

## Supporting Information

### Aptasensor for quantifying pancreatic polypeptide

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KEYWORDS: aptamer, biosensor, SELEX, pancreatic polypeptide, pancreatic cancer, gold nanoparticles, colorimetric aptasensor

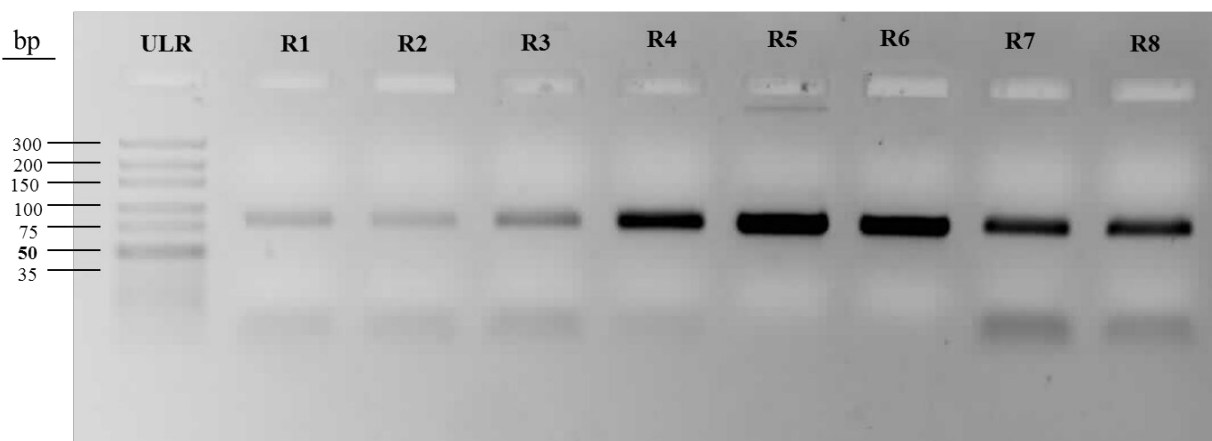
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**Table S1.** List of sequences of the ssDNA library and primers used in SELEX with corresponding modification.

Name	Sequence	Modification
D3 library	5'-GCTGTGTGACTCCTGCAA-N43-GCAGCTGTATCTTGTCTCC-3'	---
Forward primer	5'-GCTGTGTGACTCCTGCAA-3'	---
Phosphate-reverse primer	5'-GGAGACAAGATACAGCTGC-3'	5'-phosphate
Cy5-forward primer	5'-GCTGTGTGACTCCTGCAA-3'	5'-Cy5

**Table S2.** Summary for the SELEX rounds.

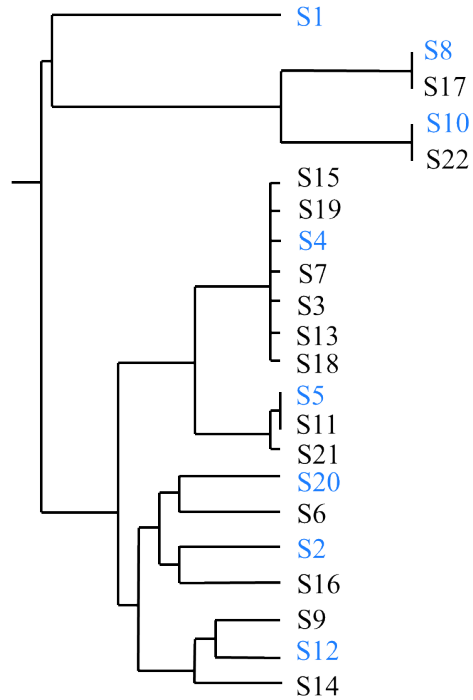
Round	Incubation				Washing		PCR		
	Target (nmol)	ssDNA (pmol)	Counter Target	Negative Selection	Conditions	Time	Number	Cycles	Volume (μL)
1	7.5	500	FCS (10%)	---	1mM CaCl <sub>2</sub> 1mM MgCl <sub>2</sub> 30 min, 25 °C, 800 rpm 200 μL total incubation volume	30 sec	3x	14	800
2	7.5	40		---		30 sec		15	
3	7.5	40		1x Empty beads		30 sec		18	
4	5	40		---		30 sec		18	
5	5	40		---		1 min		18	
6	5	40		1x Empty beads		1 min		18	
7	5	40		1x Empty beads		2 min		17	
8	5	40		1x Empty beads		2 min		22	



