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Supporting Information

Large-scale investigation of the effects of nucleobase sequence on fluorescence excitation and Stokes shifts of DNA-stabilized silver clusters

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DNA-stabilized silver cluster synthesis. The 1,880 DNA oligomers studied were subjects of previous studies.[1–4] All oligomers are 10 bases in length. DNA was ordered from Integrated DNA Technologies with standard desalting, pre-suspended in DNase-free water at 40 µM in 384 well plates. A Beckman Coulter Biomek 2000 pipetting robot was used for parallel Ag_N-DNA synthesis in low volume 384 well clear bottom polystyrene microplates with nonbinding surface (Corning). First, 10 µL of an aqueous solution of 400 µM $AgNO_3$ and 40 mM NH_4OAc, pH 7, is pipetted into each well. Then, 20 µL of 40 µM DNA is added, followed by mixing *via* pipetting. After 18 minutes, silver-DNA solutions are reduced by 10 µL of freshly prepared 200 µM $NaBH_4$, followed by mixing *via* pipetting. Finally, microplates are centrifuged for < 60 seconds at low speed to remove any small bubbles that may cling to sides of microplate wells. Final concentrations are 20 µM DNA, 100 µM $AgNO_3$, and 50 µM $NaBH_4$; stoichiometries were selected to maximize the number of brightly fluorescent wells and the range of fluorescence colors for 10-base DNA oligomers.[2] Well plates were stored in the dark at 4 °C until measurement, which was performed one week after synthesis to ensure time stability of measured products.

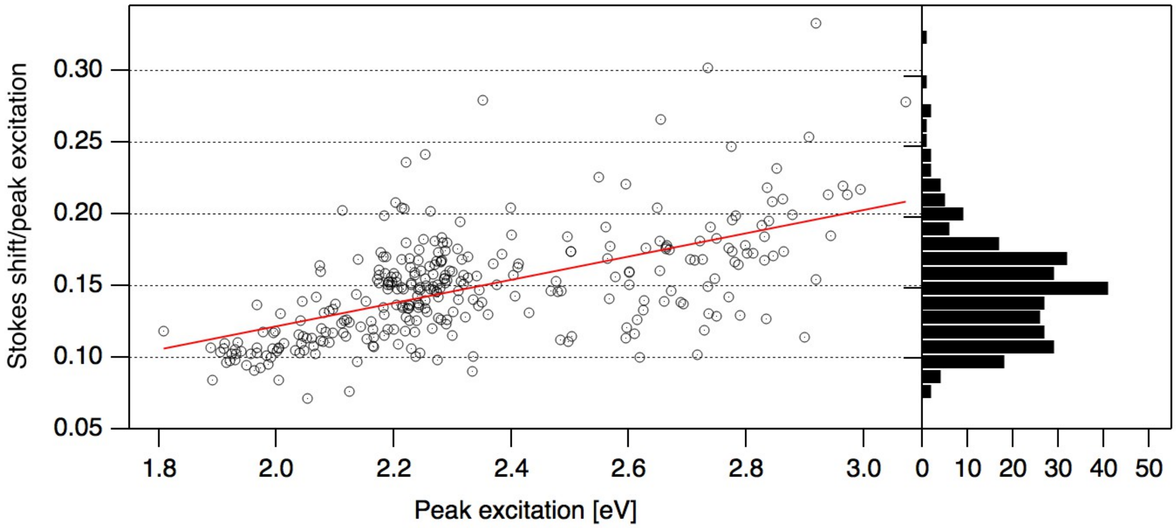

Figure S1: Left: Stokes shift (as a fraction of peak excitation energy) *versus* peak excitation energy for single-peaked Ag$_N$-DNA. A linear fit to the data is in red. **Right:** Histogram of Stokes shift as a fraction of peak excitation energy.

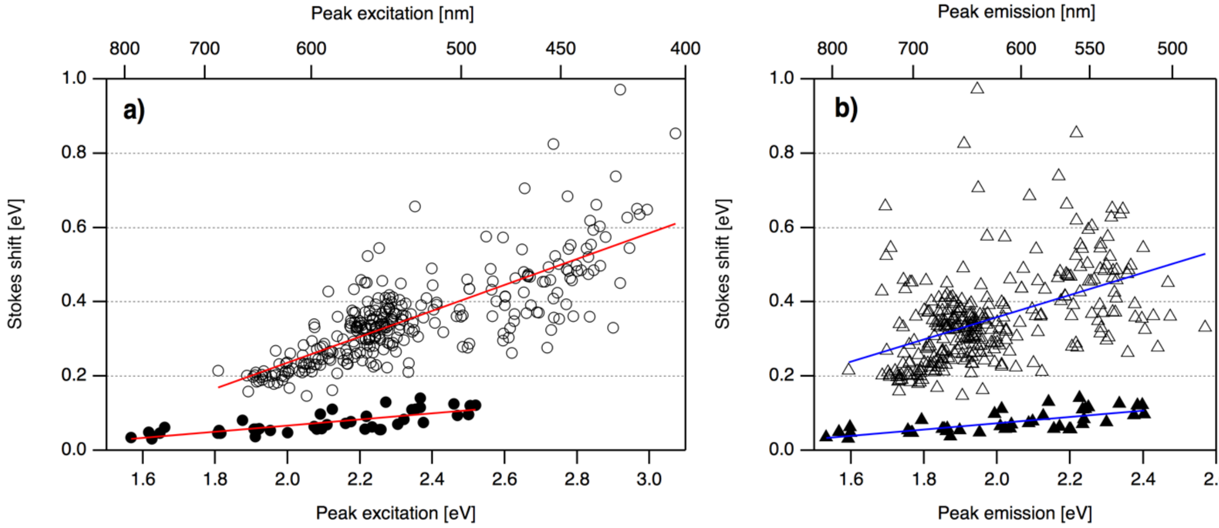

Figure S2: Comparison of Stokes shifts for Ag$_N$-DNAs (hollow markers) and common organic fluorophores (solid markers). **a)** Stokes shift as a function of peak excitation (circles), with linear least squares fits (red lines). **b)** Stokes shift as a function of peak emission (triangles), with linear least squares fits (blue lines). Stokes shift scales 4.2 times more strongly with peak excitation and 3.6 times more strongly with peak emission for Ag$_N$-DNA than for the common organic fluorophores, as determined by the ratio of the linear slopes. (Ag$_N$-DNA: SS = 0.35*E_{ex} - 0.46, SS = 0.30*E_{em} - 0.24; organic dyes: SS = 0.083*E_{ex} - 0.098, SS = 0.084*E_{em} – 0.096)

