

Supplementary Information

Auto-SELEX: A Fully Automated Microfluidic Platform for Rapid Discovery of High-Affinity Aptamers

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SUPPLEMENTARY MOVIES

Movie S1. Video microscopy illustrating the Auto-SELEX workflow using food dyes to visualize fluid transport, where blue represents the sample (target-library mixture), red represents the PCR mix containing forward primers and AuNRs, green represents magnetic beads, and brown represents the elution buffer containing AuNRs. The video is played at $2 \times$ the recorded speed.

Movie S2. Video fluorescence microscopy demonstrating continuous-flow electrophoretic separation of aptamer-IgE complexes from unbound ssDNA sequences through the 2D CW sieve under increasing electric field strengths applied orthogonal to the focused sample stream. The video is played at $2 \times$ the recorded speed and corresponds to Fig. 3C in the main text.

SUPPLEMENTARY FIGURES

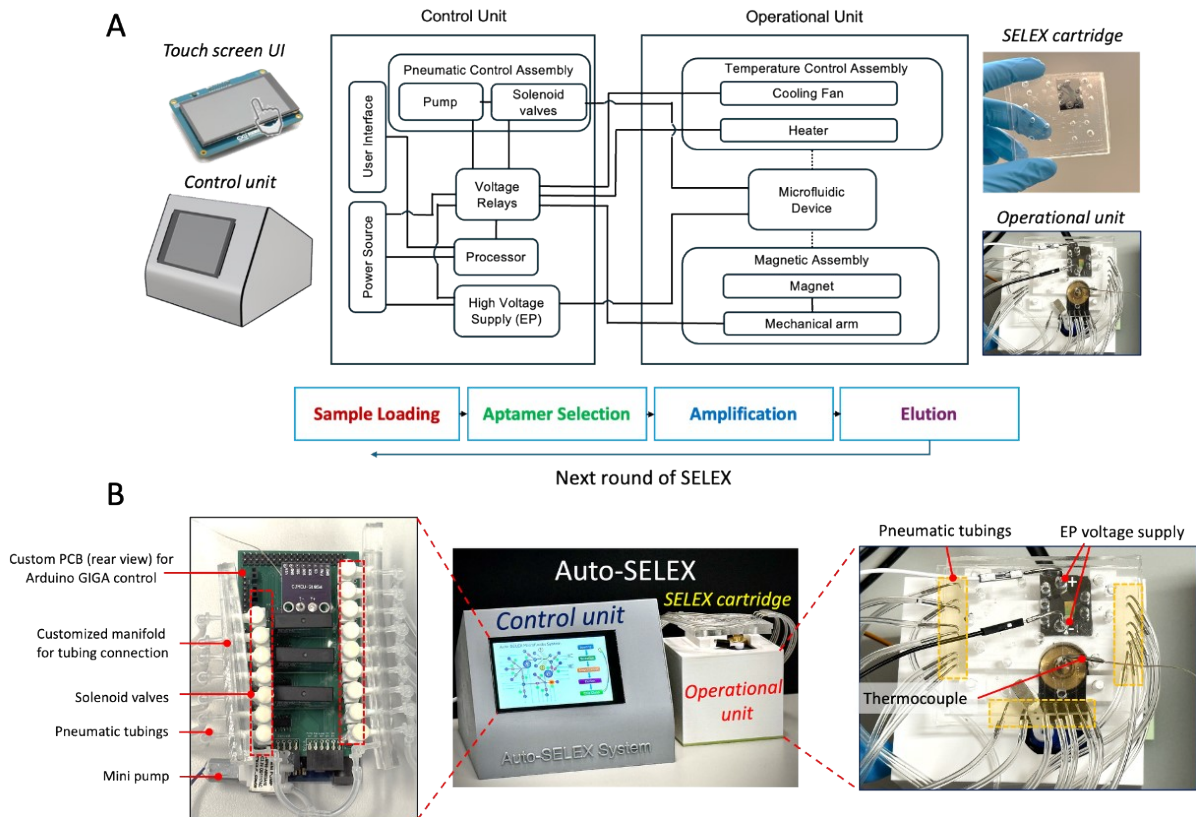


Fig. S1. Auto-SELEX system overview. (A) Block diagrams of the control and operational units highlighting the core components, key process steps, and photographs of the SELEX cartridge and operational unit. (B) Photographs of the Auto-SELEX system.

