

Supplementary information

1. Selection procedures and conditions in every round of WB-SELEX

Table S1. The selection conditions of aptamers to *P. aeruginosa*.

Round	Bacterial cells (μl)	ssDNA (pmol)	Binding time (h)	Washing times	PCR cycles
1	50+50+50 ^a	1300	0.5	0	30
2	500	800	1.5	1	25
3	500	750	1.5	1	25
4	500	625	1	2	25
5	500	725	1	2	20
6	500	300	1	2	20
7	200	300	0.5	3	20
8	200	300	0.5	3	15
9	100+100+10 0 ^b	300	1	0	15
10	100	300	0.5	3	15
11	50	100	0.5	4	15
12	50	100	0.5	5	15
13	100+100+10 0 ^b	50	1	0	15
14	100+100+10 0 ^b	50	1.5	0	15
15	50	50	0.5	6	15

^a Volumes of each counter-selection bacteria (*E. coli* ATCC 25922, *B. subtilis* ATCC 6051 and *S. aureus* ATCC 12600) added in the reaction system in the first round. The volume is as equal as 50 μl and the cell density from the culture of each counter-selection bacteria was at 1×10^7 CFU ml^{-1} .

^b Volumes of each counter-selection bacteria (*E. coli* ATCC 25922, *B. subtilis* ATCC 6051 and *S. aureus* ATCC 12600) added in the reaction systems at the other rounds of counter-selection. The volume is as equal as 100 μl and the cell density from the culture of each counter-selection bacteria was at 1×10^7 CFU ml^{-1} .

2. Sequence abundances for five aptamer candidates identified by HTS

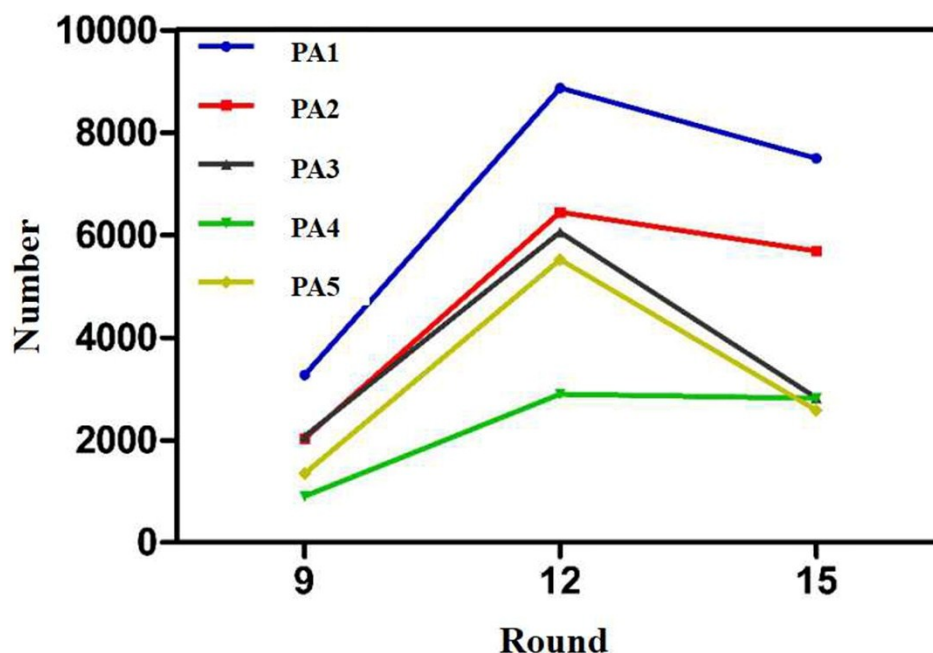


Fig. S1. Strand numbers for aptamer candidates with top five highest abundances in ssDNA pools from the 9th, the 12th and the 15th rounds revealed by HTS. The strand number for PA1, PA2, PA3 PA4, PA5 in the ssDNA pool from the 9th round was 3273, 2028, 2071, 902 and 1349, respectively. The total strand number obtained by HTS was 1820659. The strand number for PA1, PA2, PA3 PA4, PA5 in the ssDNA pool from the 12th round was 8874, 6446, 6056, 2898 and 5521, respectively. The total strand number obtained by HTS was 1712478. The strand number for PA1, PA2, PA3 PA4, PA5 in the ssDNA pool from the 15th round was 7498, 5686, 2824, 2814 and 2583, respectively. The total strand number obtained by HTS was 1729984. The abundances of these aptamer candidates reached their maximum at the round of 12th.

