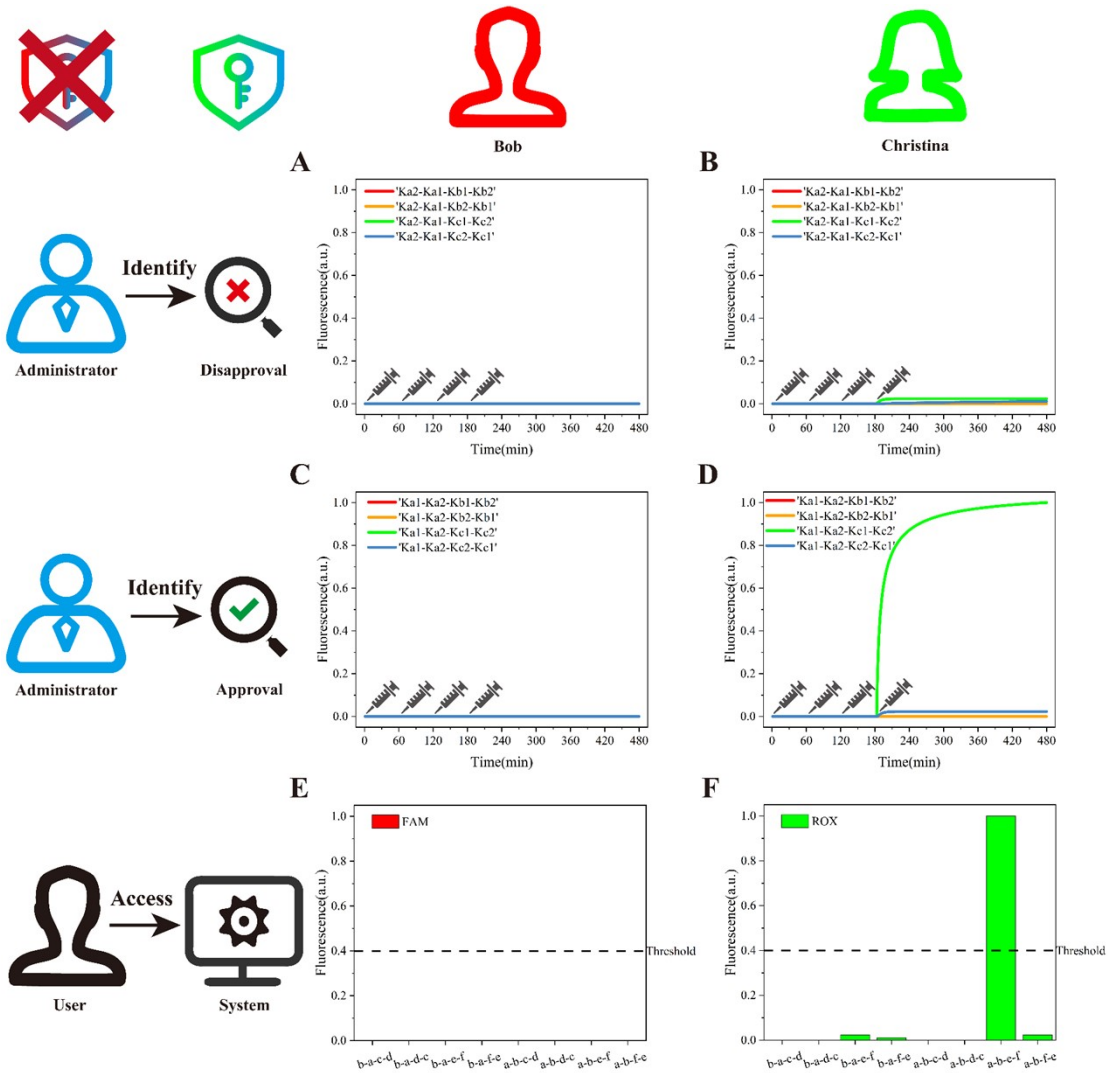

Fig. S13 Fluorescence analysis of different users accessing the system in the presence of authorization key only for Christina. Fluorescence kinetic curves of (A) user Bob, and (B) user Christina accessing the system when administrator authentication had failed in the presence of authorization key only for Christina. Fluorescence kinetic curves of (C) user Bob, and (D) user Christiana accessing the system when administrator authentication had been successful in the presence of authorization key only for Christina. Histograms of the output signals after (E) user Bob, and (F) user Christina access the system with authorization key only for Christina. In (E) and (F), a represents strand Ka1, b represents strand Ka2, c represents strand Kb1, d represents strand Kb2, e represents strand Kc1 and f represents strand Kc2. The black dashed line indicates a threshold of 0.4, which is used to differentiate between output results 0 and 1. [DSL1] = [DSL2] = [DSL3] = [EHairpin1] = [EHairpin2] = [EHairpin3] = [LK-ab] = [LK-ac] = [Ka1] = [Ka2] = [Kb1] = [Kb2] = [Kc1] = [Kc2] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

