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

Supporting Information

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Table S1. Oligonucleotide sequences

Name	Sequence (length) 5′ - 3′
N40 template	GCG CTC GCG CGG CGT GCN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN CTG TTG GCG CAG GCC GAC GC (77)
Selection Primer	Biotin-GCG TGC CrCrG rUCT GTT GGT TTT GCG TCG GCC TGC GCC AAC AG (41)
Selection Primer - no Biotin	GCG TGC CrCrG rUCT GTT GGT TTT GCG TCG GCC TGC GCC AAC AG (41)
PCR primer forward (1st_amp_2)	Phos-GCG TCG GCC TGC GCC AAC AG (20)
PCR primer back (1st_amp_1)	GCG CTC GCG CGG CGT GC (17)

TABLE S2. Summary of selection conditions

Selection Round	Incubation Time (min)	Washes (100 μL)	tRNA+ BSA
1	60	2	No
2	60	2	No
3	45	2	No
4	45	2	Yes
5	45	2	Yes
6	45	3	Yes
7	35	2	Yes
8	35	2	Yes
9	35	3	Yes
10	25	2	Yes
11	25	2	Yes
12	25	2	Yes

Table S3. Cloned Sequences

Clone[a]	N40 Region Sequence (5′ - 3′)[b]	% dU^{y}s
8.1A	ACAACAAATGTGACCATGCGATTCCCCATATCCAGGCACA	17.5
8.2A	GATGCGTGTGGTGTGGAGTTGTGTGAGTGGTCTGCGTTGT	35
8.3A	CGAGGGAATGACTTTGGTCCATGCGCTTCGGTACTCAGCT	27.5
8.4A	AGAACAACACAAGCAGCATGGAACCAGTGCGCACGGTCTA	10
8.5A	TGTCGTGCTCGCTATGGTGTATTGTGAAGAGTCCAATATT	37.5
8.6A	TGTGCGTGCAGTATGGCGGTCTGTGTGTGGCATGTGCGGT	32.5
8.7A	TGATAACCGCTGCCGGAACTGTGCCTGCTTCTGGTTCCCA	27.5
8.8A	TGTGTGTATGCGTTCATGTGGTGAGGTCTTGCGTCTGTTT	45
8.9A	TGGGGGGGGTGGTGGGTGGGCTTGGTTCGGTACGNCTGT	28
8.10A	GAGTGTGTGTGGGTCCGAGTGGGTGGTCAGGGTTTGTTT	36
8.11A	CCGCGAACCCCTAACCTATTCCTTGACTAACCTTGTTCAG	25
8.12A	TGATAGAAATGTCGGGAGCGAACTAGTTCGAATTACGAAA	22.5
8.13A	AGGGGAGTGTAAGGGGCTGATTGTTGTGTTGCGTTCTCCT	35
8.14A	TGAAGTTCCAGCAGGCCACACCGCATGACGTTTTTCAGCA	22.5
8.15A	TACGGACTCATGAAGCCAGCCATTTCTTAGTCACACACCA	22.5
8.16A	GATGCGTGTGGTGTGGTGGTATGTGTGTGGCTTGTGCTGT	40
8.17A	AGTGCATGCGTGTTTATCTGGCGTGGTTTTACGTGTGTTT	45
8.18A	TGTGCTTTGGTGGCGTTGTGTAGTGGTTCGTCCTGTGGTA	42.5
8.20A	ATGGATCGGGACGGTTGAGCAAAACTTCATGGCTTTGACA	25
8.21A	GATGCGTGTGGTGTGGAGTTGTGTGAGTGGTCTGCGTTGT	37.5
8.22A	TGTGCTTGTGGCGCGTGGGTGTGTAGGTGGTCTATGCAT	36
8.23A	AAGTGGTGAGTGTCAGTGTGGTCTGTTGTGTTCCGTGTAT	40
8.24A	TGTGTTTGTGGTACGAGCGTGTGTGGATGGTCCGTGTCA	36
8.26A	ACTGTGTGCGTGCTCAAGTAGGGTGGTATTTTGTGAGCCT	35
8.28A	TCCTCGCGTTTGGATTCATGTTGGTTTGTCGGTGTATTGT	47.5
8.30A	ACAGAAAGTGTGGCCATGTGTTGTGTCCCTGGCAGGTTAGTTTA	32
8.1B	AGGTGTGGTGCATGTGGTATGTGTTGTTGGCCTGTTAGCT	40
8.2B	TTGAGTCAATGACACACCACGCACTAAATCTCGGCACTCT	22.5
8.3B	TTGGTGGTGTGTGCCTTGGTGTTGTGTGTCGTTGGGTCA	43.5
8.4B	TCCAATGTCTCGTACGCAACGGGCGTGGTCTAAGGATAAT	25
8.5B	TTCATGCCCTGTGTCTTGCTCTTGTGAGTTGTTGTGTCA	46
8.6B	ACCATCACGCACCTGCACCGTCGCCTCTATCCTTCACTT	25.5
8.7B	ACCACCCCCTCGTAACACGTCTCCCGTCCTCGCCATGTTA	22.5
8.8B	AGTGTGTGTGGTGTGGTGATATGCTGTTGGTCTATCTTCA	42.5
8.10B	TTTGTTATGGCTGTGTTGTGTTGTGGCTAGTGTGGTGGCA	45
8.11B	ATGGTGGTCTGTGTCTCTGTGTTGTGCGTTAGTGGGTCA	41
8.14B	TCTGTGTGCGGTGTTATGCGGGTTGGGTTGTTTGTGTTT	48.5
8.15B	TGCGTCCTGTGCTGCAGTCTTTGTGTGTCCCCTTAGTCCT	40
8.16B	TTTGCGTCCGGGTTTATGCGGGTTGTCTCGTGTCTGTTT	46
8.17B	TCTTGTTGGGTCGACGGTCTGTTCATGTGGGTGTTGTCCC	40
8.18B	TTGTGTTCACGTCATTTCGCACTCCTCTCAGCTACGTTTT	42.5
8.21B	GTTGGAGGTGCGTGGTACGGGTGTGTGCGTGTTGTTCCA	33
8.27B	CATGCGTGTGGGTCATGGTGAGCTGGTCCTGTCGTTGTCT	35
8.28B	TTAGTGTGTGCCAGGGGGTTGTGTGGTTGGTTTGCGTTTG	42.5