Table S1: Excitation and emission energies and Stokes shifts for common organic molecule fluorophores. Taken from the list of fluorophore modifications available from Integrated DNA Technologies.[5]

Dye	Ex. [eV]	Em. [eV]	Stokes shift [eV]
Alexa Fluor® 488 (NHS Ester)	2.520	2.398	0.122
6-FAM (Fluorescein)	2.505	2.384	0.120
Fluorescein dT	2.505	2.384	0.120
6-FAM (NHS Ester)	2.500	2.403	0.097
6-FAM (Azide)	2.500	2.403	0.097
ATTOTM 488 (NHS Ester)	2.470	2.375	0.095
Rhodamine GreenTM-X (NHS Ester)	2.460	2.335	0.125
TETTM	2.375	2.300	0.075
MAX (NHS Ester)	2.366	2.226	0.140
Yakima Yellow®	2.366	2.250	0.116
Alexa Fluor® 532 (NHS Ester)	2.353	2.242	0.111
JOE (NHS Ester)	2.344	2.234	0.110
ATTOTM 532 (NHS Ester)	2.322	2.238	0.084
HEX	2.305	2.234	0.071
5-TAMRA TM (Azide)	2.271	2.141	0.129
TYE™ 563	2.258	2.202	0.056
Cy3TM	2.254	2.198	0.056
Alexa Fluor® 546 (NHS Ester)	2.234	2.171	0.063
TAMRATM	2.218	2.127	0.091
TAMRA (NHS Ester)	2.218	2.127	0.091
ATTOTM 550 (NHS Ester)	2.214	2.156	0.058
ATTOTM 565 (NHS Ester)	2.175	2.098	0.077
Rhodamine RedTM-X (NHS Ester)	2.160	2.087	0.073
Alexa Fluor® 594 (NHS Ester)	2.123	2.013	0.110
ROX (NHS Ester)	2.109	2.039	0.069
ATTOTM Rho101 (NHS Ester)	2.094	2.036	0.058
ATTOTM 590 (NHS Ester)	2.091	1.993	0.097
TEX 615	2.080	2.023	0.058
Texas Red®-X (NHS Ester)	2.073	2.009	0.064
Lightcycler® 640 (NHS Ester)	2.000	1.953	0.047
ATTOTM 633 (NHS Ester)	1.953	1.899	0.054
TYE™ 665	1.922	1.864	0.058
Cy5TM	1.913	1.856	0.057
WellRED D4 Dye	1.913	1.862	0.052

ATTOTM 647N (NHS Ester)	1.910	1.873	0.038
Alexa Fluor® 647 (NHS Ester)	1.907	1.851	0.057
Alexa Fluor® 660 (NHS Ester)	1.876	1.794	0.081
WellRED D3 Dye	1.815	1.769	0.047
5' IRDye® 700	1.813	1.766	0.046
Cy5.5TM	1.810	1.756	0.054
TYE 705	1.807	1.761	0.046
Dy 750 (NHS Ester)	1.660	1.598	0.062
Alexa Fluor® 750 (NHS Ester)	1.647	1.600	0.047
WellRED D2 Dye	1.625	1.594	0.031
5' IRDye® 800CW (NHS Ester)	1.616	1.567	0.049
5' IRDye® 800	1.567	1.533	0.035