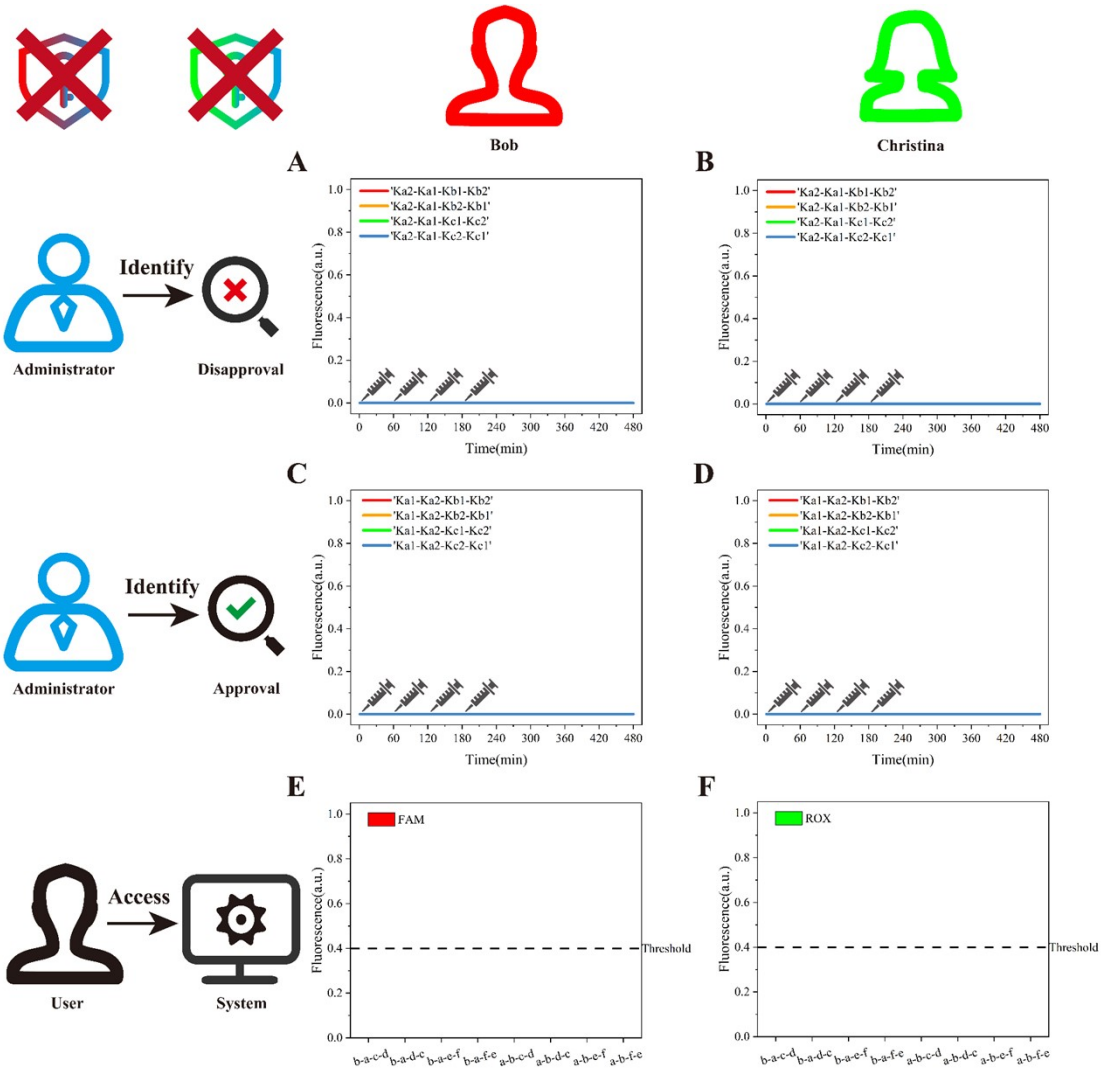

Fig. S14 Fluorescence analysis of different users accessing the system without any authorization key. Fluorescence kinetic curves of (A) user Bob, and (B) user Christina accessing the system when administrator authentication had failed without any authorization key. Fluorescence kinetic curves of (C) user Bob, and (D) user Christiana accessing the system when administrator authentication had been successful without any authorization key. Histograms of the output signals after (E) user Bob, and (F) user Christina access the system without any authorization key. In (E) and (F), a represents strand Ka1, b represents strand Ka2, c represents strand Kb1, d represents strand Kb2, e represents strand Kc1 and f represents strand Kc2. The black dashed line indicates a threshold of 0.4, which is used to differentiate between output results 0 and 