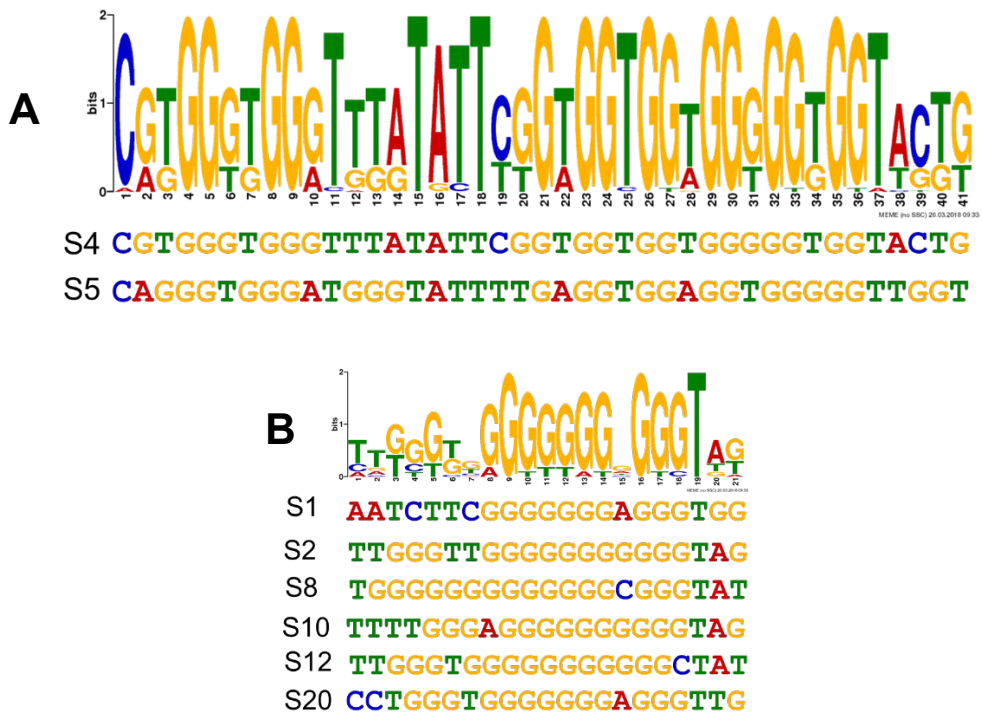
**Figure S1.** Progress of selection process. 4% agarose gel electrophoresis for PCR product of the selection rounds (R1, R2, R3, R4, R5, R6, R7 and R8) parallel to ultra-low range ladder (ULR). A single band of 80 bp corresponding to expected amplification product was detected in all lanes.

**Table S3.** List of unique sequences with the corresponding frequencies.

Name	Random region sequence	Frequency
S1	TGGCTTTGTTATTACTATTTTCAATCTTCGGGGGGGAGGGTGG	2/47
S2	TAAAAGATCTTGGGTGGGGGGGGGGGTAGAGCATCTTTGCTG	2/47
S3	CGTGGGTGGGCTTATATTCGGTGGTGGTGGGGGTGGTACTGTT	1/47
S4	CGTGGGTGGGTTTATATTCGGTGGTGGTGGGGGTGGTACTGTT	15/47
S5	CCAGGGTGGGATGGGTATTTTGAGGTGGAGGTGGGGGTGGTT	6/47
S6	TGCGATCCTGGGTAGGGTGGGTGGGTATTATGAGAGCTTGTT	1/47
S7	CGTGGGTGGGTTTATATTTGGTGGTGGTGGGGGTGGTACTGTT	2/47
S8	CGTTTTATAGATGGGGGGGGGGGGCGGGTATTTATGTAATTCGG	1/47
S9	TTCATAAATACATTTGGGCGGGTGTGGTGGGTTTTTTTTTTGA	1/47
S10	TGCTGTTTTGGGAGGGGGGGGGGTAGAAAACAGTCTAATGAG	2/47
S11	CCAGGGTGGGATAGGTATTTTGAGGTGGAGGTGGGGGTGGTT	1/47
S12	TGAACAAATGGATTTGGGTGGGGGGGGGGCTATTTGTGCGAGT	1/47
S13	CGTGGGTGGGTTTATGTTTCGGTGGTGGTGGGGGTGGTACTGTT	2/47
S14	CGGGTGGGGGGAGGGTGTGCTTAGAGTCGGTTTCCTAGGA	1/47
S15	CGTGGGTGGGTTTATACTCGGTGGTGGTGGGGGTGGTACTGTT	2/47
S16	ATTTGGGTGGGTGGGGGGTAACTAAGGTGTCACAATTAGAT	1/47
S17	GGGTTTTCAAGTGTGACTTAGCAGCGTCGGGTTGGGTGGGGGG	1/47
S18	CGTGGGTGGGTTTATATTCGGTGGCGGTGGGGGTGGTACTGTT	1/47
S19	CGTGGGTGGGTTTATATTCGGTGGTGTGGGGGTGGTACTGTT	1/47
S20	TGTGTGCCTGGGTGGGGGGAGGGTTGGTATAGAAACGTTGAA	1/47
S21	CCAAGGTGGGATGGGTATTTTGAGGTGGAGGTGGGGGTGGTT	1/47
S22	TGATTAAATAGGGTGGGTTTCGGGGGGGTGTCGGGTAGGTGAT	1/47



