Whole cell-SELEX of aptamers with a tyrosine-like side chain against live bacteria

Supporting Information
Renders, Miller, Lam and Perrin

Table S1. Oligonucleotide sequences

<table>
<thead>
<tr>
<th>Name</th>
<th>Sequence (length) 5’ - 3’</th>
</tr>
</thead>
<tbody>
<tr>
<td>N40 template</td>
<td>GCG CTC GCG CGG CGT GCN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN CTG TTG GCG CAG GCC GAC GC (77)</td>
</tr>
<tr>
<td>Selection Primer</td>
<td>Biotin-GCG TGC CrCrG rUCT GTT GGT TTT GCG TCG GCC TGC GCC AAC AG (41)</td>
</tr>
<tr>
<td>Selection Primer - no Biotin</td>
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</tr>
<tr>
<td>PCR primer forward (1st_amp_2)</td>
<td>Phos-GCG TCG GCC TGC GCC AAC AG (20)</td>
</tr>
<tr>
<td>PCR primer back (1st_amp_1)</td>
<td>GCG CTC GCG CGG CGT GC (17)</td>
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</tbody>
</table>
TABLE S2. Summary of selection conditions

<table>
<thead>
<tr>
<th>Selection Round</th>
<th>Incubation Time (min)</th>
<th>Washes (100 μL)</th>
<th>tRNA+ BSA</th>
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<td>2</td>
<td>No</td>
</tr>
<tr>
<td>2</td>
<td>60</td>
<td>2</td>
<td>No</td>
</tr>
<tr>
<td>3</td>
<td>45</td>
<td>2</td>
<td>No</td>
</tr>
<tr>
<td>4</td>
<td>45</td>
<td>2</td>
<td>Yes</td>
</tr>
<tr>
<td>5</td>
<td>45</td>
<td>2</td>
<td>Yes</td>
</tr>
<tr>
<td>6</td>
<td>45</td>
<td>3</td>
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<tr>
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<td>25</td>
<td>2</td>
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</tr>
<tr>
<td>11</td>
<td>25</td>
<td>2</td>
<td>Yes</td>
</tr>
<tr>
<td>12</td>
<td>25</td>
<td>2</td>
<td>Yes</td>
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## Table S3. Cloned Sequences