1. [DSL1] = [DSL2] = [DSL3] = [EHairpin1] = [EHairpin2] = [EHairpin3] = [LK-ab] = [LK-ac] = [Ka1] = [Ka2] = [Kb1] = [Kb2] = [Kc1] = [Kc2] = 200 nM, and a.u. = arbitrary units. The scanning interval was once per min.

Supplementary Text S1 Reaction Simulations Model

In the detailed model, the following reactions were used to model the desired pathways:

$$Hairpin + I \xrightarrow{k_{h1}} M1 \quad (1)$$

$$DSL + I1 \xrightarrow{k_1} Intermediate1 \quad (2)$$

$$Intermediate1 + I2 \xrightarrow{k_2} Intermediate2 \quad (3)$$

$$DSL1 + Ka1 \xrightarrow{k_1} IA1 \quad (4)$$

$$IA1 + Ka2 \xrightarrow{k_2} IA2 \quad (5)$$

$$CDSL2 + CKb1 \xrightarrow{k_4} CIB1 \quad (6)$$

$$CIB1 + CKb2 \xrightarrow{k_5} CIB2 \quad (7)$$

$$DSL2 + Kb1 \xrightarrow{k_1} IB1 \quad (8)$$

$$IB1 + Kb2 \xrightarrow{k_2} IB2 \quad (9)$$

$$DSL3 + Kc1 \xrightarrow{k_1} IC1 \quad (10)$$

$$IC1 + Kc2 \xrightarrow{k_2} IC2 \quad (11)$$

The following reactions were used to simulate signal inhibition and substrates loss:

$$EHairpin + I1 \xrightarrow{k_{s1}} EI \quad (12)$$

$$EHairpin + I2 \xrightarrow{k_{s2}} W1 \quad (13)$$

$$W1 + I1 \xrightarrow{k_{s3}} W2 \quad (14)$$

$$EHairpin1 + Ka1 \xrightarrow{k_{s1}} EKa \quad (15)$$

$$EHairpin1 + Ka2 \xrightarrow{k_{s2}} WA1 \quad (16)$$

$$WA1 + Ka1 \xrightarrow{k_{s3}} WA2 \quad (17)$$

$$CEHairpin2 + CKb1 \xrightarrow{k_{s4}} CEKb \quad (18)$$

$$CEHairpin2 + CKb2 \xrightarrow{k_{s5}} CWB1 \quad (19)$$

$$CWB1 + CKb1 \xrightarrow{k_{s6}} CWB2 \quad (20)$$

$$EHairpin2 + Kb1 \xrightarrow{k_{s1}} EKb \quad (21)$$

$$EHairpin2 + Kb2 \xrightarrow{k_{s2}} WB1 \quad (22)$$

$$WB1 + Kb1 \xrightarrow{k_{s3}} WB2 \quad (23)$$

$$EHairpin3 + Kc1 \xrightarrow{k_{s1}} EKc \quad (24)$$

$$EHairpin3 + Kc2 \xrightarrow{k_{s2}} WC1 \quad (25)$$

$$WC1 + Kc1 \xrightarrow{k_{s3}} WC2 \quad (26)$$

The following reactions were used to simulate output signal generation:

$$M1 + R \xrightarrow{k_{h2}} M2 + F \quad (27)$$

$$Intermediate2 + Report \xrightarrow{k_3} ODSL + S \quad (28)$$

$$IA2 + Report1 \xrightarrow{k_3} ODSL1 + FAM \quad (29)$$

$$CIB2 + CReport2 \xrightarrow{k_6} CODSL2 + Cy5 \quad (30)$$

$$IA2 + LK - ab + IB2 \xrightarrow{k_7} PAB + Sab \quad (31)$$

$$IA2 + LK - ac + IC2 \xrightarrow{k_7} PAC + Sac \quad (32)$$

According to the above reaction model, we can find there are three types of

reactions. The first is a reaction of two reactants and one product that can be abstracted into the following equation:

$$A + B \xrightarrow{k_{r1}} C \tag{33}$$

The second is a reaction of two reactants and two products that can be abstracted into the following equation:

$$A + B \xrightarrow{k_{r2}} C + D \tag{34}$$

The third is a reaction of three reactants and two products that can be abstracted into the following equation:

$$A + B + C \xrightarrow{k_{r3}} D + E \tag{35}$$

Therefore, their rate equations can be derived separately by the above equations (33)(34)(35). For example, the rate equation of the first reaction type can be derived:

$$\frac{d[C]}{dt} = k_{r1}[A][B] \tag{36}$$

The rate equation of the second reaction type can be derived:

$$\frac{d[C]}{dt} = \frac{d[D]}{dt} = k_{r2}[A][B] \tag{37}$$

The rate equation of the third reaction type can be derived:

$$\frac{d[D]}{dt} = \frac{d[E]}{dt} = k_{r3}[A][B][C] \tag{38}$$

When t = 0, the initial concentration of the substrates is set to be A[0], B[0], or C[0], and the above differential equations (36)(37)(38) can be converted to the following difference equations by discretization.

The first reaction type results in the following difference equations:

$$A[i+1] = A[i] - k_{r1}[A][B] \tag{39}$$

$$B[i+1] = B[i] - k_{r1}[A][B] \tag{40}$$

$$C[i+1] = C[i] + k_{r1}[A][B] \tag{41}$$

The second reaction type results in the following difference equations:

$$A[i+1] = A[i] - k_{r2}[A][B] \tag{42}$$

$$B[i+1] = B[i] - k_{r2}[A][B] \tag{43}$$

$$C[i+1] = C[i] + k_{r2}[A][B] \tag{44}$$

$$D[i+1] = D[i] + k_{r2}[A][B] \tag{45}$$

The third reaction type results in the following difference equations:

$$A[i+1] = A[i] - k_{r3}[A][B][C] \tag{46}$$

$$B[i+1] = B[i] - k_{r3}[A][B][C] \tag{47}$$

$$C[i+1] = C[i] - k_{r3}[A][B][C] \tag{48}$$

$$D[i+1] = D[i] + k_{r3}[A][B][C] \tag{49}$$

$$E[i+1] = E[i] + k_{r3}[A][B][C] \tag{50}$$

According to the above equations, we calculate the concentration of reactants and products at each point in time by python program. In the python program, we first set

the initial concentration of each reactant, and then according to the input order and addition time of the reaction, we successively set the initial concentration for different inputs, and calculate the differential equations at each point in time, to get the final simulation experiment results.