3. Secondary structure of aptamer candidates

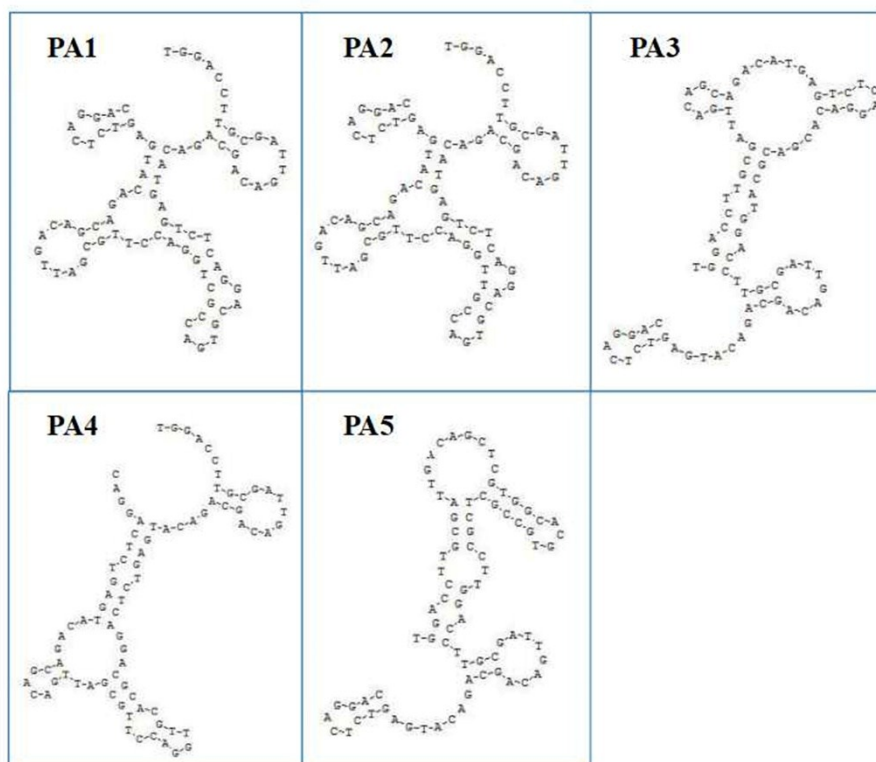


Fig. S2. Secondary stem-loop structure for each of the five aptamer candidates given by *Mfold*.

