

A

Mismatch sequence:

5'- AACACTGACAAGTGGCCCTATGGA -3'
 3'- TTGTGACTGTTCCCGGGGATACCT -5'

Exact match sequence:

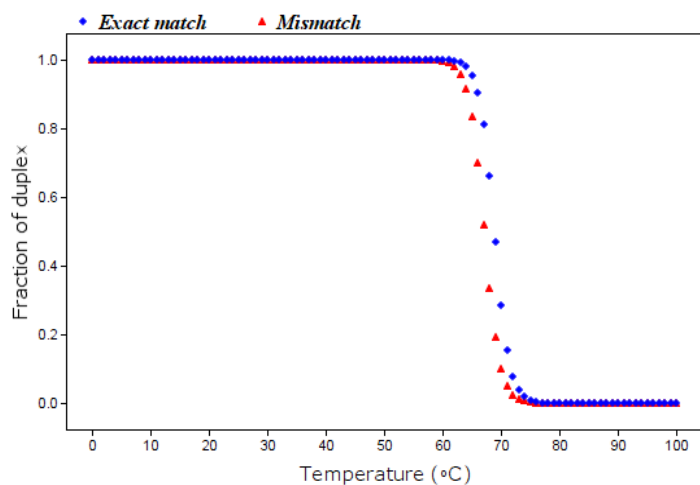
5'- AACACTGACAAGTGGCCCTATGGA -3'
 3'- TTGTGACTGTTCCACCGGGGATACCT -5'

| | T_m [°C] | Gibbs Energy (ΔG_{37}) [kcal/mol] | Enthalpy (ΔH) [kcal/mol] | Entropy (ΔS) [cal/(K·mol)] |
|--------------------|---------------|--|---------------------------------------|---|
| Mismatch | 67.10 | -24.48 | -174.90 | -485.00 |
| Exact match | 68.84 | -26.07 | -183.30 | -506.95 |
| Difference | 1.73 | -1.59 | -8.40 | -21.96 |

Duplex Length: 24

Oligo Conc: 0.45 μ M Na⁺, K⁺ Conc: 50.00 mM dNTPs Conc: 0.20 mM
 Target Conc: 0.00 μ M Mg²⁺ Conc: 1.50 mM

Hybridization profile



B

Mismatch sequence:

5'- AACACTGACAAGTGGCCCTATGGA -3'
 3'- TTGTGACTGTTCCACCGGGGATAGCT -5'

Exact match sequence:

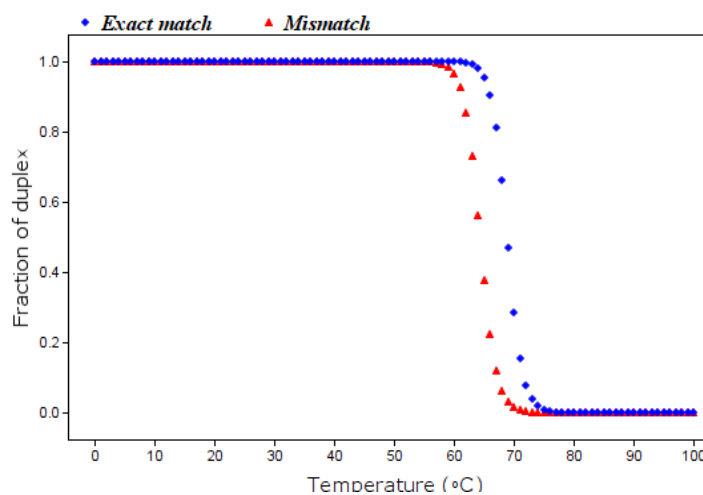
5'- AACACTGACAAGTGGCCCTATGGA -3'
 3'- TTGTGACTGTTCCACCGGGGATACCT -5'

| | T_m [°C] | Gibbs Energy (ΔG_{37}) [kcal/mol] | Enthalpy (ΔH) [kcal/mol] | Entropy (ΔS) [cal/(K·mol)] |
|--------------------|---------------|--|---------------------------------------|---|
| Mismatch | 64.33 | -22.78 | -170.10 | -475.01 |
| Exact match | 68.84 | -26.07 | -183.30 | -506.95 |
| Difference | 4.51 | -3.29 | -13.20 | -31.95 |