For the reaction model of the exploration on the loop domain base numbers of the hairpin structure, all possible reactions that can occur are (1) (27).

For the reaction model of the conformational changes in DSL structures, all possible reactions that can occur are (2) (3) (28).

For the reaction model of the EHairpin-driven double-stem-loop programmable allosteric strategy, all possible reactions that can occur are (2) (3) (12) (13) (14) (28).

For the reaction model of the molecular-switch-response circuit for multiple input signals, all possible reactions that can occur are (4) (5) (6) (7) (15) (16) (17) (18) (19) (20) (29) (30).

For the reaction model of the EHairpin-driven molecular secure access control system, all possible reactions that can occur are (4) (5) (8) (9) (10) (11) (15) (16) (17) (21) (22) (23) (24) (25) (26) (31) (32).

Supplementary Table S1 - Table S6

Table S1 Sequence of conformational changes in DSL structures.

Strand	Sequence (5'->3')
L1	GAGGTGAGATGGCAGTGGTAGTAGTAGGAGTGACTCGGTC TCTCTCTGCTCCGAGTCACTCTTGGTGTGTGTGTGTG
L2	CACACACACACACCTTCTACTACTACCTTTTTTTTACTGCC ATCTCACCTC
I1	CACACACACACACCAAGAGTGACTCGGAGCAGAGAGAGA
I2	GGTAGTAGTAGTTGGTGTGTGTGTGTG
S	AGTAGGAGTGACTCGG-FAM
H	BHQ1-CCGAGTCACTCCTACTACTACC
Sa	TTTTTTTTTTTTTTGAGGTGAGATGGCAGT
Sb	GGTAGTAGTAGTTTTTTTTTTTTT
Sc	TTTTTTTTTTTTTTGAGTGACTCGG
Se	TTTTTTTTTTTGGTGTGTGTGTGTG

Table S2 Sequence of loop domain base length probing of hairpin structures.

Strand	Sequence (5'->3')
Hairpin-6	GGTAGTAGTAGGAGTGACTCGGTGCTCTCCGAGTCACTC
Hairpin-8	GGTAGTAGTAGGAGTGACTCGGTGCTCTCTCCGAGTCACTC
Hairpin-10	GGTAGTAGTAGGAGTGACTCGGTGCTCTCTCTCCGAGTCACTC
Hairpin-12	GGTAGTAGTAGGAGTGACTCGGTGCTCTCTCTCTCCGAGTCACTC
Hairpin-14	GGTAGTAGTAGGAGTGACTCGGTGCTCTCTCTCTCTCCGAGTCACTC
Hairpin-16	GGTAGTAGTAGGAGTGACTCGGTGCTCTCTCTCTCTCTCCGAGTCACTC
Hairpin-18	GGTAGTAGTAGGAGTGACTCGGTGCTCTCTCTCTCTCTCTCCGAGTCACTC
I-6	GAGTGACTCGGAGAGCA
I-8	GAGTGACTCGGAGAGAGCA
I-10	GAGTGACTCGGAGAGAGAGCA
I-12	GAGTGACTCGGAGAGAGAGAGCA
I-14	GAGTGACTCGGAGAGAGAGAGAGCA
I-16	GAGTGACTCGGAGAGAGAGAGAGAGCA
I-18	GAGTGACTCGGAGAGAGAGAGAGAGAGCA
FAM	FAM-GGTAGTAGTAG
BHQ1	ACTCCTACTACTACC-BHQ1

Table S3 Sequence of EHairpin-driven double-stem-loop programmable allosteric strategy.