4. Characterization of synthesized CDs and aptamer-CDs conjugates

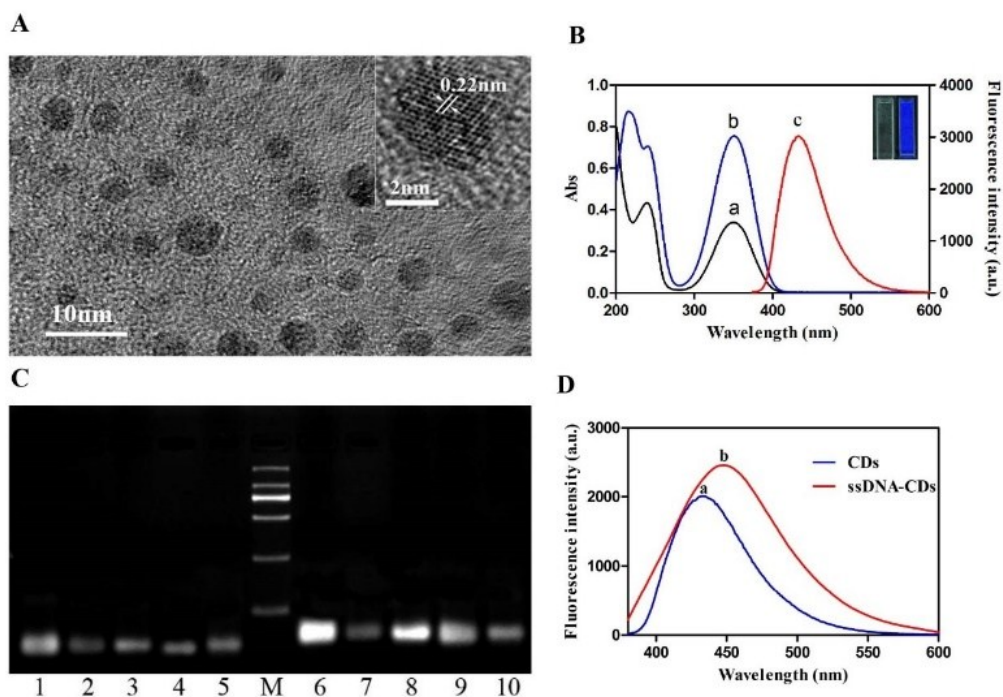


Fig. S3. (A) The HRTEM characterization of CDs, the average diameter of as-prepared CDs in this work was 4.05 nm with the lattice spacing of 0.22 nm; (B) UV-vis spectra (curve a, black), photoluminescence excitation (curve b, blue) and photoluminescence emission spectra (curve c, red) of CDs. In the UV-vis spectra, the peak wavelength was at 350nm (Fig. 3S-B, curve a). The fluorescence excitation and emission spectra demonstrated that the maximum excitation wavelength of the as-prepared CDs was 355 nm (Fig. 3S-B, curve b) and the maximum emission wavelength of them was 437 nm (Fig. 3S-B, curve c). The CDs could exhibit a blue color under the irradiation of a UV lamp; (C) Agarose gel electrophoresis of aptamer candidates and aptamer-CDs conjugates. Lane 1-5: ssDNA aptamer candidates of PA1, PA2, PA3, PA4, PA5, respectively. Lane 6-10: PA1-CDs, PA2-CDs, PA3-CDs, PA4-CDs PA5-CDs, respectively. M: DL2000 DNA marker, 100bp, 250bp, 500bp, 750bp, 1000bp, 2000bp, from bottom to top. (D) The redshift of photoluminescence emission peak for PA1-CDs as a representative.

5. Determination of K_d values for aptamer candidates

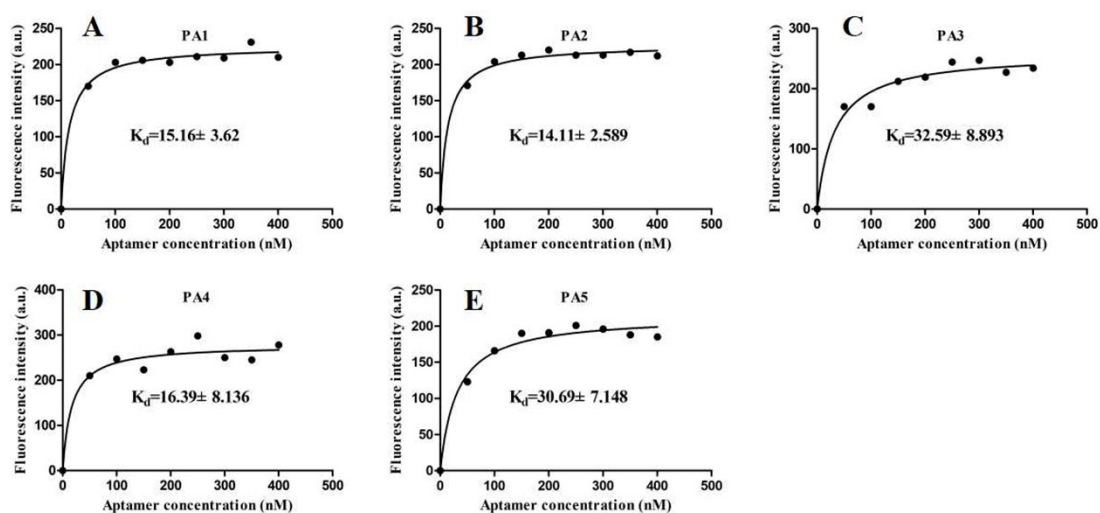


Fig. S4. Binding affinity of each aptamer candidate with the cells of *P. aeruginosa* determined by the corresponding aptamer-CDs probe. The equilibrium dissociation constants (K_d) were calculated by non-linear regression analysis.

