Supplementary Material:
Paradigms for Computational Nucleic Acid Design

Robert M. Dirks[*], Milo Lin[¶], Erik Winfree[†‡] and Niles A. Pierce[§‡]

[*]Chemistry, [¶]Undergraduate, [†]Computer Science and Computation & Neural Systems,
[§]Applied & Computational Mathematics, [‡]Bioengineering,
California Institute of Technology, Pasadena, CA 91125.

Table 2. Sequence designs for DNA multiloop designs of Figure 7.

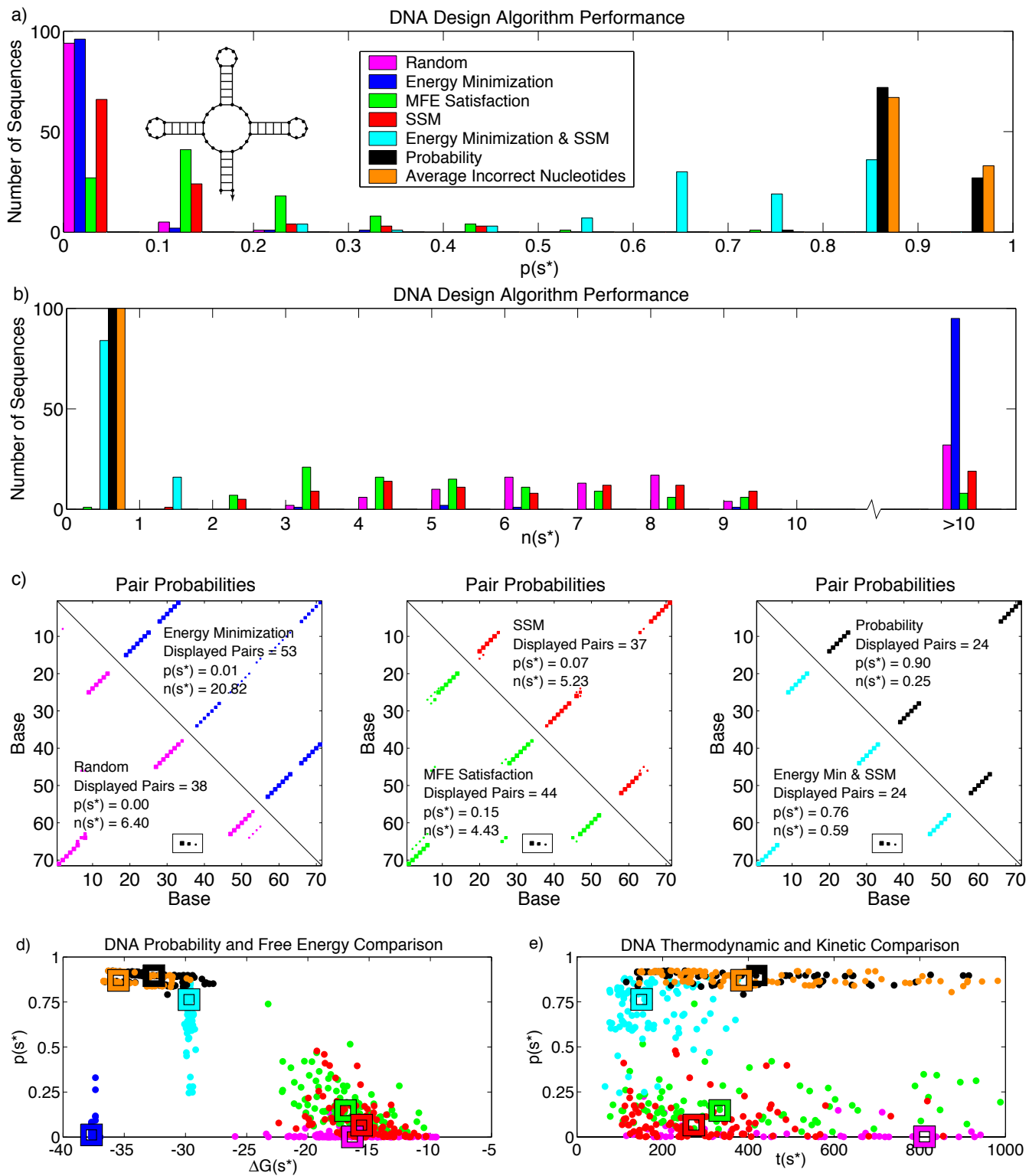| Design Method	$p(s^*)$	$n(s^*)$	CG content	Entropy	Top-ranked based on $p(s^*)$
					((((((..((((((.....))))))..((((((.....))))))..((((((.....))))))..))))))
Random	0.00	8.27	0.50	1.00	ATGGGTTATCACTGCGGCTCAGTGAAACAAGCGTCGTTCGCTTGGGACGTCTATATAAGACGTTTACCCAT
Energy Minimization	0.01	23.67	0.78	0.32	GCGCGGAACGCGCGGTATGCGCGCGAACGCGCGGTCAGCGCGCGAACGCGCGGACTGACGCGCGAACCGCGC
MFE Satisfaction	0.15	5.31	0.50	0.98	CGCGGGGTCGGAACCTAGTGTTCCGTGGGAGCCTTGACGGCTCCTTCTGGGTCCCTCACCCAGGGCCCGCG
SSM	0.07	7.06	0.50	0.99	CGACGCAAACGAAGTTACCCTTCGTGGGGACTCGGTGTGAGTCCTACTATGAAAGCATCATAGCGGCGTCG
Energy Min & SSM	0.76	0.58	0.65	0.72	CGGCACAAGCGAGGAGTCACCTCGCAACGGGCGGTCTACGCCCGAACCCAGCATAAGGCTGGGAAGTGCCG
Probability	0.90	0.34	0.63	0.48	CGCCCGAACGGCGCAAAAAGCGCCGAACGCCGCAAAAAGCGGCGAACGCGGCAAAAAGCCGCGAACGGGCG
Average Incorrect Nucleotides	0.87	0.28	0.68	0.46	CGCCCGAACGGCGCAAAAAGCGCCGAACGCCGCAAAAAGCGGCGAACGCGCGAAAAACGCGCGAACGGGCG