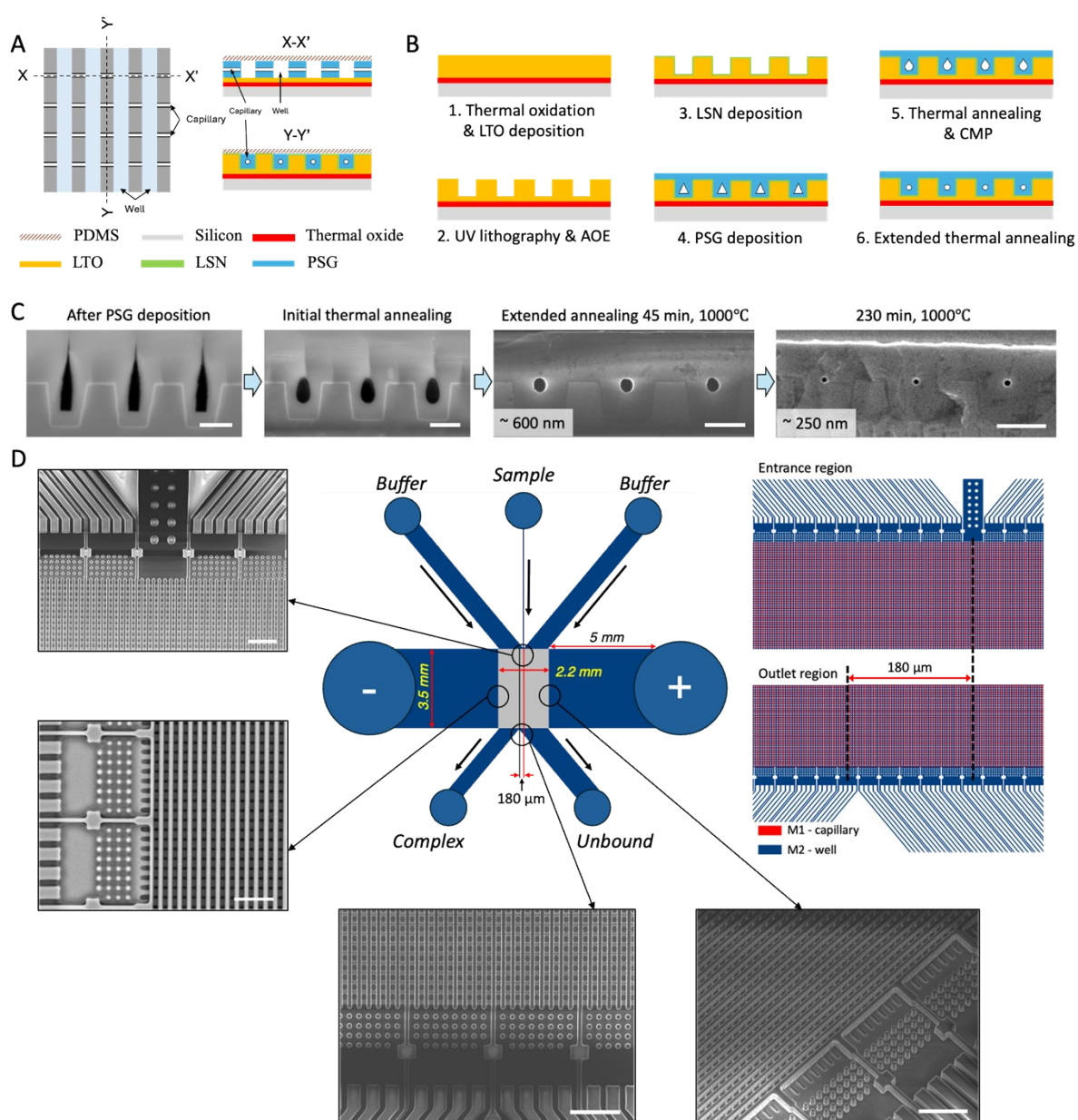


Fig. S2. Fabrication and design layout of the 2D CW sieve. (A) Schematic descriptions of the sieve array showing the top view and cross-sectional views of an array segment along the x- and y-axes. (B) Process flow diagrams in cross-sectional views illustrating the key fabrication steps. LTO: low-temperature oxide; LSN: low-stress nitride; CMP: chemical mechanical polishing; AOE: Advanced oxide etch; PSG: phosphosilicate glass. The second UV lithography step and subsequent AOE for forming the reservoirs and microchannels are not illustrated. (C) Scanning electron microscopy (SEM) images demonstrating tuning of the capillary diameter

through thermal annealing of PSG. Cross-sectional views of the sieve show three adjacent capillaries (self-enclosed channels) following PSG deposition, initial thermal annealing and then extended thermal annealing first for 45 min and subsequently for 230 min both at 1000 °C. Auto-SELEX system utilizes an optimized capillary diameter of ~700 nm. Scale bars: 2 μm. (D) Design layout with accompanying SEM images revealing microstructural details at various sieve sites. The inlet is aligned with the default outlet (Outlet II), while the alternative outlet (Outlet I) is laterally offset from the inlet by 180 μm. Scale bars: 20 μm.

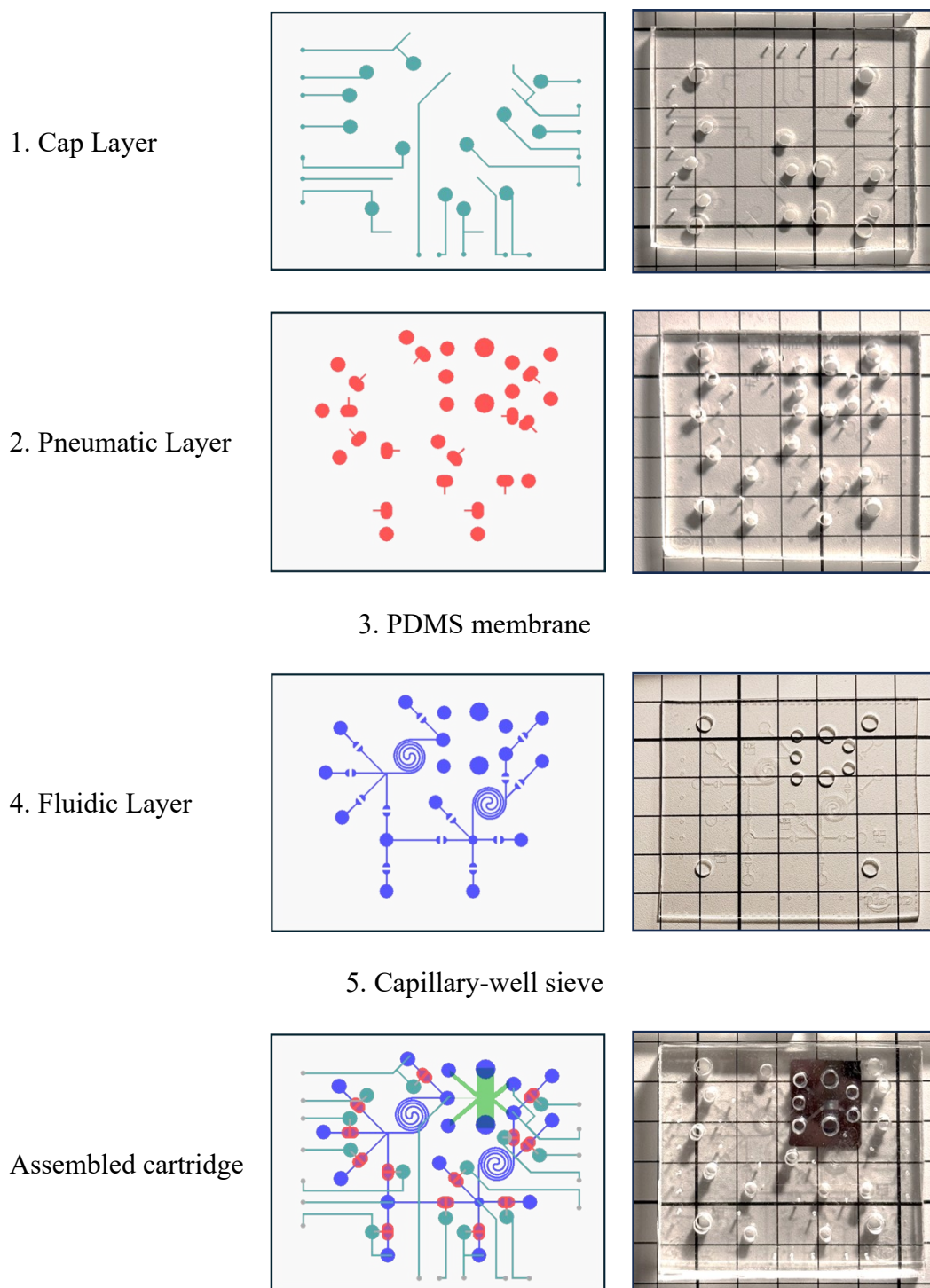


Fig. S3. Layouts of the cartridge layers (from top to bottom) and an assembled cartridge shown along with their pictures.