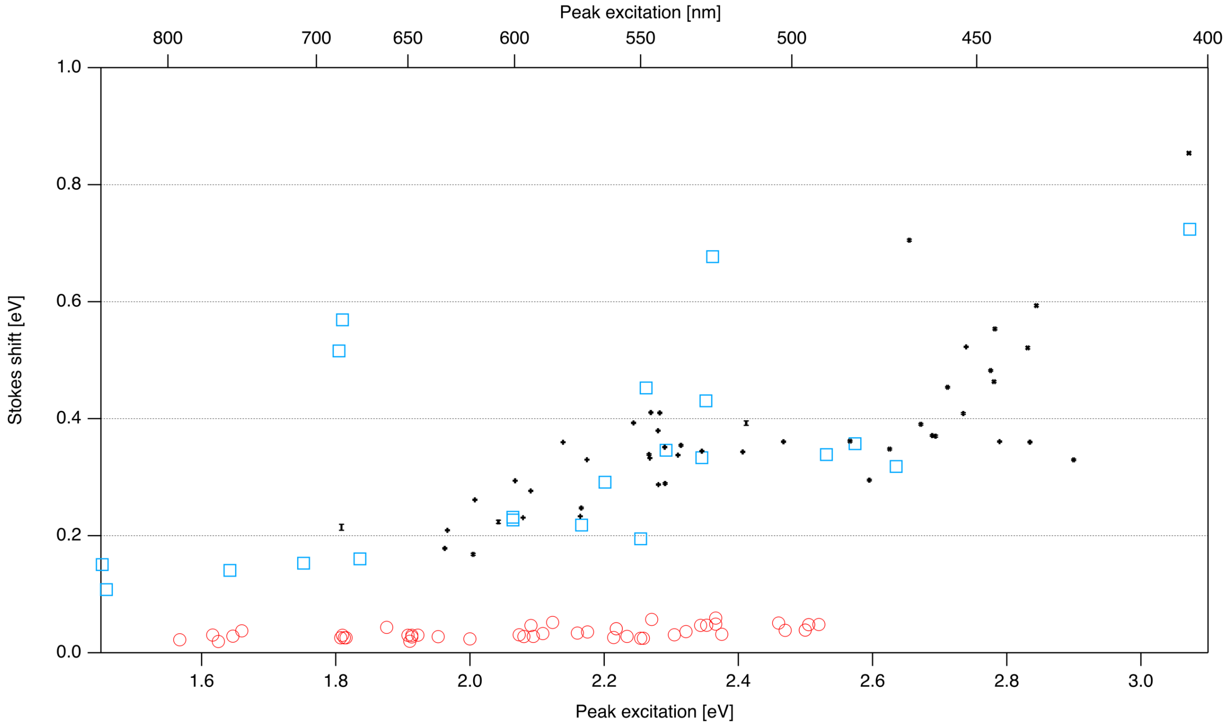

Figure S3: *SS versus E_{ex}* for spectrally pure solutions of Ag$_N$-DNAs (black) with randomly selected DNA template sequences only,[1] as compared to the full set of data shown in main text Figure 3. Previously characterized HPLC-purified Ag$_N$-DNAs (cyan squares). Organic fluorophores which are commonly used to label oligonucleotides (red circles).[5] Vertical and horizontal error bars of black points represent standard deviations; other markers are larger in size than associated standard deviations.

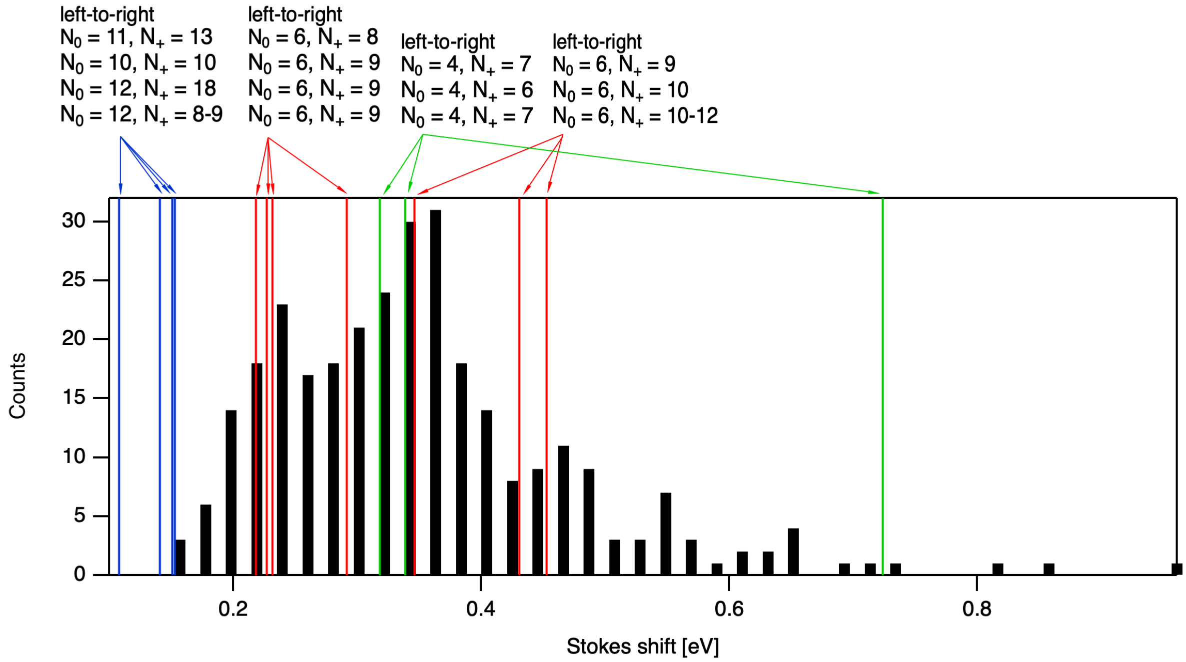

Figure S4: Histogram of *SS* values for spectrally pure solutions of Ag$_N$-DNAs (black). Fourteen colored vertical lines represent *SS* values of purified Ag$_N$-DNAs with N_0 = 4 (green), N_0 = 6 (red), and N_0 = 10 to 12 (blue), as determined by high-resolution mass spectrometry (HR-MS).[6,7,28,29] The composition of each purified Ag$_N$-DNA is listed above the histogram, including both neutral silver content N_0 and cationic silver content N_+.