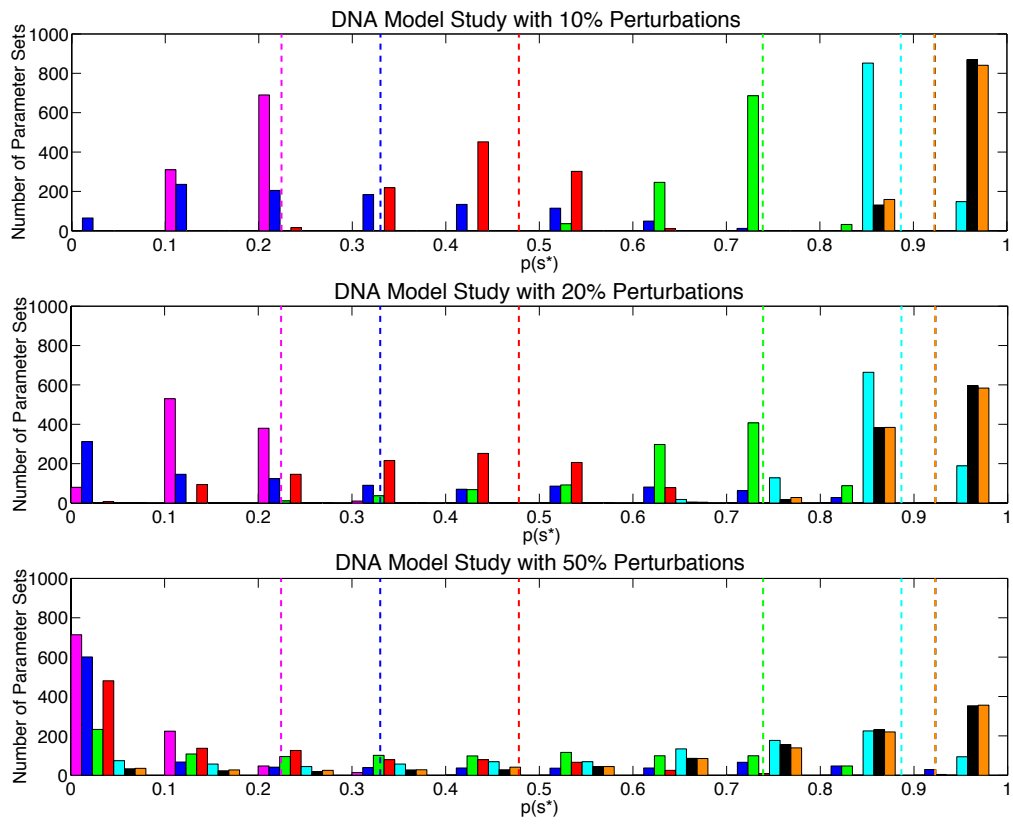**Figure 7.** DNA Multiloop: See caption for Figure 2.