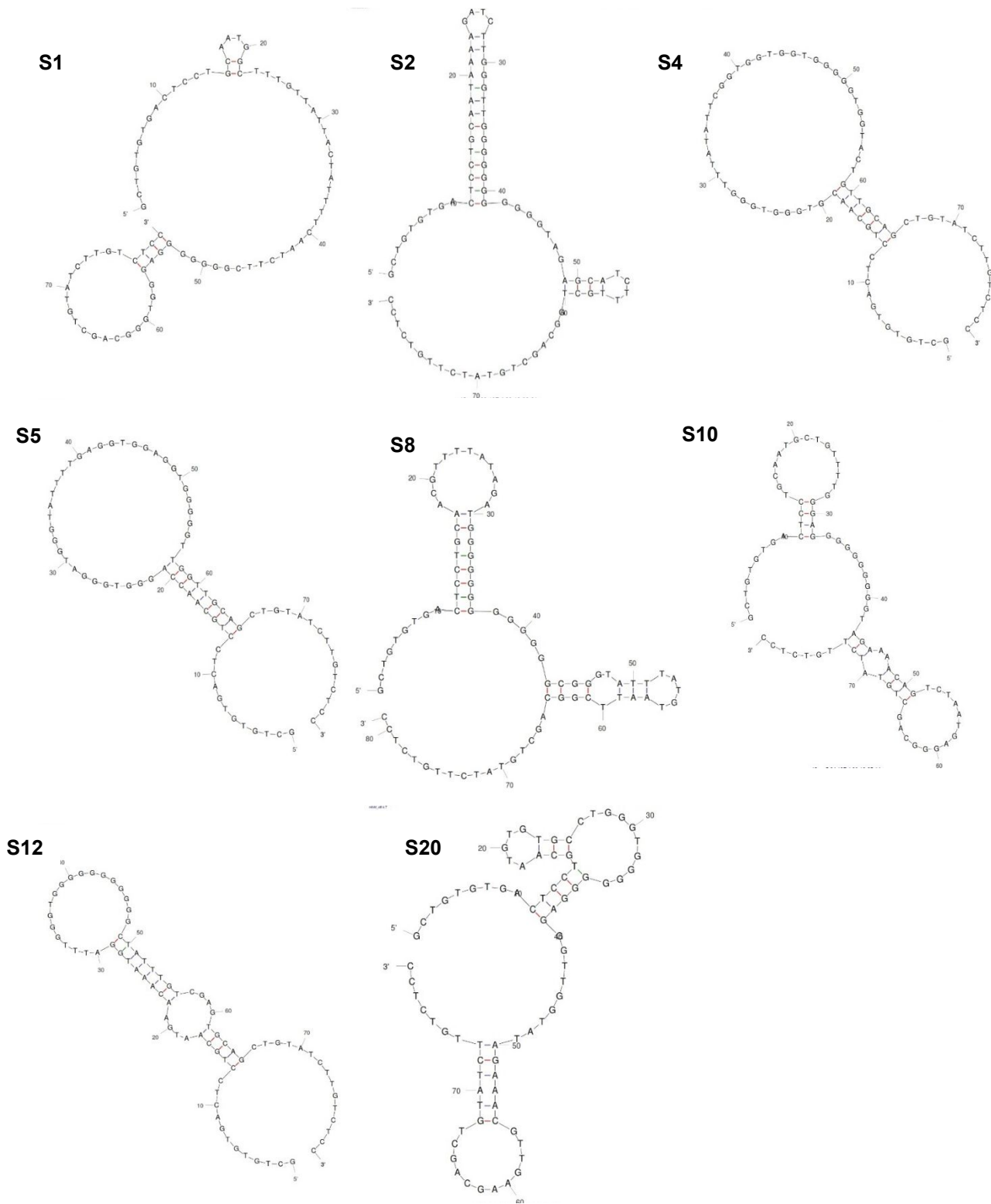
**Figure S2.** Phylogenetic tree of sequences. One sequence from each branch (indicated by blue color) was selected for further characterizations.