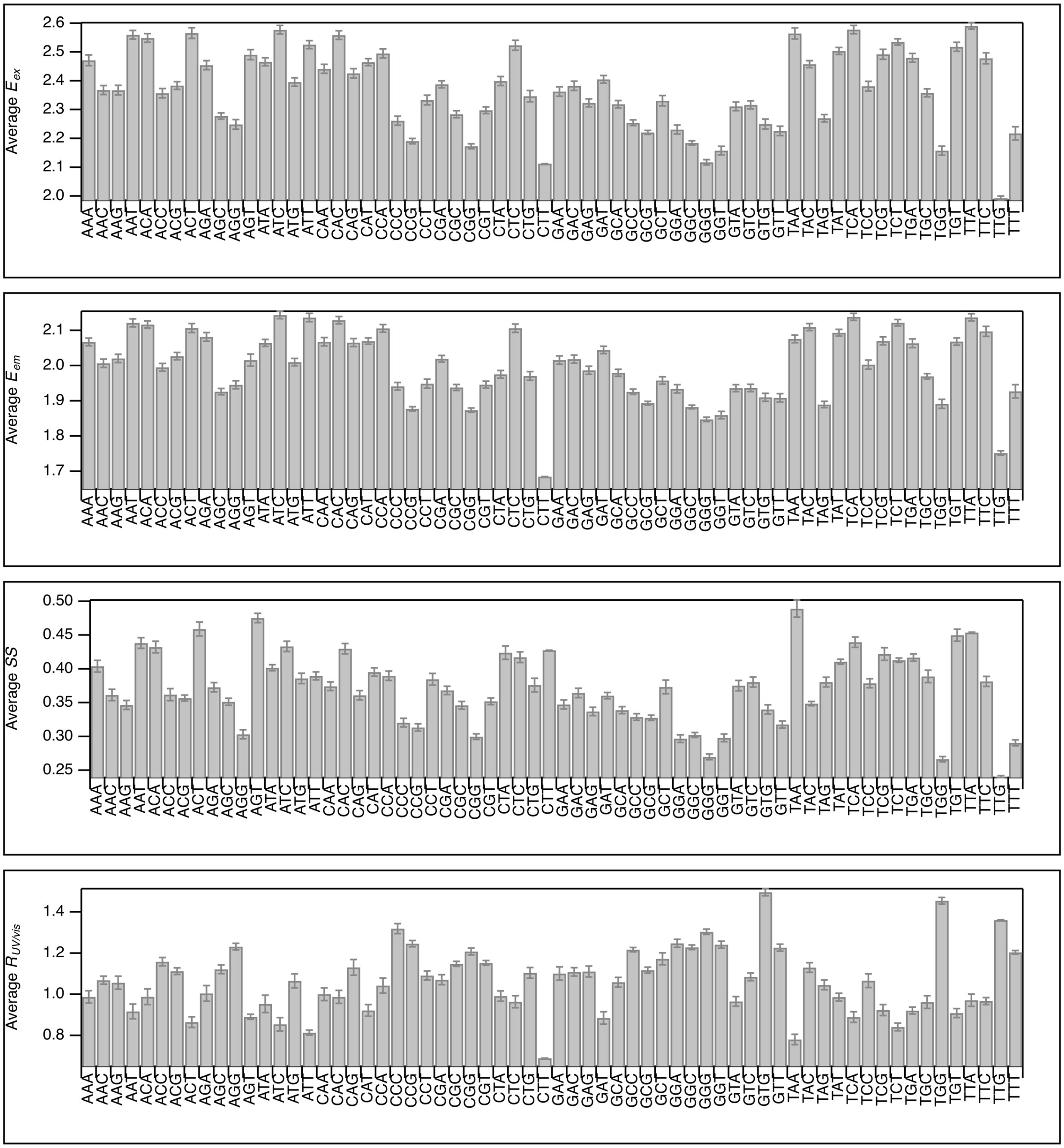

Figure S5: Mean values of (a) E_{ex}, (b) E_{em}, (c) *SS*, and (d) $R_{UV/vis}$ for each instance of the 64 possible three-base motifs in the set of DNA template sequences for the 305 spectrally pure Ag_N-DNAs. Error bars represent standard error, as a measure of precision of the mean. Note: there is only one occurrence of motif CTT in the 305 DNA sequences; thus, error bars for this motif have zero width.

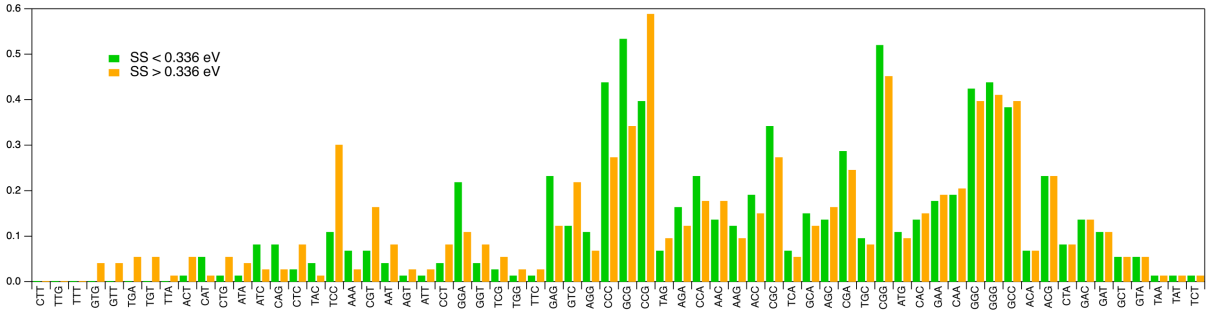

Figure S6: Correlations of 3-base patterns with *SS* for 2.15 eV < E_{ex} < 2.45 eV only. Green: *SS* < 0.336 eV. Orange: *SS* > 0.336 eV. Motifs are sorted left to right in order of greatest relative difference between orange and green bars.

