

Talking molecules: the networks that shape the living world March 19-20, 2018, Warsaw, Poland



FOLDING AND BINDING LANDSCAPES OF G-QUADRUPLEX (G4) DNA STRUCTURES

How <u>not</u> to run a biophysics core facility...

Jonathan B. Chaires

James Graham Brown Cancer Center

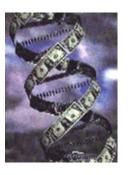
University of Louisville

Louisville, Kentucky USA



Supported by:

NIH Grants GM077422 & CA35635 NIH/NCRR COBRE P20RR018733 The James Graham Brown Foundation





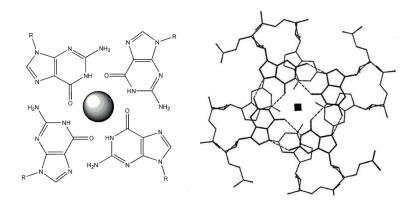






A Brief History of Quadruplex DNA...







Ivar Bang

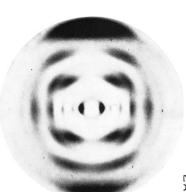


Fig. 4. Side view of successive residues in a single (232) chain of the four-stranded structure of poly(I) or poly (G) The helix axis is represented by the vertical line. Atoms in a nucleotide are labelled. The intramolecular hydrogen bond 0-6 · · · · O-3 is shown by a dashed line.

Bang, I. (1910). Untersuchungen über die Guanylsäure. Biochemische Zeitschrift, 26, 293–311.

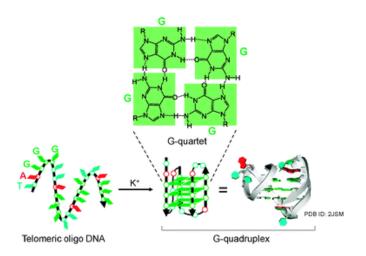
David Davies



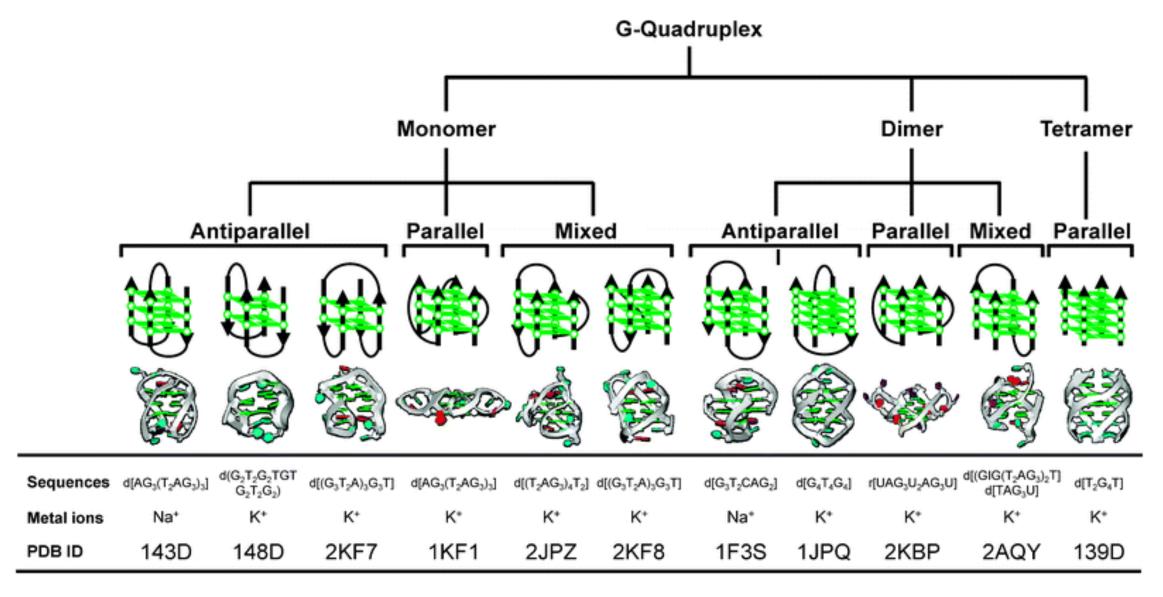


Gellert, M., Lipsett, M. N., & Davies, D. R. (1962). Helix formation by guanylic acid. Proc. Nat. Acad. Sci. USA, 48, 2013–2018.

Struther Arnott, R. Chandrasekaran and C. M. Martilla (1974) Structures for Polyinosinic Acid and Polyguanylic Acid. Biochem. J. 141: 537-543