Duplex Length: 24

Oligo Conc: 0.45 μ M Na⁺, K⁺ Conc: 50.00 mM dNTPs Conc: 0.20 mM
 Target Conc: 0.00 μ M Mg²⁺ Conc: 1.50 mM

Hybridization profile



C

Mismatch sequence:

5'- TCCGATCGGTTTTCGAATAACGGGT -3'
 3'- AGGCAGCCAAAGCTTATTGCCCA -5'

Exact match sequence:

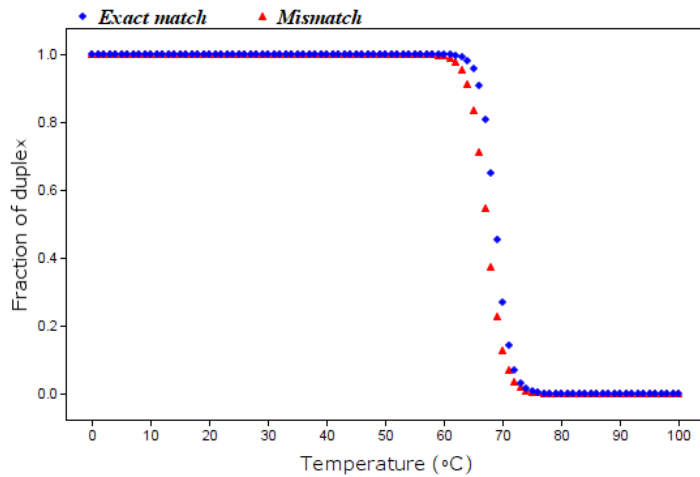
5'- TCCGATCGGTTTTCGAATAACGGGT -3'
 3'- AGGCTAGCCAAAGCTTATTGCCCA -5'

| | T_m [°C] | Gibbs Energy (ΔG_{37}) [kcal/mol] | Enthalpy (ΔH) [kcal/mol] | Entropy (ΔS) [cal/(K·mol)] |
|--------------------|---------------|--|---------------------------------------|---|
| Mismatch | 67.26 | -23.52 | -163.30 | -450.69 |
| Exact match | 68.77 | -26.58 | -189.20 | -524.32 |
| Difference | 1.51 | -3.06 | -25.90 | -73.63 |

Duplex Length: 24

Oligo Conc: 0.45 μ M Na⁺, K⁺ Conc: 50.00 mM dNTPs Conc: 0.20 mM
 Target Conc: 0.00 μ M Mg²⁺ Conc: 1.50 mM

Hybridization profile



D

Mismatch sequence:

5'- ACGATCTCCGAGAACGCACTGAACA -3'
 3'- TGTAGAGGCTCTTGCGTGACTTGT -5'

Exact match sequence:

5'- ACGATCTCCGAGAACGCACTGAACA -3'
 3'- TGCTAGAGGCTCTTGCGTGACTTGT -5'

| | T_m [°C] | Gibbs Energy (ΔG_{37}) [kcal/mol] | Enthalpy (ΔH) [kcal/mol] | Entropy (ΔS) [cal/(K·mol)] |
|--------------------|---------------|--|---------------------------------------|---|
| Mismatch | 66.79 | -25.40 | -186.30 | -518.77 |
| Exact match | 70.40 | -28.49 | -199.70 | -552.02 |
| Difference | 3.61 | -3.09 | -13.40 | -33.25 |

Duplex Length: 25

Oligo Conc: 0.40 μ M Na⁺, K⁺ Conc: 50.00 mM dNTPs Conc: 0.20 mM
 Target Conc: 0.00 μ M Mg²⁺ Conc: 1.50 mM

Hybridization profile