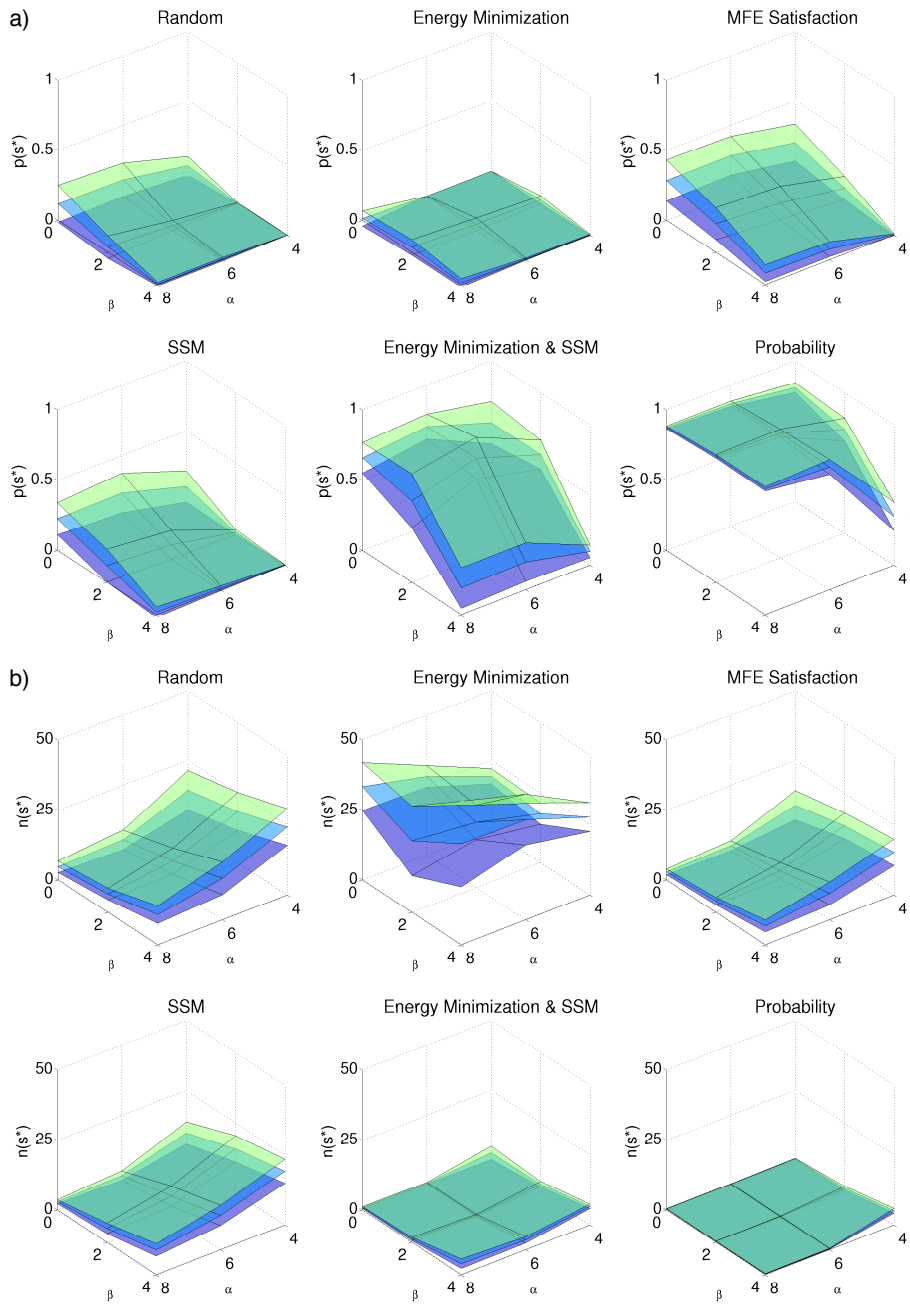**Figure 8.** DNA model perturbation study. See caption for Figure 3.