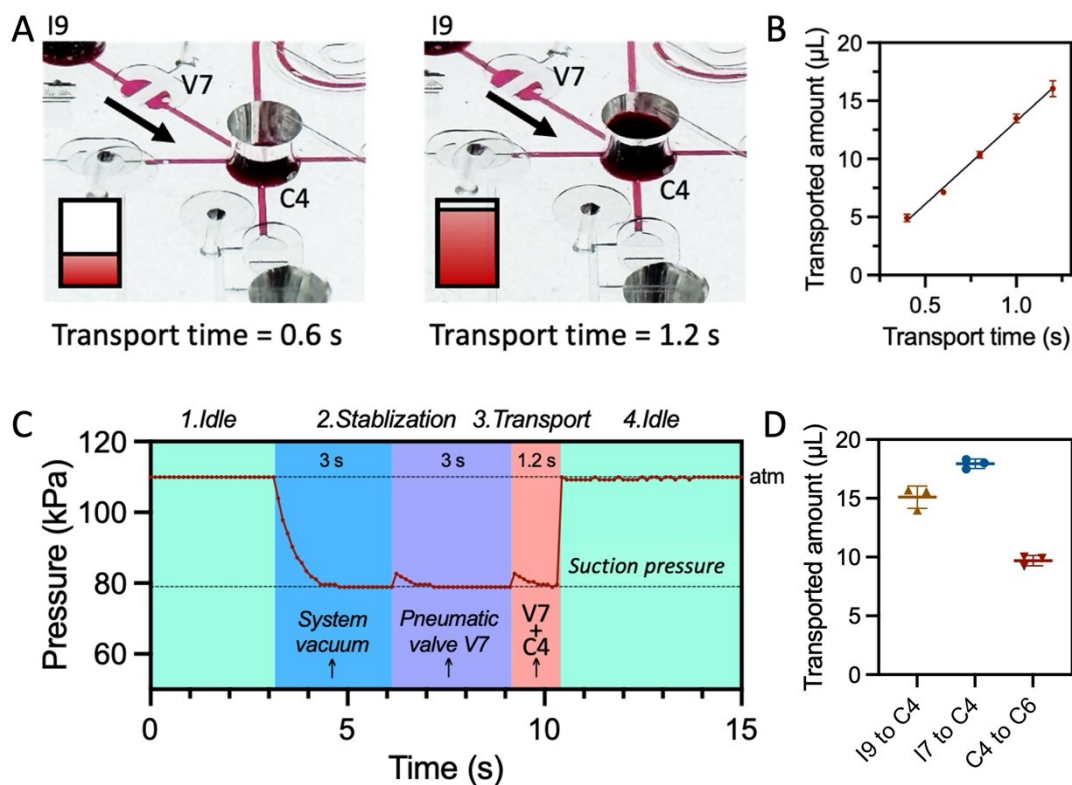


Fig. S4. Vacuum-driven liquid transfer within the cartridge. (A) Food dye (red) is transferred from reservoir I9 to the PCR chamber (C4) via valve V7. Sequential images show partial and near-complete filling of chamber C4 after transfer durations of 0.6 and 1.2 s, respectively. (B) The plot shows a linear relationship ($R^2 = 0.99$) between transferred volume and transfer duration (mean \pm SD; $n = 5$). (C) The plot shows the vacuum profile applied during transfer. Liquid transfer is initiated by opening V7 followed by application of vacuum to chamber C4, and is metered by controlling the duration of concurrent vacuum application to V7 and C4, enabling programmable volumetric dosing. (D) The plot shows cartridge-to-cartridge reproducibility of transferred volume through three representative fluidic paths (I9 to C4 via V7, I7 to C4 via V4, and C4 to C6 via V8) under a fixed valve-opening duration of 1.2 s. Error bars represent standard deviations based on measurements from three independent cartridges.

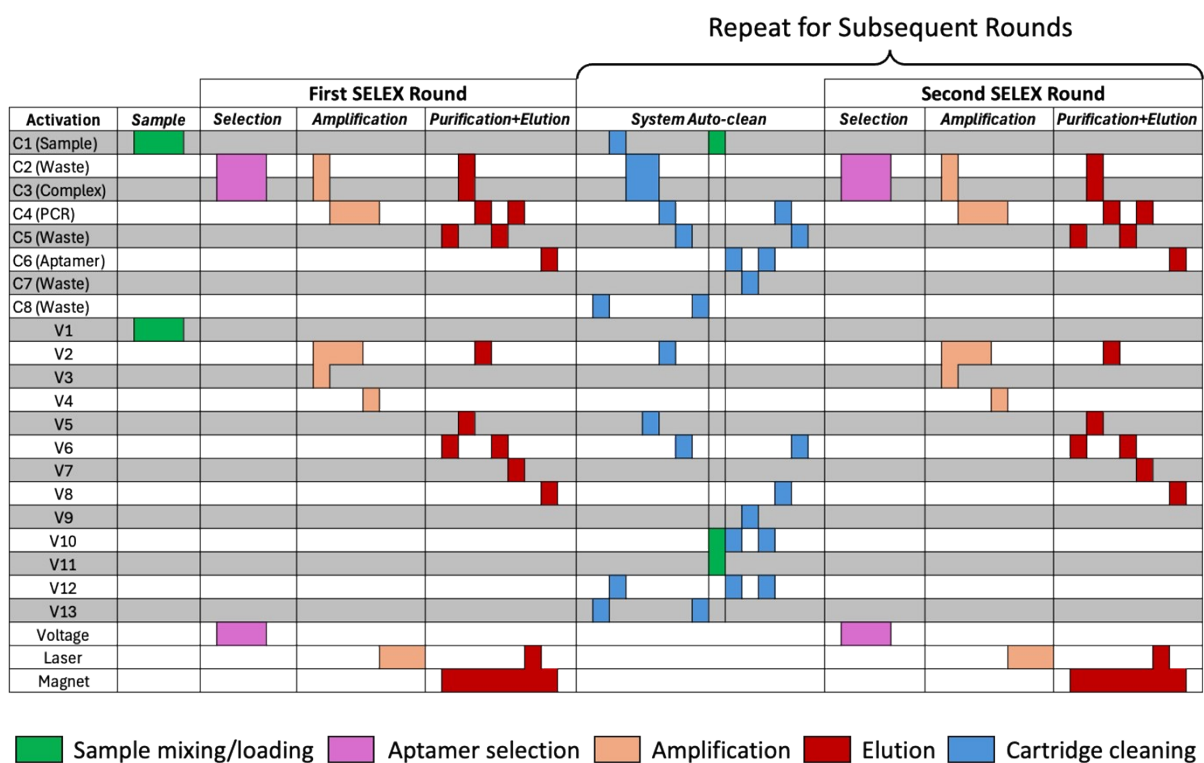


Fig. S5. Auto-SELEX workflow activation sequence.