8.30B	ATGGTGGTCTGTGTCTCTGTGTTGTGCGTTAGTGGGTCAG	40

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 dU^y 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

	expt 1	expt 2	expt 3	AVG	STDEV	AVG/AVG E coli DH5a
8.10A						
E. coli DH5a	10.9	8.3	14.3	11.2	1.0	1.0
E. coli K12	8.9	10.6	1.4	7.0	1.6	0.4
E. coli O14:K7	7.7	8.2	1.9	5.9	1.2	0.3
S. cerevisiae	4.0	3.9	2.2	3.4	0.3	0.2
B. subtilis	0.8	2.4	11.3	4.8	1.9	0.7
P. fluorescens	3.0	3.0	0.8	2.3	0.4	0.1
A. tumefaciens	1.6	10.7	0.7	4.3	1.8	0.3
unmod crtl[1]	1.2	1.0		1.1	0.1	0.1
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 crtl[1]	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 crtl[1]	0.7	1.4		1.1	0.2	0.1
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 crtl[1]	1.1	1.5		1.3	0.1	0.0

[1] The unmodified control represents the aptamer sequence synthesized in the presence of TTP instead of dU^{y}TP

Table S5. Raw data for the saturation binding assay of aptamer 8.28A

	expt 1	**expt 2**	**expt 3**	**expt 4**
10 nM	0.024777	0.041087	0.133967	0.087347
30 nM	0.287719	0.161289	0.211164	0.305874
60 nM	0.316635	0.150469	0.354631	0.312408
100 nM	0.201232	0.330069	0.172031	0.434172
300 nM	0.628187	0.557381	0.467786	0.67916
600 nM	0.740967	0.521801	0.680914	0.788071
1000 nM	1	1	1	1