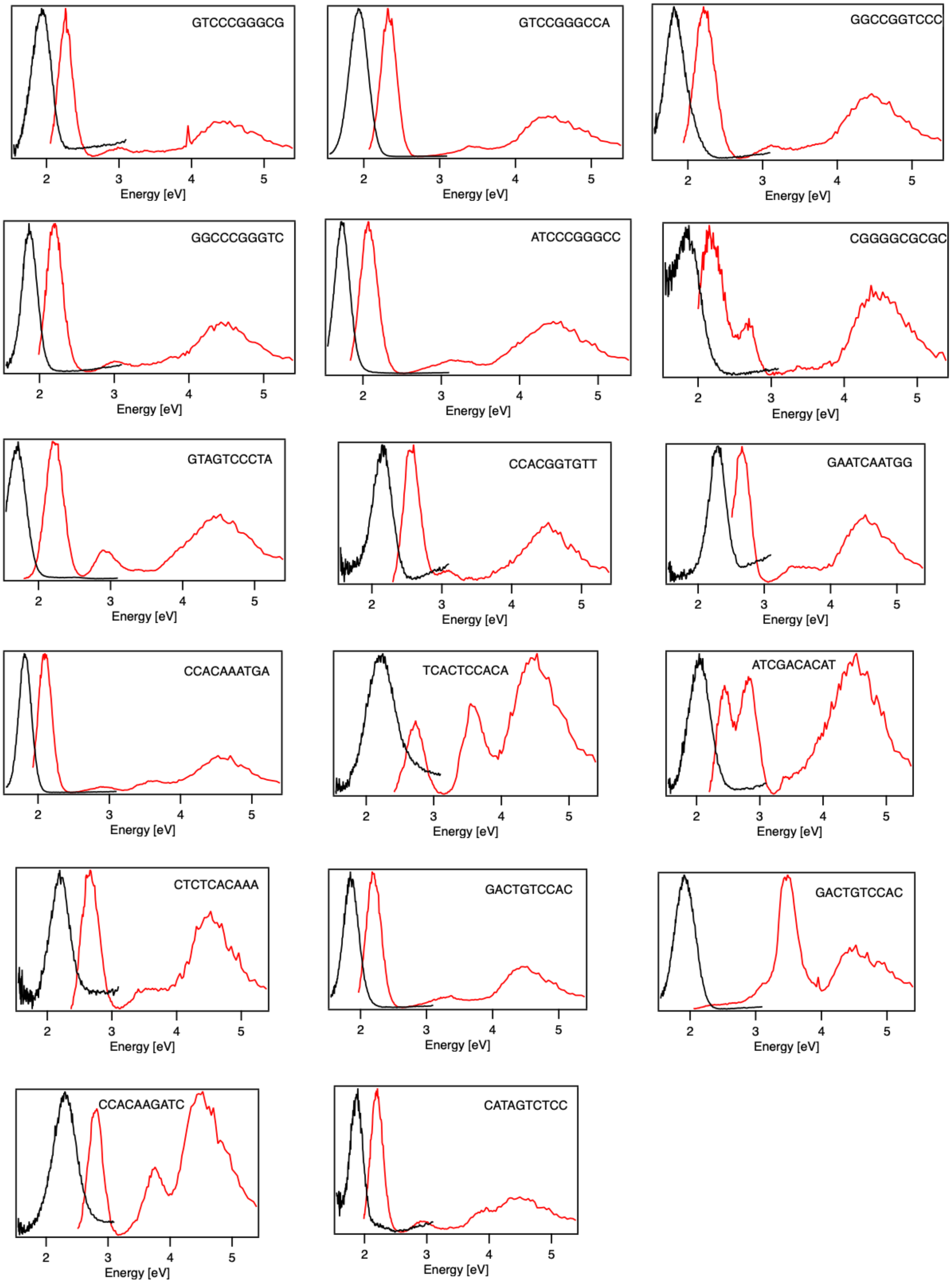

Figure S7: Examples of normalized excitation spectra (red) and emission spectra (black) for Ag$_N$-DNAs identified to have single Gaussian peaks in emission spectra but multiple peaks in excitation spectra in the near UV to visible to NIR ranges.

Table S2: DNA sequences and values for E_{ex}, E_{em}, SS, and $R_{UV/vis}$ for the samples identified to have single-peaked excitation and emission spectra.

Sequence	E_{ex} [eV]	E_{em} [eV]	SS [eV]	$R_{UV/vis}$
CGGTTTGGCC	1.81	1.59	0.21	1.42
CCTGGGGAAA	1.89	1.69	0.20	1.70
TAGGGCTCCG	1.89	1.73	0.16	1.82
CCCCTGGGGT	1.90	1.71	0.20	1.51
TGGGGTTCCG	1.91	1.71	0.20	1.63
CCAGGGGTCC	1.91	1.70	0.21	1.75
CAAGGGACCC	1.91	1.73	0.18	1.63
CCGGGGCGGC	1.92	1.73	0.19	1.81
CCGGGGAGGG	1.92	1.73	0.20	1.67
CCCGGGTGGT	1.93	1.73	0.20	1.50
CCGGGGGACC	1.93	1.74	0.19	1.66
CCCGGGGAAC	1.93	1.73	0.20	1.61
CCCGGAGAAG	1.93	1.72	0.21	1.28
CCCCGGTTCC	1.94	1.74	0.20	1.46
CCCGGCGGGG	1.95	1.76	0.18	1.68
CCCGGGGGGA	1.96	1.76	0.20	1.60
GGGTGGGGTA	1.96	1.78	0.18	1.63
GGGGGGAACC	1.97	1.76	0.20	1.32
GACGGGTCCC	1.97	1.76	0.21	1.25
GCGCAAGATG	1.97	1.70	0.27	0.99
CCGGAGGGGG	1.97	1.79	0.18	1.23
CCCCGGGCGC	1.98	1.74	0.23	1.70
TCGGTCCCGG	1.98	1.78	0.20	1.33
CGGGGAAGAA	1.99	1.80	0.19	1.46
CGGGTCCCGC	1.99	1.79	0.20	1.31
CCCCGGGCCG	1.99	1.78	0.21	1.46
TCCCCCGGGG	1.99	1.76	0.23	1.92
CCCCGGGGCC	2.00	1.76	0.24	1.63
CGGCCCGGGG	2.00	1.79	0.21	1.43
AAGCCCGGGG	2.00	1.79	0.21	1.65
ATCCCCCCCG	2.00	1.79	0.21	2.01
CGGGGGGAGC	2.00	1.84	0.17	1.31