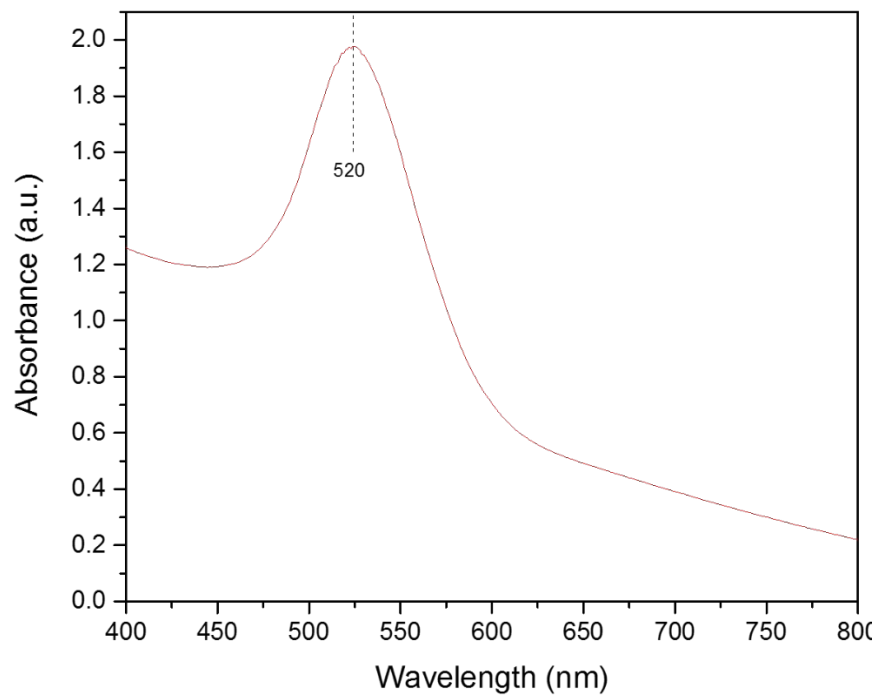
**Figure S3.** The most shared motifs represented in the selected sequences. (A) motif 1, (B) motif 2.