(1) One base sequence is as follows:

Strand	Sequence (5'->3')
L1	GAGGTGAGATGGCAGTGGTAGTAGTAGGAGTGACTCGGTC TCTCTCTGCTCCGAGTCACTCTTGGTGTGTGTGTGTG
L2	CACACACACACACCTTCTACTACTACCTTTTTTTTACTGCC ATCTCACCTC
I1	CACACACACACACCAAGAGTGACTCGGAGCAGAGAGAGA
I2	GGTAGTAGTAGTTGGTGTGTGTGTGTG
E	CACACACACACACCAACCGAGTCACTCTTGGTGTGTGTG
S	AGTAGGAGTGACTCGG-FAM
H	BHQ1-CCGAGTCACTCCTACTACTACC

(2) Another different base sequence is as follows:

Strand	Sequence (5'->3')
L1	GAGGTGAGATGGCAGTCTTGCTGACTTTCAGTGTCATGACT CTGTACTTGCATGACACTGATTGACGACTGGTGCCT
L2	AGGCACCAGTCGTCTTAAGTCAGCAAGTTTTTTTTACTGCC ATCTCACCTC
I1	AGGCACCAGTCGTCAATCAGTGTCATGCAAGTACAGAGT
I2	CTTGCTGACTTTTGACGACTGGTGCCT
E	AGGCACCAGTCGTCAACATGACACTGATTGACGACTGGT
S	GACTTTCAGTGTCATG-Cy5
H	BHQ3-CATGACACTGAAAGTCAGCAAG

Table S4 Sequence of conditional optimization of the EHairpin-driven double-stem-loop programmable allosteric strategy.

Strand	Sequence (5'->3')
L1-12	GAGGTGAGATGGCAGTGGTAGTAGTAGGAGTGAC TCGGTCTCTCTCTGCTCCGAGTCACTCTTGGTGTGT GTGTG
L1-14	GAGGTGAGATGGCAGTGGTAGTAGTAGGAGTGAC TCGGTCTCTCTCTGCTCCGAGTCACTCTTGGTGTGT GTGTGTG
L1-16	GAGGTGAGATGGCAGTGGTAGTAGTAGGAGTGAC TCGGTCTCTCTCTGCTCCGAGTCACTCTTGGTGTGT GTGTGTGTG
L2-12	CACACACACACCTTCTACTACTACCTTTTTTTTACT GCCATCTCACCTC
L2-14	CACACACACACACCTTCTACTACTACCTTTTTTTTA CTGCCATCTCACCTC
L2-16	CACACACACACACACCTTCTACTACTACCTTTTTTT TACTGCCATCTCACCTC
I1-12	CACACACACACCAAGAGTGACTCGGAGCAGAGAG AGA
I1-14	CACACACACACACCAAGAGTGACTCGGAGCAGAG AGAGA
I1-16	CACACACACACACACCAAGAGTGACTCGGAGCAG AGAGAGA
I2-12	GGTAGTAGTAGTTGGTGTGTGTGTG
I2-14	GGTAGTAGTAGTTGGTGTGTGTGTGTG
I2-16	GGTAGTAGTAGTTGGTGTGTGTGTGTGTG
E-12-6	CACACACACACCAACCGAGTCACTCTTGGTGTG
E-12-8	CACACACACACCAACCGAGTCACTCTTGGTGTGTG
E-12-10	CACACACACACCAACCGAGTCACTCTTGGTGTGTG TG
E-12-12	CACACACACACCAACCGAGTCACTCTTGGTGTGTG TGTG
E-14-8	CACACACACACACCAACCGAGTCACTCTTGGTGTG TG
E-14-10	CACACACACACACCAACCGAGTCACTCTTGGTGTG TGTG

E-14-12	CACACACACACACCAACCGAGTCACTCTTGGTGTG TGTGTG
E-14-14	CACACACACACACCAACCGAGTCACTCTTGGTGTG TGTGTGTG
E-16-10	CACACACACACACACCAACCGAGTCACTCTTGGTG TGTGTG
E-16-12	CACACACACACACACCAACCGAGTCACTCTTGGTG TGTGTGTG
E-16-14	CACACACACACACACCAACCGAGTCACTCTTGGTG TGTGTGTGTG
E-16-16	CACACACACACACACCAACCGAGTCACTCTTGGTG TGTGTGTGTGTG
S	AGTAGGAGTGACTCGG-FAM
H	BHQ1-CCGAGTCACTCCTACTACTACC

Table S5 Sequence of molecular-switch-response circuit for multiple input signals.