Sequence	E_{ex} [eV]	E_{em} [eV]	SS [eV]	$R_{UV/vis}$
GTGGAGAATG	2.01	1.75	0.26	5.49
CCGGGAAAGC	2.01	1.79	0.22	1.45
GTGGGGAACC	2.03	1.82	0.21	1.53
AGGGCAACGC	2.04	1.80	0.24	1.42
GGCCCTGCGA	2.04	1.83	0.21	1.47
GGGGGCGCGC	2.04	1.79	0.26	0.95
ACCTGGACCG	2.04	1.82	0.22	1.10
CCGGGCGAAG	2.04	1.76	0.28	1.60
CCCGGAGGGC	2.04	1.81	0.23	1.31
GCGTGCATGG	2.05	1.83	0.21	0.88
TCCCGAACAG	2.05	1.82	0.23	1.49
GGCTCGCCAA	2.05	1.91	0.15	1.57
ATCCCCCTGC	2.06	1.83	0.23	1.76
CCCGGAAGGG	2.06	1.84	0.22	1.38
CCCGGACGAC	2.07	1.85	0.21	1.40
CCTGGCTAGC	2.07	1.77	0.29	1.37
ATCCCGGGCC	2.07	1.73	0.34	0.88
CCCGGAAGGC	2.07	1.84	0.23	1.38
GAACGTGCGG	2.07	1.74	0.33	0.94
CGGGGCCCGG	2.08	1.83	0.25	1.38
GCGTTGGCCC	2.08	1.85	0.23	1.29
GAACTAACCC	2.08	1.81	0.27	0.91
CCCCCCCGGG	2.08	1.84	0.25	1.70
CCCCGTTGTT	2.09	1.81	0.28	1.37
ACGGGGCAAA	2.09	1.86	0.23	1.49
CAGGGCCCGG	2.10	1.85	0.25	1.37
CCACAAATGA	2.10	1.82	0.28	1.21
GGCCCCGGGA	2.10	1.81	0.29	1.46
GGGCTGCCCG	2.11	1.85	0.26	1.53
GCAAGAGCTT	2.11	1.69	0.43	0.69
CGGGGCGAAA	2.11	1.87	0.25	1.64
GCAAGCCCGC	2.12	1.85	0.27	1.45
GCCAACTAAT	2.12	1.87	0.24	1.09
GGCCCCGGAG	2.12	1.85	0.27	1.37

Sequence	E_{ex} **[eV]**	E_{em} **[eV]**	*SS* **[eV]**	$R_{UV/vis}$
GCCGTCCCCA	2.12	1.96	0.16	1.81
GCCGGGAAGC	2.12	1.86	0.26	1.41
TGGAGAACCC	2.14	1.83	0.31	0.97
GCAAGGGGCC	2.14	1.93	0.21	1.47
ACGTCAACGT	2.14	1.78	0.36	1.73
GCCGGGAATC	2.14	1.88	0.26	1.12
CCGGGCGGAC	2.15	1.85	0.30	1.16
GCCGGGAATG	2.15	1.91	0.24	1.45
CCCACACGCC	2.16	1.89	0.27	1.75
ATCACAGGGC	2.16	1.93	0.23	1.94
GGCGGGCAAA	2.16	1.91	0.26	1.45
GGCAAGATGC	2.17	1.93	0.23	1.51
CGAAAGGGAA	2.17	1.92	0.25	1.15
GGGGGAGCGC	2.17	1.84	0.33	1.02
GGCTAGCGCG	2.17	1.84	0.33	1.32
CGCGCAATGT	2.17	1.83	0.34	1.11
CCAACTAACG	2.18	1.82	0.35	0.67
TCGAACGCGC	2.18	1.80	0.38	1.17
AGCTGACTCA	2.18	1.81	0.37	1.38
GCGCGGGCCG	2.18	1.89	0.29	1.29
GTGAGTCCCT	2.18	1.75	0.43	0.87
TCCAACCCGG	2.18	1.93	0.25	1.45
CGGCGCCGGA	2.18	1.90	0.28	1.21
TCGTAGCGTA	2.19	1.84	0.35	0.88
GGGGTAGGCC	2.19	1.81	0.37	1.13
GAAGCCCCAC	2.19	1.93	0.26	1.69
CCAGCCCGGA	2.19	1.86	0.33	1.85
GCGCGGATCC	2.19	1.87	0.32	0.99
CCGGGCGGGC	2.19	1.86	0.33	1.09
CGGTCCGGGG	2.19	1.86	0.33	1.03
CATAGTCTCC	2.19	1.86	0.33	1.15
GACTGTCCAC	2.20	1.85	0.34	1.23
GGCCCGGGTC	2.20	1.86	0.33	1.00
GGCCGGGGCA	2.20	1.85	0.35	1.00

Sequence	E_{ex} [eV]	E_{em} [eV]	*SS* [eV]	$R_{UV/vis}$
GCCGGCCGGG	2.20	1.94	0.26	0.97
CCGGAATCCG	2.20	1.74	0.46	0.74
GGGCCGGGCG	2.20	1.86	0.34	1.15
CCATCGAATG	2.20	1.90	0.30	1.18
AGGCCGGGCG	2.20	1.87	0.34	0.97
GAGCGATGCC	2.21	1.88	0.33	0.82
GCGACCCCAG	2.21	1.97	0.24	2.19
ACCCGGCGCG	2.21	1.84	0.37	1.02
CCGGTCCCCT	2.21	1.88	0.33	1.33
GCGCGCAATT	2.21	1.76	0.45	0.96
CGGCCGGGAG	2.21	1.92	0.30	1.09
CGCGCAGAAG	2.22	1.91	0.30	1.17
GCCGGGAGCG	2.22	1.89	0.33	1.03
TTCCCAACGA	2.22	1.77	0.45	0.87
AGGCTACCCC	2.22	1.96	0.26	1.57
CGCGCAAGAA	2.22	1.94	0.28	1.18
GGCCGGTCCC	2.22	1.82	0.40	0.94
GTAGTCCCTA	2.22	1.70	0.52	0.74
GTCCCCAACG	2.22	1.93	0.30	1.29
ACGGCAACCA	2.22	1.92	0.30	1.14
CACCCGGCGG	2.22	1.93	0.30	1.12
CTCCGGGCCG	2.23	1.85	0.38	1.02
CGACACGAGA	2.23	1.95	0.28	1.82
AGAGCCCCCA	2.23	1.92	0.30	1.67
GTCCTGGGCG	2.23	1.87	0.36	0.93
GTCACGCCCC	2.23	1.89	0.34	1.44
GACGCGGCCC	2.23	1.89	0.34	1.10
GGGGCGTAAA	2.23	1.99	0.24	1.15
CCGGGAGGCG	2.24	1.88	0.36	0.98
ACCCGATGCA	2.24	1.97	0.26	1.55
ACCAATGACC	2.24	1.88	0.35	1.07
TGCAAGATTC	2.24	2.01	0.22	0.71
AGGCGCGGGA	2.24	1.96	0.28	1.26
CAAGGCGGGG	2.24	1.92	0.32	0.98

