

Supporting information for Wilmes and Bell (December 26, 2001) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.012578499.

Table 3. B2 mutant sequences

Sequence	% Plasmid loss/generation	SD of plasmid loss	Best match to ACS/11	Helical stability, Kcal/Mol	No. of As/11	No. of Ts/11
CCAATCTTTAA	1.6	1.9	7	6.2	4	4
AAATGCTAATC	1.6	2.9	6	5.8	5	3
AATGCGAAAAC	1.8	1.6	7	7.7	6	1
CTAAACCTCTA	2.0	0.9	8	6.7	4	3
AAACAAATATA	2.1	1.9	8	3.4	8	2
AAACAAATATA	2.5	2.3	8	3.4	8	2
TAACATAACAA	2.6	1.1	8	4.4	7	2
ATTATCGTTAA	2.9	1.8	8	4.5	4	5
GTTTACAAAAC	2.9	1.5	7	6.3	5	3
AAAATGATATA	2.9	0.4	8	3.2	7	3
AACTACTAAAT	3.2	2.0	7	3.8	6	3
CATACATAACT	3.3	1.3	8	5.0	5	3
AAACAAATATA	3.6	1.5	8	3.4	8	2
ATTAAAATGCT	3.6	3.5	6	4.4	5	3
CCAAACAAAAC	3.7	1.7	8	8.0	7	0
TACCAATTATA	3.7	0.5	6	4.0	5	4
TCAATGTTTAA	3.8	1.0	8	4.8	4	5
CAAAAAGATTA	3.8	1.3	7	5.0	7	2
GTAAAAGACT	3.9	0.8	6	5.6	5	3
CTAAATAGATA	3.9	1.9	9	3.8	6	3
CACAAACTTAA	3.9	1.0	7	6.2	6	2
TATTCCTAAT	3.9	0.7	6	5.0	3	5
AATTACGAAAT	4.0	0.7	7	4.5	6	3
CTAAACAAAAG	4.0	0.5	9	6.1	7	1
GCAAATGTTAA	4.0	1.5	9	6.3	5	3
GACATAAACAC	4.1	2.0	6	7.1	6	1

ATAAAAATGTC	4.1	0.4	7	4.8	6	3
TACATTCAAAA	4.1	1.1	8	4.8	6	3
CAACAGTAAAT	4.1	1.2	8	5.6	6	2
TAACTAACGCT	4.2	1.6	7	5.2	5	3
TTAAATTCGCG	4.2	1.8	6	7.3	3	4
CAACATGAATA	4.2	1.0	8	6.0	6	2
GTTTATTTCCA	4.2	0.9	6	6.3	2	6
CAACAAGACGT	4.3	1.7	5	8.3	5	1
TATAAAATTAC	4.3	1.8	7	2.8	6	4
GTTAATGTACC	4.3	1.0	8	6.9	3	4
CGGCTAAATAC	4.4	1.1	4	8.1	4	2
TGATAAACGCT	4.5	0.6	5	5.5	5	3
CGAATCTTAAA	4.5	0.9	8	6.1	4	5
ATGAATTTAGT	4.5	1.3	7	4.2	5	3
CTAAATACTGA	4.5	1.5	8	5.4	5	4
GATTAATTAAG	4.6	1.2	6	4.3	5	5
TAAAAGTATTT	4.6	1.2	8	2.9	7	3
ATAAACCGCCA	4.6	1.3	7	8.7	5	5
AATTAAAACAT	4.6	1.3	6	3.4	4	1
TGAATTATTAA	4.7	1.4	8	3.2	3	4
GAAACCGCTGA	4.7	1.8	7	10.0	7	1
TAAAAACAGGA	5.0	1.3	7	6.1	3	4
CTTTACGTATA	5.3	2.0	8	5.3	5	1
AGTACCTAAAA	5.4	3.3	8	5.7	6	2
CTTAAATTGTT	5.6	3.1	5	4.6	6	3
TCTCATGATTG	6.6		4	6.8	2	5
CTTGGCTCGCC	7.1	2.2	3	12.3	0	5
TTTCGTACCGC	7.5	0.6	4	9.6	1	4
TTCACAGACTG	7.6		5	8.1	3	3
TACCCTATTAC	7.9	0.1	6	6.2	3	4
TTACTACTCCTA	8.0	1.3	6	6.5	7	4
GTTTATTTCCA	8.5	1.7	6	6.3	2	6
GTAAACCCAT	8.6	0.6	5	7.1	2	6

TAGTGA CTTCG	9.3		3	7.8	4	5
ATCACGATGAC	9.4		6	8.3	4	3
TACATTAATTC	10.0	1.2	5	4.2	2	4
GCACAAGCACG	10.1		5	11.0	4	2
CCAATCTTTAA	10.1	6.2	7	6.2	0	3
TCTTTTAGCAT	10.4	0.6	4	5.3	2	7
CCCTTCACTAT	10.4		4	7.8	4	0
AACGTAGATCG	10.5		5	8.0	3	2
CCAAGTTTCTT	10.7	1	5	7.2	2	6
TTTTACGAGTG	10.9	5.6	5	7.0	2	4
TTGACCTGAGA	10.9		6	8.3	4	2
CTTGACCTCA	11.2		3	9.8	3	3
CCTCGTGTTTA	11.4		5	8.5	2	3
ATTTTCGATAG	11.7	3.1	5	5.7	1	5
TTATTTACTTG	11.9	1.9	5	4.3	2	5
TCCTGACTTGC	12.5		2	9.5	2	3
GTTGTCAACCA	13.5		5	8.9	3	3
GATTCCGCGGT	13.8	5.4	4	10.9	1	3
TGCTCCCAAAC	15.0	4.3	5	9.8	3	3
CTTCCTGGCTT	15.0	6.6	4	9.4	4	4
AGTCCTTTCAT	16.0	3.3	5	6.8	0	5
AATCTACCTTC	16.4	5.4	4	6.8	2	5
CTTCTCGGGTT	17.5		4	9.5	0	5
TGATCCTCACA	23.1	6.4	6	8.2	3	4