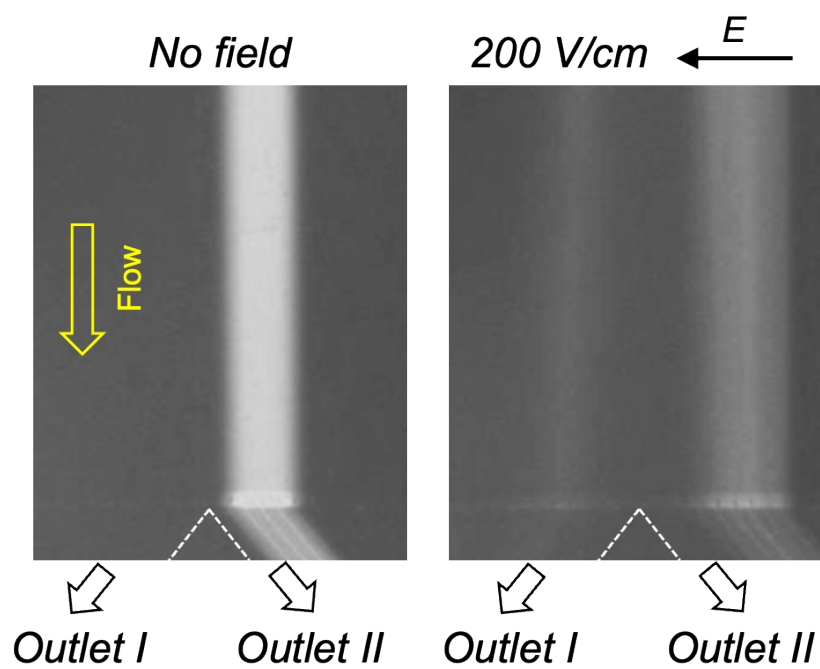


Fig. S6. Fluorescence images of a sample stream containing vitronectin ($2 \mu\text{M}$) and FAM-labelled randomized ssDNA library ($2 \mu\text{M}$) exiting the sieve in the absence and presence of an applied average electric field of 200 V/cm .

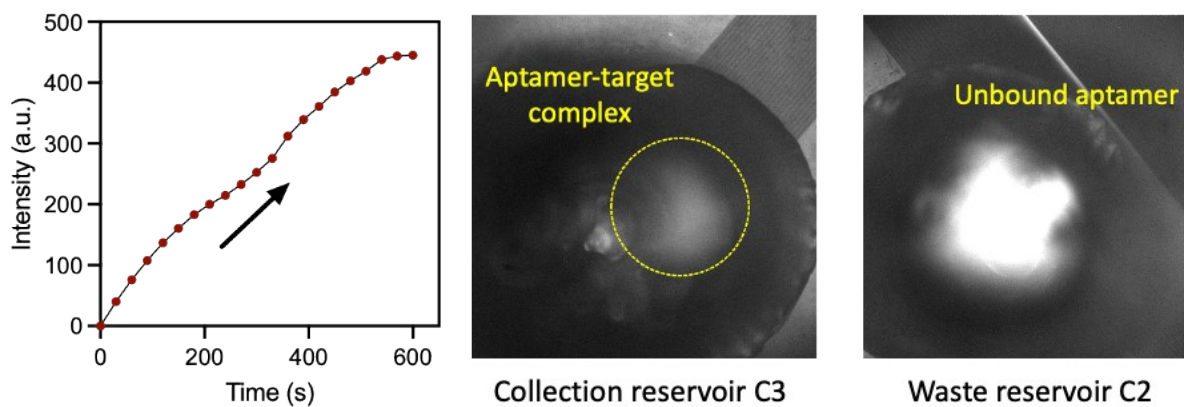


Fig. S7. Fluorescence images of chambers C2 and C3, respectively, accumulating unbound ssDNA strands and aptamer-IgE complex, acquired 5 min after the onset of continuous-flow separation through the sieve under an average electric field of 200 V/cm. The corresponding plot shows a monotonic increase in fluorescence intensity over time in chamber C3, indicating progressive accumulation of the aptamer-IgE complex over time.

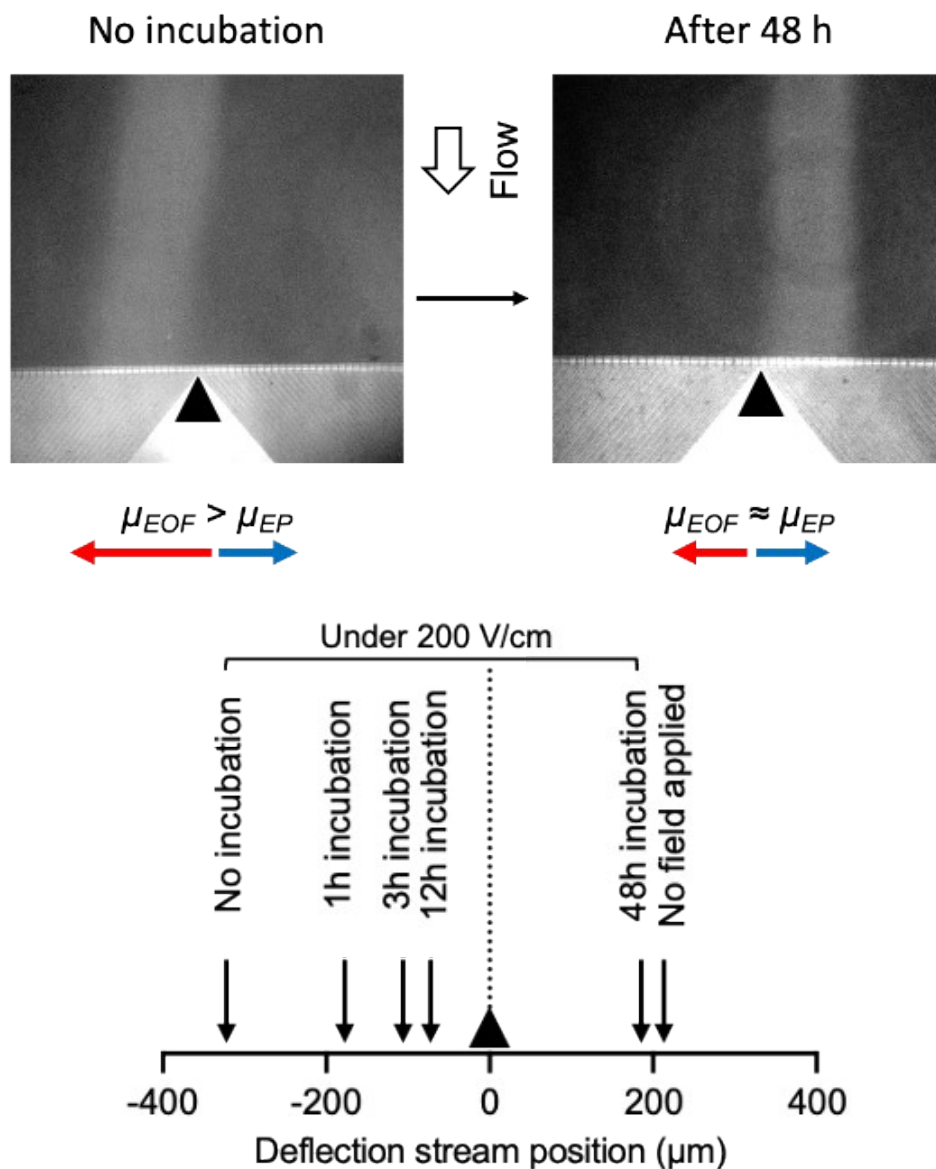


Fig. S8. Evolution of EOF with chip incubation duration in $1\times$ TGK buffer under an applied average electric field of 200 V/cm. Representative fluorescence images show the stream exiting the sieve prior to chip incubation and after 48 h of incubation. The below diagram shows the deflection extent for the unbound ssDNA stream relative to the dashed line indicating the outlet bifurcation (arrowhead), as a function of chip incubation time.