**Table S4.** Sequences with corresponding predicted G-score.

Aptamer	Sequence	G-Score
S1	GCTGTGTGACTCCTGCAATGGCTTTGTTATTACTATTTTCAATCTTCGGGGGGGAGGGTGGGCAGCTGTATCTTGTCTCC	1
S2	GCTGTGTGACTCCTGCAATAAAAGATCTTGGGTTGGGGGGGGGGTAGAGCATCTTGTGTCAGCTGTATCTTGTCTCC	1
S3	GCTGTGTGACTCCTGCAACGTGGGTGGGCTTATATTCCGGTGGTGGTGGGGGTGGTACTGTTGCAGCTGTATCTTGTCTCC	1
S4	GCTGTGTGACTCCTGCAACGTGGGTGGGTTTATATTCCGGTGGTGGTGGGGGTGGTACTGTTGCAGCTGTATCTTGTCTCC	1
S5	GCTGTGTGACTCCTGCAACCAGGTGGGATGGGTATTTTGGAGTGGAGGTGGGGGTGGTGCAGCTGTATCTTGTCTCC	1
S6	GCTGTGTGACTCCTGCAATGCGATCCTGGGTAGGGTGGGTGGGTATTATGAGAGCTTGGTGCAGCTGTATCTTGTCTCC	1
S7	GCTGTGTGACTCCTGCAACGTGGGTGGGTTTATATTGGTGGTGGTGGGGGTGGTACTGTTGCAGCTGTATCTTGTCTCC	1
S8	GCTGTGTGACTCCTGCAACGTTTTATAGATGGGGGGGGGGGGCGGGTATTTATGTAATTCGGGCAGCTGTATCTTGTCTCC	1
S9	GCTGTGTGACTCCTGCAATTCATAAATACATTTGGGCGGGTGTGGTGGGTTTTTTTTTTGAGCAGCTGTATCTTGTCTCC	1
S10	GCTGTGTGACTCCTGCAATGCTGTTTTGGGAGGGGGGGGGTAGAAAACAGTCTAATGAGGCAGCTGTATCTTGTCTCC	1
S11	GCTGTGTGACTCCTGCAACCAGGTGGGATAGGTATTTGAGGTGGAGGTGGGGGTGGTGCAGCTGTATCTTGTCTCC	1
S12	GCTGTGTGACTCCTGCAATGAACAAATGGATTTGGGTGGGGGGGGGGCTATTTGTGAGTGCAGCTGTATCTTGTCTCC	1
S13	GCTGTGTGACTCCTGCAACGTGGGTGGGTTTATGTTCCGGTGGTGGTGGGGGTGGTACTGTTGCAGCTGTATCTTGTCTCC	1
S14	GCTGTGTGACTCCTGCAACGGGTGGGGGGAGGGTGTGTTGCTTAGAGTCGGTTTTCTAGGAGCAGCTGTATCTTGTCTCC	1
S15	GCTGTGTGACTCCTGCAACGTGGGTGGGTTTATACTCGGTGGTGGTGGGGGTGGTACTGTTGCAGCTGTATCTTGTCTCC	1
S16	GCTGTGTGACTCCTGCAAAATTTGGGTTGGGTGGGGGGTAAGGTGTACAAATAGATGCAGCTGTATCTTGTCTCC	1
S17	GCTGTGTGACTCCTGCAAGGGTTTTCAAGTGTGACTTAGCAGCGTCGGGTGGGTGGGGGGCAGCTGTATCTTGTCTCC	1
S18	GCTGTGTGACTCCTGCAACGTGGGTGGGTTTATATTCCGGTGGCGGTGGGGGTGGTACTGTTGCAGCTGTATCTTGTCTCC	1
S19	GCTGTGTGACTCCTGCAACGTGGGTGGGTTTATATTCCGGTGGTGGTGGGGGTGGTACTGTTGCAGCTGTATCTTGTCTCC	1
S20	GCTGTGTGACTCCTGCAATGTGTGCCTGGGTGGGGGGAGGGTTGGTATAGAAACGTTGAAGCAGCTGTATCTTGTCTCC	1
S21	GCTGTGTGACTCCTGCAACCAAGGTGGGATGGGTATTTTGGAGTGGAGGTGGGGGTGGTGCAGCTGTATCTTGTCTCC	1
S22	GCTGTGTGACTCCTGCAATGATTAATAGGGTGGGTTTCGGGGGGGTGTCGGGTAGGTGATGCAGCTGTATCTTGTCTCC	1



**Figure S4.** Secondary structures predicted by mfold.



**Figure S5.** UV-Vis spectrum for the synthesized AuNPs.

**Table S5.** Kd values of the reported aptamers for PP

Aptamer Name	Sequence	Kd (nM)	Reference
26_17	AGCGTCGGATACCACTACTAGGCACCGCTGTTTTAGCCTCGGCTGAGACAAGGGCATCATGGAGTTCGTGGTCAG	33.15 ± 4.08	1
10_13	AGCGTCGGATACCACTACTACGTGCAATGTGCAATGCATGAGCAAACATGGCGATATCATGGAGTTCGTGGTCAG	58.81 ± 3.28	1
5_13	AGCGTCGGATACCACTACTAGGTTGATGTGCAACGAAGTAAGCATTAGCCAAAAGATCATGGAGTTCGTGGTCAG	77.39 ± 3.93	1
S2	GCTGTGTGACTCCTGCAATAAAAGATCTTGGGTTGGGGGGGGGGTAGAGCATCTTTGCTGGCAGCTGTATCTTGTCTCC	15.12 ± 0.515	Our aptamer
S12	GCTGTGTGACTCCTGCAATGAACAAATGGATTTGGGTGGGGGGGGGGCTATTTGTCGAGTGCAGCTGTATCTTGTCTCC	15.87 ± 0.510	Our aptamer
S20	GCTGTGTGACTCCTGCAATGTGTGCCTGGGTGGGGGGGAGGGTTGGTATAGAAACGTTGAAGCAGCTGTATCTTGTCTCC	13.06 ± 0.223	Our aptamer



## References:

1. Qin, S.; Chen, N.; Yang, X.; Wang, Q.; Wang, K.; Huang, J.; Liu, J.; Zhou, M., Development of Dual-Aptamers for Constructing Sandwich-Type Pancreatic Polypeptide Assay. *ACS sensors* **2017**, *2* (2), 308-315.