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<thead>
<tr>
<th>Clone&lt;sup&gt;a&lt;/sup&gt;</th>
<th>N40 Region Sequence (5' - 3')&lt;sup&gt;b&lt;/sup&gt;</th>
<th>% dU's</th>
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<tbody>
<tr>
<td>8.1A</td>
<td>ACAACAAATGTGACATCGCGATTCCCCATATCCAGGCA</td>
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<tr>
<td>8.2A</td>
<td>GATGCGTGTTGAGTTGAGTGTTGAGTGTGCAGCT</td>
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</tr>
<tr>
<td>8.3A</td>
<td>CGAGGGGATGACTTTGCTTCCATGAGCTTTCCGTAATCGCT</td>
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<td>8.4A</td>
<td>AGAAAACAAACAGCAGCATGGGGAGGTCCGCGAGGCTT</td>
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<td>8.5A</td>
<td>TGTCGTTGCTGCTATTGTTGATAAGAGCTCCACATATT</td>
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<tr>
<td>8.6A</td>
<td>TGTCGCTGCGATTGAGTGTTGAGTGTGCAGCT</td>
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<tr>
<td>8.7A</td>
<td>TGATTAACCCGTGCAGGGAAGCTTGCGCTCTTCTTGTTCCA</td>
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<tr>
<td>8.8A</td>
<td>TGGTGTGTATGCGCTGTTGAGGCTTTCGCTCTTGGCCGA</td>
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<tr>
<td>8.9A</td>
<td>TGGGGGGGTGGTGGTGCGTTGGTGAACCTACAGNTCAC</td>
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<tr>
<td>8.10A</td>
<td>GAGTGTGTTGTTGCGGATGGTGCTAGGGGTTGTTGCTT</td>
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<td>8.11A</td>
<td>CCGCGAACCCTTAACCATTTCTCTGACTAACCTTGTTCCA</td>
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<td>8.12A</td>
<td>TGATAGAAAATGTCCGGGAGGCAGCATAGTGCAATTACGAAAA</td>
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<td>8.13A</td>
<td>AGGGAGGTGAAGGGGGTATTGATGCTGCTCTCTTTCTTCTTCA</td>
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<td>8.14A</td>
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<td>8.15A</td>
<td>TACGGACTCATGAAGCCAGCAGCTTTACTCATACACACA</td>
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<td>8.16A</td>
<td>GATGCGTGTTGAGTGTTGAGTGTGCTGCTGCTGCTG</td>
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<td>8.17A</td>
<td>AGTGCACTGCGTTTATCTGGGTGGTTTACTTGGCTTGT</td>
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<tr>
<td>8.18A</td>
<td>TGTCCTTTGGTGGGCCTGGTACCTGGTCTCTCTGCTGT</td>
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<td>8.20A</td>
<td>ATGGATCCGGACGTTGACAAAATCTAGGGTCTTGAGCA</td>
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<tr>
<td>8.21A</td>
<td>GATGCGTGTTGAGTGTTGAGTGTGCTGCTGCTGCTG</td>
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<td>8.22A</td>
<td>TGTCCTTTGGTGGGCCTGGTACTGGTCTAGGGCTATAG</td>
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<td>8.23A</td>
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<td>8.26A</td>
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<td>8.28A</td>
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<td>8.1B</td>
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</tr>
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<td>8.2B</td>
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</tr>
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<td>8.3B</td>
<td>TGGGTGGTGGTGCTGCCCTGTGTTGTGCTGCTGCGTGCA</td>
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</tr>
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<td>8.4B</td>
<td>TCCAGTGTCTGCTGATACGGAACGGCAGGTGCTAAGGATATT</td>
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<td>8.5B</td>
<td>TTTCATTGCCTGTGCTCTGCTTGTTAGGTTGTTGTGCA</td>
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<td>8.6B</td>
<td>ACCATCAGCACCAGCGCCATGCCTCTTCTTCTTCACTT</td>
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<td>8.7B</td>
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<td>8.8B</td>
<td>AGTGTTGGTGTTGTTGAGTGTGCTGCTGCTGCTGCTG</td>
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</tr>
<tr>
<td>8.10B</td>
<td>TTGTGTATGGCTTGTGTTGTGCTGCTGCTGCTGCTGCTG</td>
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</tr>
<tr>
<td>8.11B</td>
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<tr>
<td>8.14B</td>
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<tr>
<td>8.15B</td>
<td>TGCGTTCTGTGCTGCGCTTTTATTGTTGCTGCCCTTTA</td>
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<tr>
<td>8.16B</td>
<td>TTGGCGTCCGGTTTATGGGAATGTTGCTGCTGCTGCTG</td>
<td>46</td>
</tr>
<tr>
<td>8.17B</td>
<td>TCTTTGGTTGGTTCAGCGTTGTATTGTTGCTGCTGCTC</td>
<td>40</td>
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<tr>
<td>8.18B</td>
<td>TTTGTTTGGTTGCTGCGCTTTATGCGGTTGCTGCTGCTG</td>
<td>42.5</td>
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<tr>
<td>8.21B</td>
<td>GCTGGAGGTGCGGGTTACGGGTTGTTGCTGCTGCTGCTG</td>
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<tr>
<td>8.27B</td>
<td>CATGCGTGTTGGCTATGGTGAGCTGTGCTGCTGCTGCTG</td>
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</tr>
<tr>
<td>8.28B</td>
<td>TTAGTTGTGTTGCCAGGTTTGTGGTTTGTTGTTGCTTTG</td>
<td>42.5</td>
</tr>
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</table>
Note: a) A and B denote different lots of clones submitted for sequencing.
b) Only the N40 region is shown. The primer regions are not included.
c) Note that dUr is read as dT during the sequencing process.
Table S4. Raw data for the specificity analysis of clones 8.10A, 8.14B, 8.18B and 8.28A

<table>
<thead>
<tr>
<th></th>
<th>expt 1</th>
<th>expt 2</th>
<th>expt 3</th>
<th>AVG</th>
<th>STDEV</th>
<th>AVG/AVG</th>
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<tbody>
<tr>
<td><strong>8.10A</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>E. coli DH5a</td>
<td>10.9</td>
<td>8.3</td>
<td>14.3</td>
<td>11.2</td>
<td>1.0</td>
<td>1.0</td>
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<tr>
<td>E. coli K12</td>
<td>8.9</td>
<td>10.6</td>
<td>1.4</td>
<td>7.0</td>
<td>1.6</td>
<td>0.4</td>
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<tr>
<td>E. coli O14:K7</td>
<td>7.7</td>
<td>8.2</td>
<td>1.9</td>
<td>5.9</td>
<td>1.2</td>
<td>0.3</td>
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<tr>
<td>S. cerevisiae</td>
<td>4.0</td>
<td>3.9</td>
<td>2.2</td>
<td>3.4</td>
<td>0.3</td>
<td>0.2</td>
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<tr>
<td>B. subtilis</td>
<td>0.8</td>
<td>2.4</td>
<td>11.3</td>
<td>4.8</td>
<td>1.9</td>
<td>0.7</td>
</tr>
<tr>
<td>P. fluorescens</td>
<td>3.0</td>
<td>3.0</td>
<td>0.8</td>
<td>2.3</td>
<td>0.4</td>
<td>0.1</td>
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<tr>
<td>A. tumefaciens</td>
<td>1.6</td>
<td>10.7</td>
<td>0.7</td>
<td>4.3</td>
<td>1.8</td>
<td>0.3</td>
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<tr>
<td>unmod crtl¹</td>
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<td>1.0</td>
<td>1.1</td>
<td>0.1</td>
<td>0.1</td>
<td></td>
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</tbody>
</table>