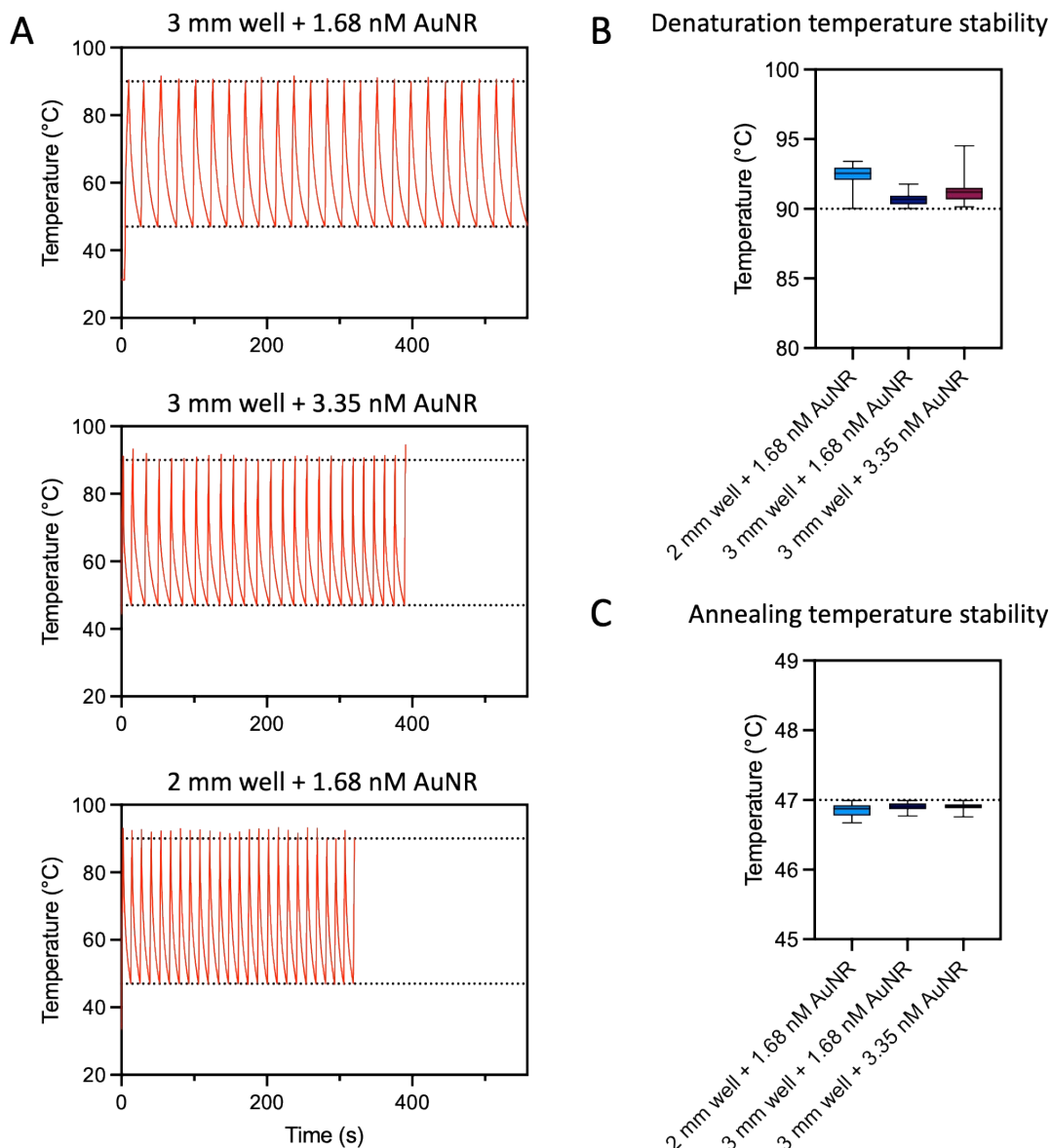


Fig. S9. Thermal cycling performance of bead-based plasmonic PCR within 2-mm- and 3-mm-diameter vacuum-driven chambers using 1.68 nM and 3.35 nM AuNRs. (A) Temperature profiles over 25 cycles. Cycle-to-cycle temperature stability during (B) denaturation (target: 92 °C) and (C) annealing/extension (target: 47 °C). The PCR chamber contains a 16 μ L reaction mixture consisting of 1 \times KOD One™ PCR Master Mix supplemented with 1 μ M FAM-labeled forward primer, 1.68 nM or 3.35 nM AuNRs, 5 nM ssDNA library template, and 60 μ g reverse primer-functionalized magnetic beads.