Sequence	E_{ex} [eV]	E_{em} [eV]	*SS* [eV]	$R_{UV/vis}$
CCGGGTGGCG	2.24	1.87	0.38	1.08
GTAGCGATCA	2.24	1.93	0.31	0.46
GCGGCGCCTA	2.24	1.94	0.30	1.09
GCTACGCGCC	2.24	1.91	0.33	1.29
GCCGCGAGGG	2.24	1.94	0.31	1.03
CGGGACAGAC	2.24	1.85	0.39	0.93
CGGCTGGGCG	2.24	2.01	0.23	1.49
GCCGGAGGGG	2.24	1.92	0.33	1.03
CCGCGATGCG	2.25	1.91	0.33	0.98
CAAAGAGCGG	2.25	1.89	0.36	1.01
CGGTCCGGCA	2.25	1.84	0.41	1.05
CCGTCCCGCC	2.25	1.71	0.54	0.97
CGCCCGGGCC	2.25	1.90	0.35	1.12
CGACAACCGT	2.25	1.94	0.32	1.23
ACGTAGCGTC	2.25	1.95	0.30	1.16
AGGGGCCGAA	2.26	1.92	0.34	1.17
GGGCCGGGAG	2.26	1.96	0.30	0.95
CCGGGCCGGA	2.26	1.89	0.37	1.34
GCACGATGCC	2.26	1.81	0.46	0.79
GTCCCGGGCG	2.26	1.93	0.33	0.99
ACGGCAACCG	2.26	1.99	0.27	1.64
CCAGCTCCCG	2.27	1.91	0.36	1.28
CGTCCGTGTT	2.27	1.93	0.34	1.16
GCCGACCTAT	2.27	1.94	0.33	1.50
GGTTCCGGGC	2.27	1.86	0.41	0.96
CGGGAGAACG	2.27	1.90	0.37	0.91
CCGAGCGTCC	2.27	1.89	0.38	1.35
GTAGCGACCC	2.27	1.94	0.33	1.14
GCGCCCAAAC	2.27	1.94	0.33	1.38
TCCCACGATA	2.27	1.93	0.34	1.10
CCGAGAGAAG	2.27	2.05	0.22	1.54
TCCGGGCGCC	2.28	1.88	0.39	1.08
GCACGCCCCA	2.28	1.99	0.29	1.34
GGCGCGGACC	2.28	1.95	0.32	1.00

Sequence	E_{ex} [eV]	E_{em} [eV]	SS [eV]	$R_{UV/vis}$
CCAAGAACGC	2.28	1.94	0.34	1.30
CTAGCGTCGC	2.28	1.90	0.38	1.13
ACGAACATGC	2.28	1.99	0.29	1.45
GAACCGATGC	2.28	1.90	0.38	0.71
CCGGGCCCGT	2.28	1.86	0.42	0.99
GAATCCGGGC	2.28	1.90	0.38	1.01
GCTCGTCTAT	2.28	1.87	0.41	1.12
GGGCGCGGGC	2.29	1.93	0.35	0.93
GCCACGATGC	2.29	1.93	0.35	1.00
CTGCAAGATT	2.29	1.89	0.40	0.65
AGCCGGGCGG	2.29	1.93	0.36	0.90
CGGGAACGCG	2.29	1.94	0.35	1.09
GATCCGGGAG	2.29	2.01	0.28	0.45
TGTCAACAAA	2.29	1.94	0.35	1.10
GTCGACGCCC	2.29	2.00	0.29	1.02
CGTCCGGGCG	2.29	1.88	0.41	0.97
CCGAGCCGGG	2.29	1.93	0.37	1.03
ACGCACCCAG	2.30	2.03	0.27	1.41
CGACCAAGAA	2.30	1.93	0.37	0.89
GGCCGACCCA	2.30	2.00	0.30	1.54
TCAAGGCCCA	2.31	1.90	0.40	1.00
GGCGCGGGAG	2.31	1.99	0.32	1.08
GCCGATACCC	2.31	1.97	0.34	1.51
GCCGGGACCC	2.31	1.86	0.45	1.13
TCCTCCGGCC	2.31	1.96	0.35	1.17
ACTCCGGCCG	2.32	1.93	0.39	1.08
CCACGCGCCG	2.32	1.95	0.36	1.11
ACCGAACGTC	2.32	1.97	0.35	1.09
CCAACGAGAA	2.32	2.02	0.30	0.97
GTCCGGGCCA	2.33	1.93	0.40	1.06
CGACACGATG	2.33	1.96	0.36	1.21
AACCAATCAG	2.33	2.12	0.21	1.41
ACGGAGAGAA	2.34	2.10	0.24	1.08
CTACGCGAAG	2.34	2.01	0.33	1.26