Strand	Sequence (5'->3')
La1	GAGGTGAGATGGCAGTGGTAGTAGTAGGAGTGACTCGGTC TCTCTCTGCTCCGAGTCACTCTTGGTGTGTGTGTGTG
La2	CACACACACACACCTTCTACTACTACCTTTTTTTTACTGCC ATCTCACCTC
Ka1	CACACACACACACCAAGAGTGACTCGGAGCAGAGAGAGA
Ka2	GGTAGTAGTAGTTGGTGTGTGTGTGTG
Ea	CACACACACACACCAACCGAGTCACTCTTGGTGTGTGTG
Sa	AGTAGGAGTGACTCGG-FAM
Ha	BHQ1-CCGAGTCACTCCTACTACTACC
Lb1	GAGGTGAGATGGCAGTCTTGCTGACTTTCAGTGTCATGACT CTGTACTTGCATGACACTGATTGACGACTGGTGCCT
Lb2	AGGCACCAGTCGTCTTAAGTCAGCAAGTTTTTTTTACTGCC ATCTCACCTC
Kb1	AGGCACCAGTCGTCAATCAGTGTCATGCAAGTACAGAGT
Kb2	CTTGCTGACTTTTGACGACTGGTGCCT
Eb	AGGCACCAGTCGTCAACATGACACTGATTGACGACTGGT
Sb	GACTTTCAGTGTCATG-Cy5
Hb	BHQ3-CATGACACTGAAAGTCAGCAAG

Table S6 Sequence of EHairpin-driven molecular security access control system.

Strand	Sequence (5'->3')
La1	GAGGTGAGATGGCAGTGGTAGTAGTAGGAGTGACTCGGTC TCTCTCTGCTCCGAGTCACTCTTGGTGTGTGTGTGTG
La2	CACACACACACACCTTCTACTACTACCTTTTTTTTACTGCC ATCTCACCTC
Ka1	CACACACACACACCAAGAGTGACTCGGAGCAGAGAGAGA
Ka2	GGTAGTAGTAGTTGGTGTGTGTGTGTG
Ea	CACACACACACACCAACCGAGTCACTCTTGGTGTGTGTG
Lb1	GAGGTGAGATGGCAGTCTTGCTGACTTTCAGTGTCATGACT CTGTACTTGCATGACACTGATTGACGACTGGTGCCT
Lb2	AGGCACCAGTCGTCTTAAGTCAGCAAGTTTTTTTTACTGCC ATCTCACCTC
Kb1	AGGCACCAGTCGTCAATCAGTGTCATGCAAGTACAGAGT
Kb2	CTTGCTGACTTTTGACGACTGGTGCCT
Eb	AGGCACCAGTCGTCAACATGACACTGATTGACGACTGGT
Sab	AGTAGGAGTGACTCGGT-FAM-AGGCTTGCTGACTTTCAGT
Hab	CATGACACTGAAAGTCAGCAAGCCT-BHQ1- ACCGAGTCACTCCTACTACTACC
Lc1	GAGGTGAGATGGCAGTCAGTCGTCAGTGAAGTCGTCGGTC GACTAGATGTCCGACGACTTCTTCAGATCAAGCTCAC
Lc2	GTGAGCTTGATCTGTTACTGACGACTGTTTTTTTTACTGCC ATCTCACCTC
Kc1	GTGAGCTTGATCTGAAGAAGTCGTCGGACATCTAGTCGA
Kc2	CAGTCGTCAGTTTCAGATCAAGCTCAC
Ec	GTGAGCTTGATCTGAACCGACGACTTCTTCAGATCAAGC
Sac	AGTAGGAGTGACTCGGT-ROX-AGGCAGTCGTCAGTGAAGT
Hac	CCGACGACTTCACTGACGACTGCCT-BHQ2- ACCGAGTCACTCCTACTACTACC