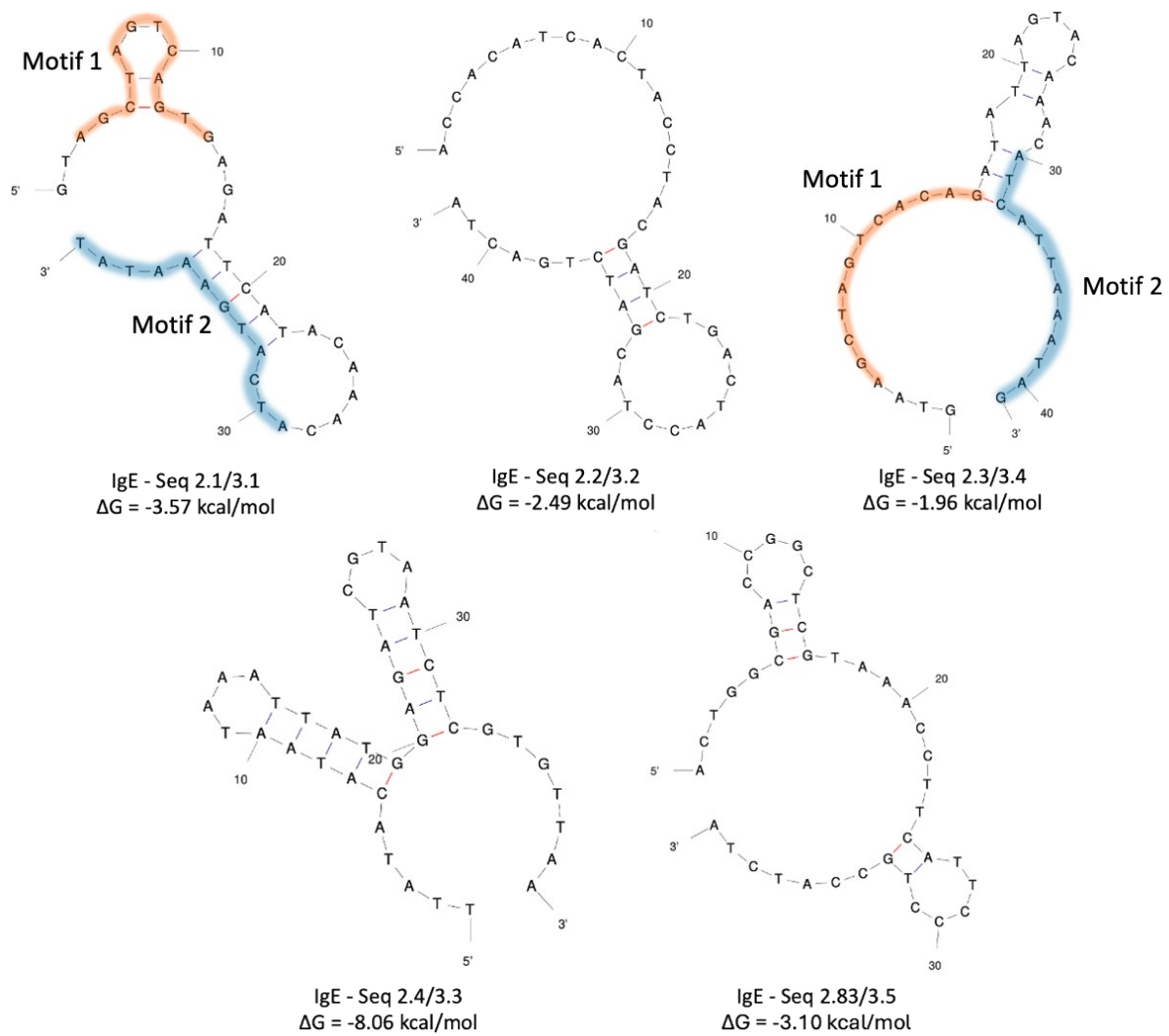


Fig. S10. Predicted secondary structures of selected aptamers against human IgE.

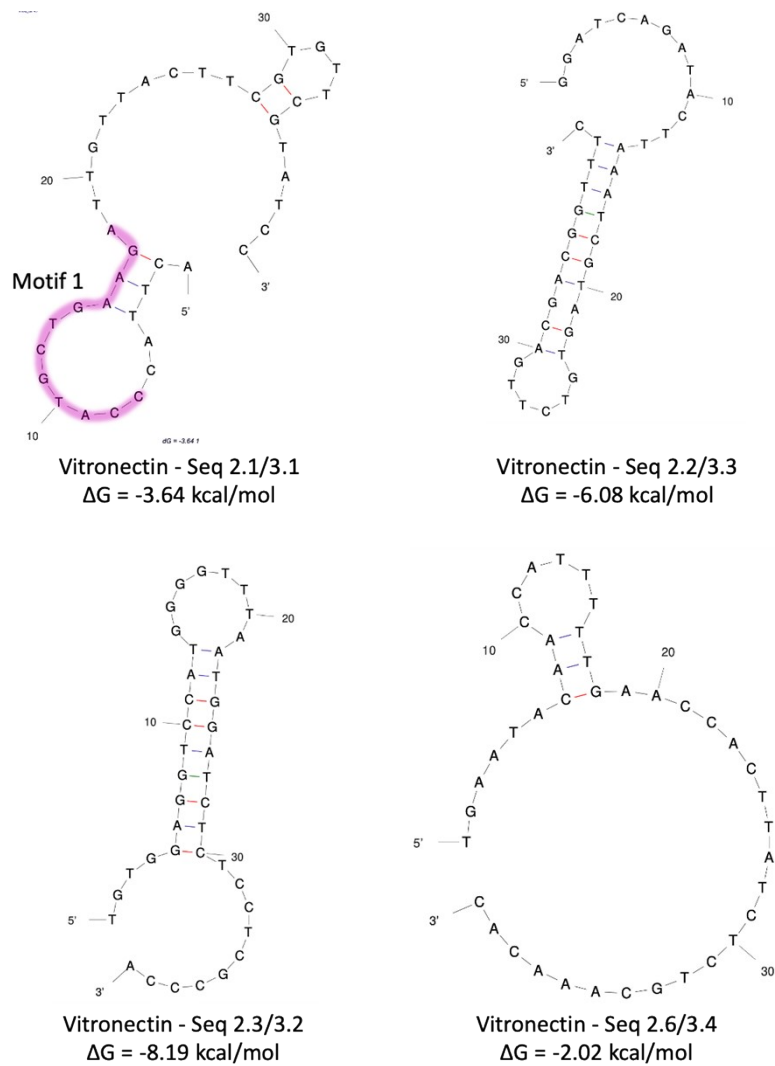


Fig. S11. Predicted secondary structures of selected aptamers against human vitronectin.

