Watson-Crick Base Pairing





Stability and Sequence

Table N. 2. Table^a of thermodynamic data for contributions made by base pair doublets in duplex melting. Each sequence can be seen as two dinucleotides that complement each other. For example, AT/TA is 5'-AT-3'/3'-TA-5'.

	ΔH _{melt}	ΔS_{melt}	ΔG_{melt}
ΑΤ/ΤΑ	(Kca l/III0I) 7.2	20.4	1 1
TA/AT	7.2	21.3	0.9
CT/GA	7.8	21	1.5
AA/TT	7.9	22.2	1.3
GG/CC	8	19.9	2.1
GA/CT	8.2	22.2	1.6
GT/CA	8.4	22.4	1.7
CA/GT	8.5	22.7	1.7
GC/CG	9.8	24.4	2.5
CG/GC	10.6	27.2	2.5

^a. SantaLucia (1998) Proc. Natl. Acad. Sci. USA **95**, 1460-5.



FIG. 1 (color online). Schematic of single-molecule atomicforce microscopy measurements of ssDNA molecules (the figure is not to scale).

hannin

FIG. 3 (color online). (a) three typical force-extension measurement curves for poly(dT), (b) comparison between poly(dA) and poly(dT) on a normalized extension basis. We assume that at a force of 600 pN, ssDNA is fully stretched, and the distance between two neighboring phosphates is 0.7 nm.

Base Stacking and Stability



Du	plex	Τ_m (°C)	∆G _{melt} (^{kcal} / _{mol})
5 ′	CTTTTC T TTCTT	43.2	12.6
3′	GAAAAG <mark>A</mark> AAGAA	13.2	12.0
5 ′	CTTTTC <mark>0</mark> TTCTT	22 0	70
3′	GAAAAG <mark>A</mark> AAGAA	22.0	7.0
5′	CTTTTC <mark>0</mark> TTCTT	41.6	12.1
3′	GAAAAG <mark>P</mark> AAGAA	11.0	*~**

Matray and Kool (1998) JACS 120, 6191

The Overhang Experiment 5' - xcgcgcg GCGCGCX - 5'

Χ	$\mathbf{T}_{\mathbf{m}}(\mathbf{C})$	ΔH_{melt}	ΔH_{melt} ΔS_{melt}	
		(kcal/mol)	(cal/molK)	(kcal/mol)
None	41.7	45.9	122	-
Thymine	48.1	47.9	125	1.1
Cytosine	46.2	50.4	133	1.0
Adenine	51.6	54.7	144	2.0
Guanine	51.5	43.3	109	1.3
Benzene	48.3	51.4	135	1.4

J. Am. Chem. Soc. 1996, 118, 8182-8183.





Spine of Hydration in AT rich DNA



CD Spectra of DNA



Proc. Natl. Acad. Sci. USA Vol. 92, pp. 6464–6468, July 1995 Biophysics

An A-DNA triplet code: Thermodynamic rules for predicting A- and B-DNA

(DNA structure/structure prediction/crystallography/circular dichroism/spectroscopy)

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Table 5. Conformations of dodecanucleotides in aqueous solution (0% TFE) and in high concentrations of TFE (concentrations shown in parentheses)

		DNA conformation		
Sequence	APE	Predicted	0% TFE	High TFE
d(GGCGGCGGCGGC)	0.10	В	В	A (71%)
d(GCGCGCGCGCGCGC)	0.71	в	В	Z (75%)
d(CCCCCGCGGGGGG)	-0.15	Α	A-like	A (68%)
d(CCCCGTACGGGG)	-0.03	Α	A-like	A (75%)

APE=A-DNA Propensity Related to $\Delta G_{solvation}(B \rightarrow A)$







RNA is Always in A Conformation



B-RNA

A-RNA

UUCG Tetraloop

Loop	T _m (°C)	$\Delta \mathbf{H}^{\circ}$	∆G°
		(^{kcal} / _{mol})	(^{kcal} / _{mol})
G(UUCG)C	60.1	-48.6	-3.4
G(UUUG)C	51.1	-39.2	-1.7
G(UUUU)C	51.5	-38.2	-1.7
G(CUCG)C	62.4	-47.5	-3.6
deoxy - G(TTCG)C	44.7	-31.2	-1.4







Figure 2. Sequences and Structures of RNA Pseudoknots

Staple DW, Butcher SE (2005) Pseudoknots: RNA Structures with Diverse Functions. PLoS Biol 3(6): e213. doi:10.1371/journal.pbio.0030213

http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.0030213



tRNA Structure



Non Watson-Crick Base Pairs



Tertiary Structure in RNA





Mg²⁺ stabilizes dense phosphates