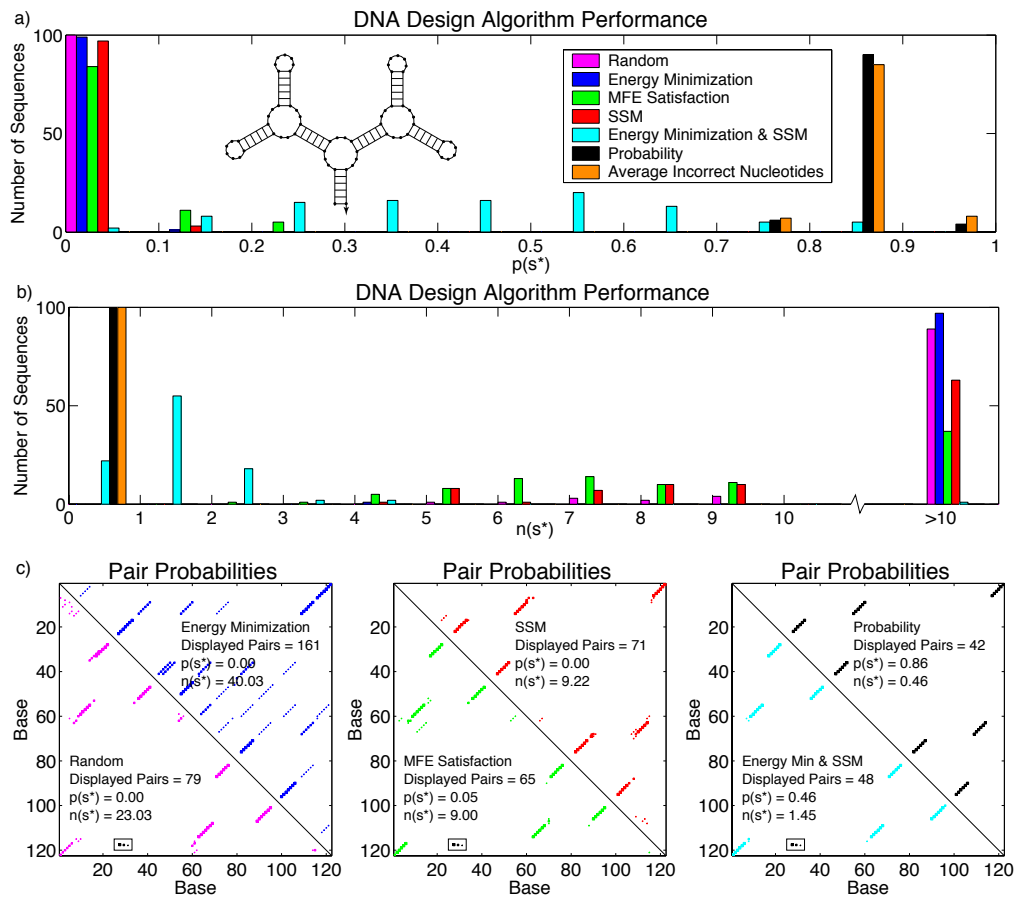**Figure 9.** DNA Multiloop Variations: See caption for Figure 4.

Figure 10. Large DNA multiloop: See captions for Figures 2abc.