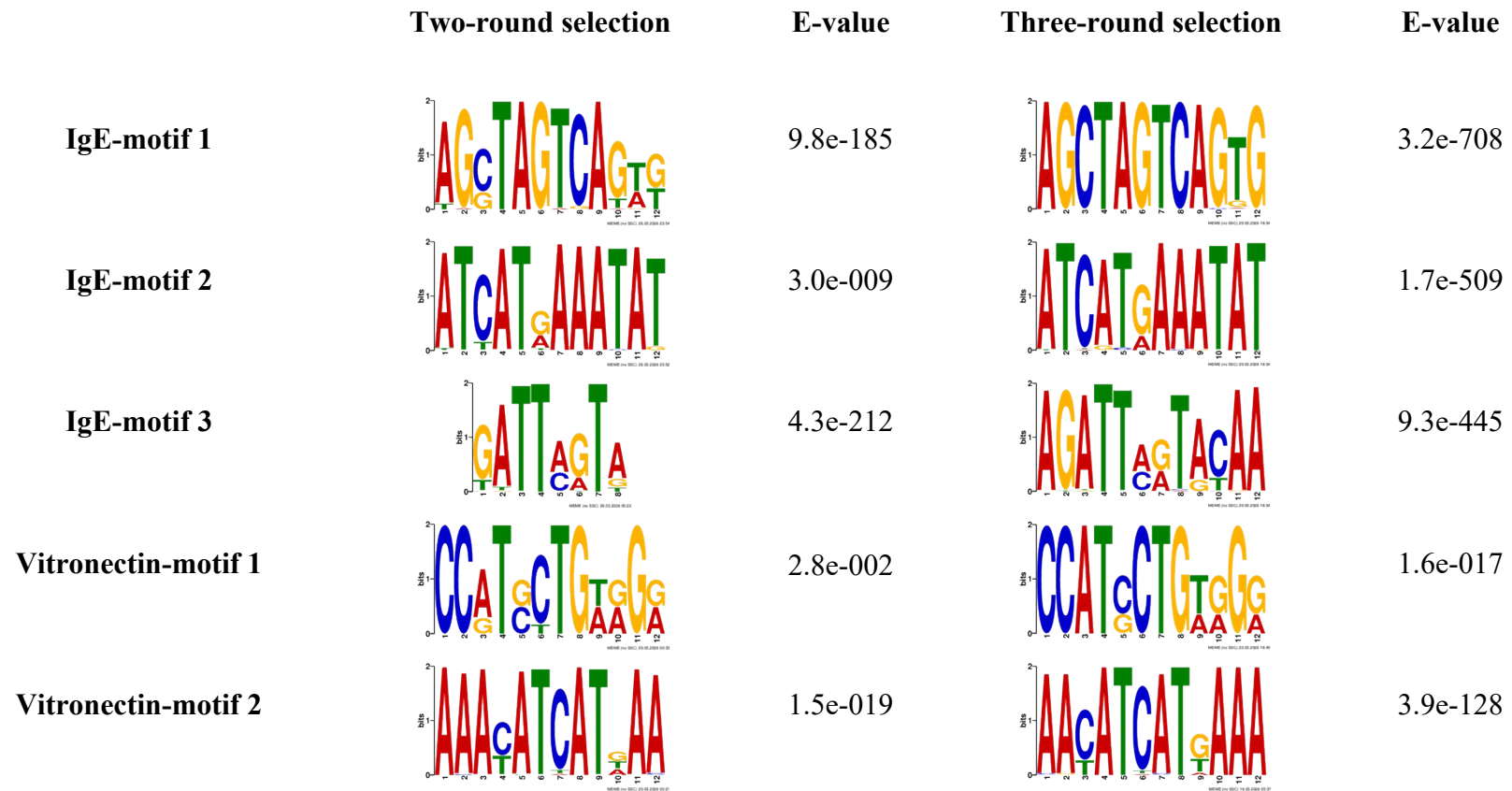


Fig. S12. Sequence logos of motifs identified by MEME Suite from independent two-round and three-round selections. Motifs with E-values ≤ 0.05 are considered statistically significant (non-random); those with E-values $\leq 10^{-5}$ represent highly significant motifs indicating strong sequence conservation.

SUPPLEMENTARY TABLES

Table S1. Auto-SELEX cartridge reservoir loading before initiating the workflow.

| Reservoir | Content | Composition & Concentration | Volume* (μL) |
|------------|---|--|---------------------------|
| I1 | Mixture of target protein & ssDNA library preincubated for 30 min (used in round 1) | IgE (50 nM) + Random ssDNA Pool (10 μM) | 15 |
| I2 | Aptamer selection buffer | 1 \times TGK | 20 |
| I3 | | | |
| I4 | | | |
| I5 | | | 40 |
| I6 | PCR reagents & AuNRs | 2 \times KOD Master Mix + Forward Primer (2 μM) + AuNR (3.35 nM) | 20 |
| I7 | Reverse primer-modified magnetic beads (2.8 μm) | 8.57 $\mu\text{g}/\mu\text{L}$ in PCR water | 20 |
| I8 | Wash buffer | 1 \times TGK | 80 |
| I9 | AuNRs (10 nm \times 41 nm) | AuNR, 1.68 nM in 1 \times TGK | 20 |
| I10 | Wash buffer | 1 \times TGK | 80 |
| I11 | Target protein (used in subsequent rounds) | IgE, 50 nM | 30 |

*The listed volumes support the selection for two rounds and they scale proportionally for additional rounds.

Table S2. Sequencing read statistics for selected pools (length analysis is based on the random region with the expected length of 40 nt).

| | Selection depth | Total reads | Reads 38–42 nt | % within 38–42 nt | Unique sequences | % Duplicate |
|-------------------------|-----------------|-------------|----------------|-------------------|------------------|-------------|
| Random Library | - | 109,893 | 109,585 | 99.72% | 100,205 | 8.56 |
| IgE Pool | two-round | 64,253 | 63,056 | 98.10% | 51,968 | 17.58 |
| | three-round | 79,756 | 79,297 | 99.40% | 53,447 | 32.60 |
| Vitronectin Pool | two-round | 150,581 | 149,571 | 99.30% | 135,411 | 9.47 |
| | three-round | 122,512 | 121,288 | 99.00% | 103,814 | 14.41 |

Table S3. Sequences of selected aptamers, without primer regions, against human IgE and vitronectin ranked according to their abundance expressed as reads per million (RPM). Aptamer binding affinity measurements exclude primer regions.

| Target | No. | Sequence (5' – 3') | Two rounds (RPM) | Three rounds (RPM) | Binding affinity (nM) |
|--------------------|----------|--|------------------|--------------------|-----------------------|
| IgE | 2.1/3.1 | GTAGCTAGTCAGTGAGATTCATACAAACATCATGAAATAT | 222 | 277 | 19.0 ± 1.95 |
| | 2.2/3.2 | ACCACATCACTACCTACGATCTGACTACCTACGATCTGACTA | 174 | 227 | 25.3 ± 0.7 |
| | 2.3/3.4 | GTAAGCTAGTCACAGATATTAGTACAAACATCATTAATAG | 127 | 151 | 25.3 ± 2.5 |
| | 2.4/3.3 | TTATACATAATAAATTATGGAGATCGTAATCTCGTGTTAA | 111 | 177 | 28.2 ± 0.8 |
| | 2.83/3.5 | ACTGGCGACCGGCTCGTAAACCTTCATTCCCTGCCATCTA | 16 | 100 | 19.9 ± 1.8 |
| Vitronectin | 2.1/3.1 | ACTTACCCATGCTGAAGATTGTTACTTCGTGTTTCGTATCC | 134 | 330 | 98.5 ± 5.5 |
| | 2.2/3.3 | GGATCAGATACTTAAATCGTAGTGTCTTGACGACGGTTTC | 94 | 124 | 108 ± 2.6 |
| | 2.3/3.2 | TGTGGAGGTCCATGGGGTTTAATGGATCTCTCCTCGCCCA | 87 | 165 | 118 ± 9.5 |
| | 2.6/3.4 | TGAATACAACCATTTTTGAACCACTTATCTCTGCAAACAC | 67 | 115 | 157 ± 13 |

Table S4. Enriched sequence motifs identified in IgE and vitronectin pools after three-round selection and their expressed abundance as reads per million (RPM).

| Target | Motif | Consensus sequence | Two-round | | Three-round | | Relative Abundance (three-round over two-round) |
|-------------|---------|---------------------------|------------|-------------|-------------|-------------|--|
| | | | Unique seq | Reads (RPM) | Unique seq | Reads (RPM) | |
| IgE | Motif 1 | AGCTAGTCAGTG | 121 | 2395 | 128 | 13509 | 5.64× |
| | Motif 2 | ATCATGAAATAT | 139 | 2783 | 89 | 11723 | 4.21× |
| | Motif 3 | AGATTMRTACAA* | 104 | 2165 | 93 | 11961 | 5.53× |
| Vitronectin | Motif 1 | CCATSCTGWRGR [#] | 28 | 2427 | 34 | 3215 | 1.32× |
| | Motif 2 | AACATCATKAAA [#] | 31 | 2513 | 32 | 3463 | 1.38× |