Sequence	E_{ex} [eV]	E_{em} [eV]	*SS* [eV]	$R_{UV/vis}$
GCCCACACAA	2.34	1.97	0.37	1.51
GCCCATGCCC	2.34	2.03	0.32	1.45
CTAGGGCCCT	2.35	2.00	0.34	1.05
CGACGGCAAA	2.35	2.02	0.32	1.05
CACCTAGCGA	2.35	1.70	0.66	0.57
CCCGCCACGT	2.36	2.05	0.31	1.00
GAGCGAATGC	2.37	1.98	0.39	0.83
GAAGCAAGAT	2.38	2.02	0.36	0.83
TGCGCCCCGC	2.38	1.97	0.41	1.32
GCCGAGCCCG	2.40	1.91	0.49	0.99
GCACGGGTTA	2.40	1.96	0.44	1.38
TGAACGGAGA	2.40	2.02	0.38	0.66
GTCAACCGCT	2.41	2.06	0.34	1.15
GCATAGAACG	2.41	2.02	0.39	1.04
CACCCGACGT	2.41	2.01	0.40	1.25
CGAGAACTCA	2.43	2.11	0.32	1.07
CTCTCGCCCG	2.47	2.11	0.36	1.18
GCAAGAGAAG	2.48	2.10	0.38	0.94
AAACGGGGTT	2.48	2.12	0.36	1.04
TGCCAGAATT	2.48	2.21	0.28	0.87
TATCATCGAC	2.48	2.12	0.36	0.76
TGAGCGATGT	2.50	2.04	0.46	0.72
TGGGACCGAA	2.50	2.22	0.28	1.10
TCACAAGCCC	2.50	2.07	0.43	1.32
GAAGAAATGT	2.50	2.07	0.44	0.77
CCACAATCCC	2.50	2.22	0.29	1.25
GACATCCATC	2.55	1.97	0.58	0.44
ACCTCCCCAA	2.56	2.07	0.49	1.21
GTCACGATCT	2.56	2.13	0.43	0.68
ATCCCCAAAC	2.57	2.20	0.36	0.99
CGACACTAAG	2.57	2.11	0.46	0.95
GAACGGCGGT	2.58	2.18	0.40	0.58
CAGTCAATGC	2.59	2.02	0.57	0.68
CCAAACATTC	2.60	2.30	0.30	0.91

Sequence	E_{ex} [eV]	E_{em} [eV]	SS [eV]	$R_{UV/vis}$
GCACGAACAG	2.60	2.28	0.31	0.73
AATCCACGTT	2.60	2.21	0.39	1.07
CCCAACTCGG	2.60	2.19	0.41	0.41
CGAGAATGCA	2.60	2.19	0.41	0.41
GAATCCACGA	2.61	2.31	0.30	1.36
TTCCCACGAT	2.61	2.29	0.33	1.03
TGATCCCTGT	2.62	2.36	0.26	1.09
GGCTCTACAA	2.63	2.28	0.35	0.66
TTTCCACGAC	2.63	2.26	0.37	0.99
AACATCACGA	2.63	2.17	0.46	0.81
TCCAAGAATG	2.65	2.11	0.54	0.32
TATCGATCAC	2.65	2.23	0.42	0.93
CCACACTCAG	2.65	2.17	0.48	0.71
TGCCCTGTCG	2.65	1.95	0.71	0.61
GAATCAATGG	2.66	2.29	0.37	0.78
CTCTCACAAA	2.66	2.20	0.47	0.65
CTGTCCACAT	2.66	2.19	0.47	0.62
TCCAATCCAC	2.66	2.19	0.47	0.91
CCCAATCTGA	2.67	2.20	0.47	0.61
AGGACGATCG	2.67	2.28	0.39	0.69
TAAGCAAGAG	2.69	2.32	0.37	0.53
GCCTACGCAA	2.69	2.32	0.37	1.05
ATCAATGCGA	2.71	2.25	0.45	0.72
CAGATGTCCA	2.71	2.26	0.45	0.63
GGAAGGACCG	2.72	2.44	0.28	1.31
TGCACAAGAA	2.72	2.23	0.49	0.53
CAATCCAGAA	2.73	2.27	0.46	1.15
CAAGACTCAC	2.73	2.40	0.32	0.68
CCGAGAATGC	2.73	1.91	0.82	0.40
ATGGTCCCGC	2.74	2.33	0.41	1.02
AATGGAGAAC	2.74	2.38	0.36	0.67
TGTGAACGTG	2.74	2.22	0.52	1.07
CCACCCCAAT	2.75	2.32	0.42	0.71
CGAGAATCAG	2.75	2.25	0.50	0.62

Sequence	E_{ex} [eV]	E_{em} [eV]	SS [eV]	$R_{UV/vis}$
CGAGAAGATG	2.75	2.40	0.35	0.84
CAATCAGGGA	2.77	2.38	0.39	0.59
CCCACATTCC	2.77	2.28	0.49	0.99
CCCTAAATCA	2.77	2.09	0.68	0.51
TGACGCTGTG	2.78	2.29	0.48	0.74
ACGACAAATC	2.78	2.23	0.54	0.66
ATACGGGTTA	2.78	2.32	0.46	0.57
GAAATCGCAC	2.78	2.23	0.55	0.65
CCACCATTCC	2.79	2.33	0.46	0.79
ACAAGCCCCA	2.79	2.43	0.36	1.02
CCACAAGATC	2.80	2.30	0.50	0.33
CACCACCAAA	2.80	2.32	0.48	0.67
ATCTAATCCC	2.81	2.33	0.48	0.68
AATCCCAATA	2.83	2.28	0.54	0.36
TCGTATTCAA	2.83	2.31	0.52	0.62
CCCTCCCCCT	2.83	2.36	0.47	0.69
GCCAACTCGT	2.83	2.47	0.36	1.11
TCGACAGAAG	2.84	2.22	0.62	0.69
CGAAGAATCA	2.84	2.28	0.55	0.54
AAAAATCCCA	2.84	2.25	0.59	0.48
TCCCACAGAA	2.85	2.36	0.49	0.28
AGTAATCCCA	2.85	2.19	0.66	0.82
ATCCCAAAGA	2.86	2.26	0.60	1.17
AGCACGAACG	2.86	2.37	0.50	0.87
GATCACTGAC	2.88	2.30	0.57	0.70
AGAGTCCAAC	2.90	2.57	0.33	1.09
ACCAATGCTC	2.91	2.17	0.74	0.44
AACTAACACC	2.92	1.95	0.97	0.84
GGAGAATCAC	2.92	2.47	0.45	0.56
TTCACCACAA	2.94	2.31	0.63	0.64
ACCAACGCCC	2.94	2.40	0.54	0.99
AAGGACACTC	2.97	2.32	0.65	0.72
TAGGACACTC	2.97	2.34	0.63	0.72
CTCCACTAAA	2.99	2.35	0.65	0.44

Sequence	**E_{ex} [eV]**	**E_{em} [eV]**	**SS [eV]**	**$R_{UV/vis}$**
ATCGCTGTCA	3.07	2.22	0.85	0.49

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