6. Optimization of reacting time for the fluorescence assay

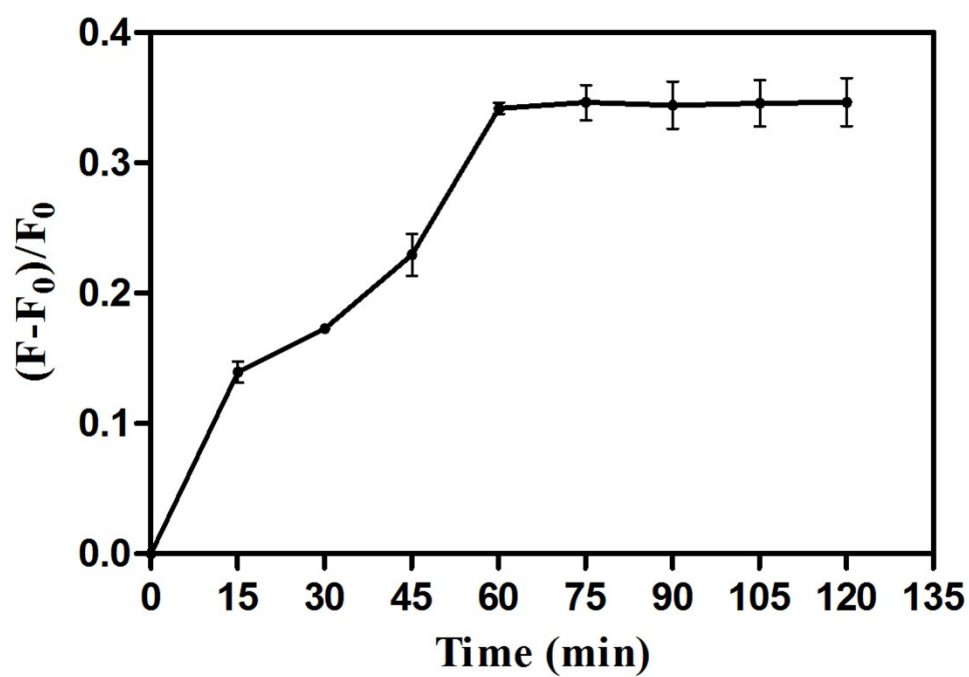


Fig. S5. Optimization of reacting time for the fluorescence assay.

7. Specificity of aptamer-CDs/GO system for *P. aeruginosa* ATCC27853 strain and different *P. aeruginosa* serotypes

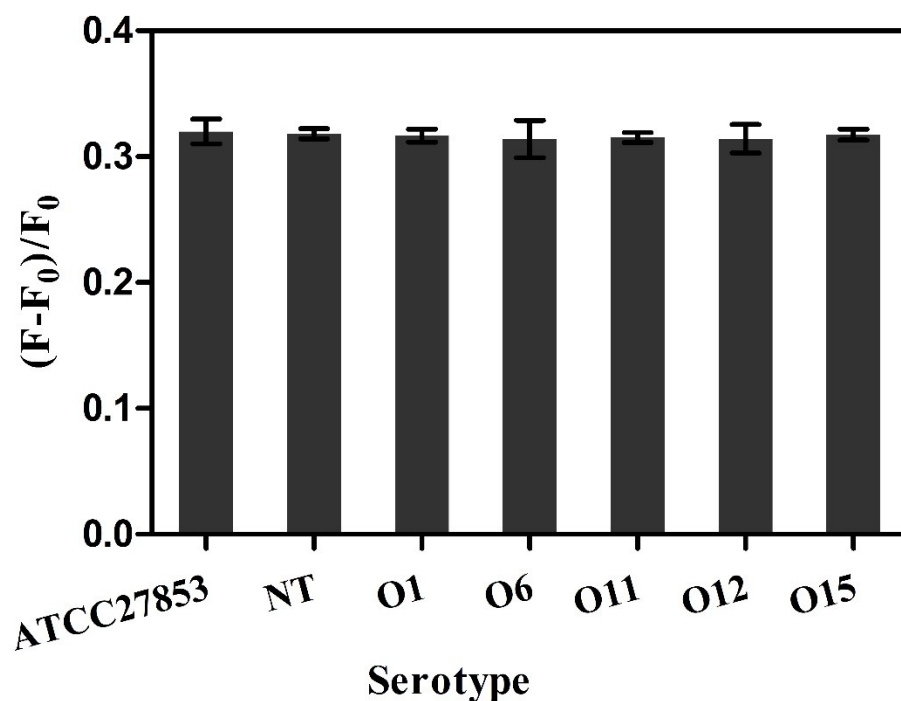


Fig. S6. Fluorescence recovery ratios of *P. aeruginosa* ATCC27853 strain and different *P. aeruginosa* serotypes. NT: not serotyped; O1: *P. aeruginosa* serotype O1; O6: *P. aeruginosa* serotype O6; O11: *P. aeruginosa* serotype O11; O12: *P. aeruginosa* serotype O12; O15: *P. aeruginosa* serotype O15. No significant difference among ATCC27853 strain and different *P. aeruginosa* serotypes was observed after calculated with the student's *t*-test.