*M = A/C, R = A/G

[#]S = G/C, W = A/T, R = A/G, K = G/T

Table S5. Performance benchmarking of fully and semi-automated microfluidic SELEX platforms

| Ref. | Partitioning | Partitioning time per round (min) | PCR | PCR time per round (min) | Total time per round (min) | Rounds | Protein target: Aptamer Affinity (Kd) | Automation level | |
|-------------------------------|---|---|-------------------------------|--------------------------|----------------------------|-----------------------|--|---------------------------------|----------------|
| Auto-SELEX (this work) | Electrokinetic free-resolution partitioning across artificial sieve | ~17 (2 min separation + 15 min incubation) | Plasmonic bead-based PCR | ~10 (25 cycles) | ~30 | 3 | IgE: 19.0 nM; Vitronectin: 98.5 nM | Fully automated | |
| Hybarger et al., 2006 | Solid-phase capture (target immobilized in microline) | ~15 (10 min binding + 3 min elution + washing) | Heating block | ~60 (40 cycles) | ~200 | 1 (for validation) | Not reported | Fully automated | |
| Huang et al., 2010 | Magnetic beads (target immobilized) | 10 (5 min incubation + 5 min washing) | On-chip microheaters | ~45 (20 cycles) | 60 | 5 | CRP: 3.51 nM | Fully automated | |
| Huang et al., 2012 | | ~10 (incubation + washing) | Array-type microheaters | ~42 (20 cycles) | 60 | 6 | AFP: 2.37 nM | Fully automated | |
| Hilton et al., 2015 | | ~90 (18 min incubation + 60 min washing + thermal elution) | | | ~30 (25 cycles) | ~120 | 2 | IgE: 83.9 nM (pool affinity) | Semi-automated |
| Kim et al., 2016 | | ~55 (10 min incubation + 5 min elution + 15 min washing + 25 min transfer) | Bead-based PCR by microheater | ~45 (25 cycles) | ~200 | 3 | IgE: 10-18 nM; Small molecule: 1-2 μ M | Semi-automated | |
| Olsen et al., 2017a | | ~110 (30 min incubation + 40 min washing + 40 min elution / transfer) | | | ~15 (20 cycles) | ~240 | 2 | IgA: Not reported | Semi-automated |
| Olsen et al., 2017b | | ~40 (estimated) | | | ~25 (20 cycles) | ~150 | 4 | IgE: 12 nM | Semi-automated |
| Sinha et al., 2018 | | Not specified | Thermoelectric heater/cooler | ~38 (20 cycles) | ~96 | 8 | NT-proBNP: 2.89 nM; hcTnI: 19.8 nM; Fibrinogen: 4.4 nM | Fully automated | |
| Olsen et al., 2023 | | ~60 (10 min incubation + 35-45 min washing + transfer) | Bead-based PCR by microheater | ~15 (12 cycles) | ~120 | 6 | Rituximab: 35.8 nM; Patient M-Ig: ~36 nM | Semi-automated | |

Table S6. Bill of materials for the Auto-SELEX system and disposable cartridge.

| Module | Item | Part Number / Source | Cost (USD) |
|-----------------------------|--|---|------------|
| Control Unit | Enclosure | In-house 3D printing | \$30 |
| | Arduino GIGA R1 WiFi, display shield, and custom PCB | Arduino (Ivrea, Italy); custom PCB in-house | \$134 |
| | Miniature pump | CJWP08-AB03A10 (Conjoin, Xiamen, China) | \$3 |
| | Pressure sensor | MPX5700AP (NXP Semiconductors) | \$26 |
| | Solenoid valves (total 17 units) | LHDA0533115H (The LEE Company, Westbrook, CT) | \$1,282 |
| | Tubings, connectors, and wiring | Cole-Parmer | \$13 |
| | Subtotal | | \$1,488 |
| Operational Unit | Enclosure | In-house 3D printing | \$26 |
| | 808-nm laser | Arm Laser, Shenzhen, China | \$77 |
| | Cooling fan | AFB0512MA (Delta Electronics, Taipei) | \$2 |
| | K-type thermocouple | Omega Engineering (Norwalk, CT) | \$1 |
| | Motorized magnet arm (SG90 servo + permanent magnet) | SG90 (TowerPro, Taipei); HuiLunTe Magnets, Jiangsu, China | \$3 |
| | Subtotal | | \$109 |
| Total (System) | | \$1,588 | |
| Disposable Cartridge | 2D CW sieve (Per dozen chips on a 4-inch wafer) | In-house cleanroom | \$16 |
| | PDMS base and curing agent (~90 g) | Sylgard 184, Dow Corning (Midland, MI) | \$11 |
| | PDMS membrane (~300 μm thick) | Westru (Hangzhou, China) | \$1 |
| | Total | | \$28 |

REFERENCES

- G. Hybarger, J. Bynum, R. F. Williams, J. J. Valdes and J. P. Chambers, *Anal. Bioanal. Chem.*, 2006, **384**, 191–198.
- C. J. Huang, H. I. Lin, S. C. Shiesh and G. B. Lee, *Biosens. Bioelectron.*, 2010, **25**, 1761–1766.
- C. J. Huang, H. I. Lin, S. C. Shiesh and G. B. Lee, *Biosens. Bioelectron.*, 2012, **35**, 50–55.
- J. P. Hilton, T. Olsen, J. Kim, J. Zhu, T. Nguyen, M. Barbu, R. Pei, M. Stojanovic and Q. Lin, *Microfluid. Nanofluid.*, 2015, **19**, 795–804.
- J. Kim, T. R. Olsen, J. Zhu, J. P. Hilton, K.-A. Yang, R. Pei, M. N. Stojanovic and Q. Lin, *Sci. Rep.*, 2016, **6**, 26139.
- T. R. Olsen, C. Tapia-Alveal, K.-A. Yang, X. Zhang, L. J. Pereira, N. Farmakidis, R. Pei, M. N. Stojanovic and Q. Lin, *J. Electrochem. Soc.*, 2017, **164**, B3122–B3129.
- T. Olsen, J. Zhu, J. Kim, R. Pei, M. N. Stojanovic and Q. Lin, *SLAS Technol.*, 2017, **22**, 63–72.
- A. Sinha, P. Gopinathan, Y.-D. Chung, H.-Y. Lin, K.-H. Li, H.-P. Ma, P.-C. Huang, S.-C. Shiesh and G.-B. Lee, *Biosens. Bioelectron.*, 2018, **122**, 104–112.
- T. R. Olsen, C. Tapia-Alveal, K. Wen, T. S. Worgall, M. N. Stojanovic and Q. Lin, *Biomed. Microdevices*, 2023, **25**, 3.