|          |        |        |        |     |       |         |
| **8.14B** |        |        |        |     |       |         |
| E. coli DH5a | 17.0   | 6.7    | 16.2   | 13.3| 1.9   | 1.0     |
| E. coli K12  | 16.3   | 4.4    | 2.0    | 7.6 | 2.6   | 0.4     |
| E. coli O14:K7 | 5.4   | 8.4    | 5.1    | 6.3 | 0.6   | 0.4     |
| S. cerevisiae | 2.6    | 3.6    | 6.6    | 4.3 | 0.7   | 0.4     |
| B. subtilis  | 1.7    | 4.8    | 9.0    | 5.2 | 1.2   | 0.5     |
| P. fluorescens | 1.8    | 2.0    | 2.1    | 2.0 | 0.1   | 0.1     |
| A. tumefaciens | 2.0    | 2.0    | 2.4    | 2.1 | 0.1   | 0.1     |
| unmod crtl¹ | 1.3    | 1.0    | 1.2    | 0.1 | 0.1   |         |

|          |        |        |        |     |       |         |
| **8.18B** |        |        |        |     |       |         |
| E. coli DH5a | 19.0   | 10.7   | 19.2   | 16.3| 1.6   | 1.0     |
| E. coli K12  | 10.3   | 3.4    | 2.3    | 5.3 | 1.4   | 0.2     |
| E. coli O14:K7 | 2.9   | 3.9    | 4.8    | 3.9 | 0.3   | 0.2     |
| S. cerevisiae | 0.0    | 0.0    | 3.0    | 1.0 | 0.6   | 0.1     |
| B. subtilis  | 1.3    | 5.1    | 6.0    | 4.1 | 0.8   | 0.3     |
| P. fluorescens | 1.6    | 2.1    | 0.8    | 1.5 | 0.2   | 0.1     |
| A. tumefaciens | 1.6    | 2.2    | 1.3    | 1.7 | 0.2   | 0.1     |
| unmod crtl¹ | 0.7    | 1.4    | 1.1    | 0.2 | 0.2   |         |

|          |        |        |        |     |       |         |
| **8.28A** |        |        |        |     |       |         |
| E. coli DH5a | 20.8   | 15.3   | 23.9   | 20.0| 1.5   | 1.0     |
| E. coli K12  | 17.5   | 10.6   | 2.4    | 10.2| 2.5   | 0.3     |
| E. coli O14:K7 | 2.8   | 2.9    | 4.0    | 3.2 | 0.2   | 0.2     |
| S. cerevisiae | 4.7    | 2.8    | 2.0    | 3.2 | 0.5   | 0.1     |
| B. subtilis  | 3.6    | 3.8    | 4.3    | 3.9 | 0.1   | 0.2     |
| P. fluorescens | 1.5    | 1.5    | 2.1    | 1.7 | 0.1   | 0.1     |
| A. tumefaciens | 2.5    | 2.4    | 1.3    | 2.1 | 0.2   | 0.1     |
| unmod crtl¹ | 1.1    | 1.5    | 1.3    | 0.1 | 0.1   | 0.0     |

¹The unmodified control represents the aptamer sequence synthesized in the presence of TTP instead of dUTP.
<table>
<thead>
<tr>
<th>Concentration (nM)</th>
<th>expt 1</th>
<th>expt 2</th>
<th>expt 3</th>
<th>expt 4</th>
</tr>
</thead>
<tbody>
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<td>30 nM</td>
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<td>60 nM</td>
<td>0.316635</td>
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</tr>
<tr>
<td>100 nM</td>
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<td>1000 nM</td>
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<td>1</td>
<td>1</td>
<td>1</td>
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Table S5. Raw data for the saturation binding assay of aptamer 8.28A.