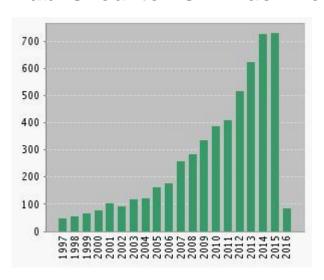


Diversity of G-quadruplex structures

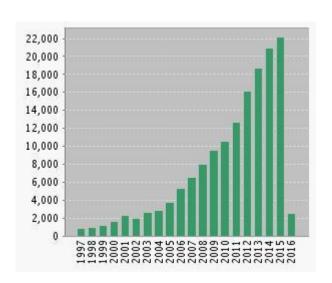


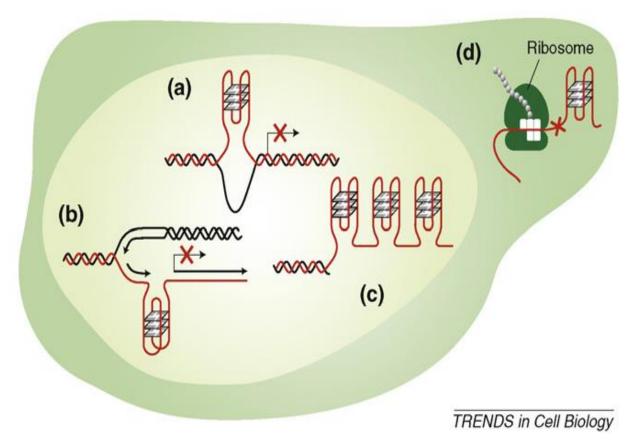
Growing interest in quadruplexes...

Published Items in Each Year



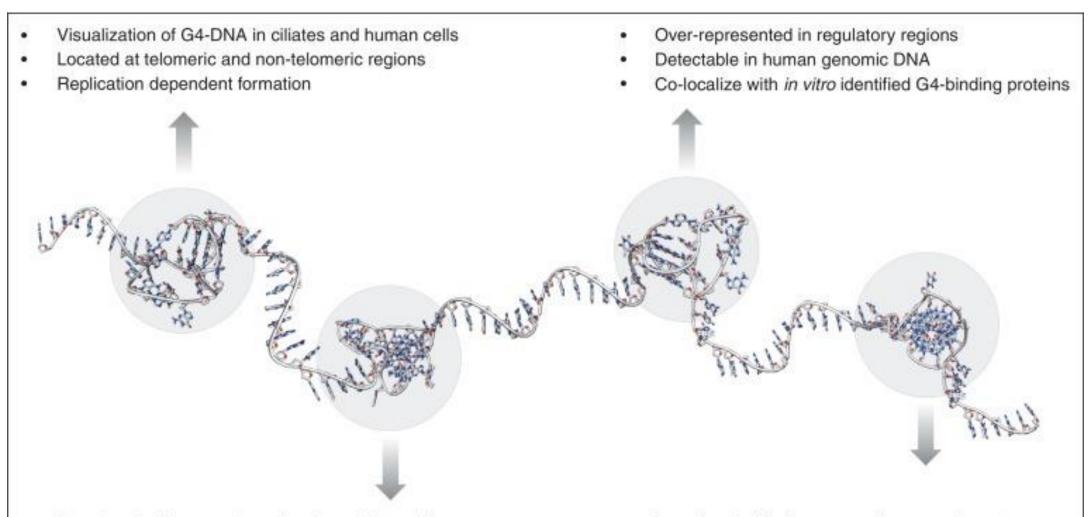
Citations in Each Year





Quadruplex-forming sequences are highly conserved and non-randomly distributed.

Transient or permanent single-strands can fold into functional non-duplex structures

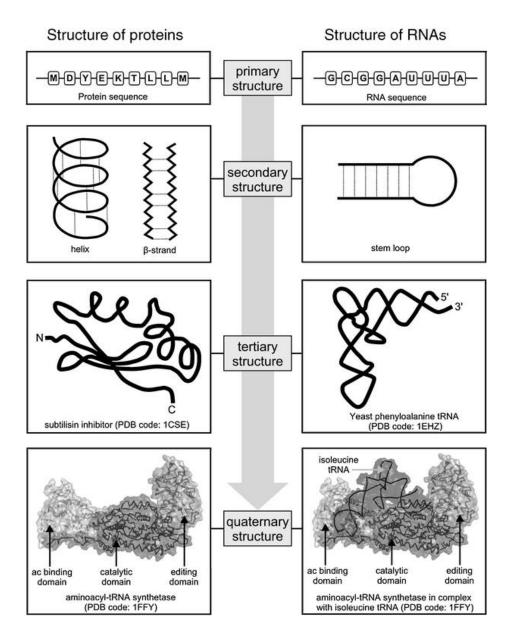


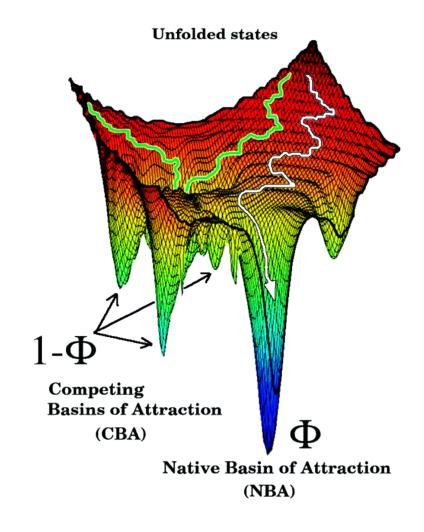
- Associated with genomic and epigenetic instability
- Processed by helicases conserved from bacteria to humans
- Promote recombination and rearrangement

- Associated with diseases and cancer phenotypes
- Relevant target for new therapies
- Potential for chemical synthetic lethality approaches

Current Opinion in Genetics & Development

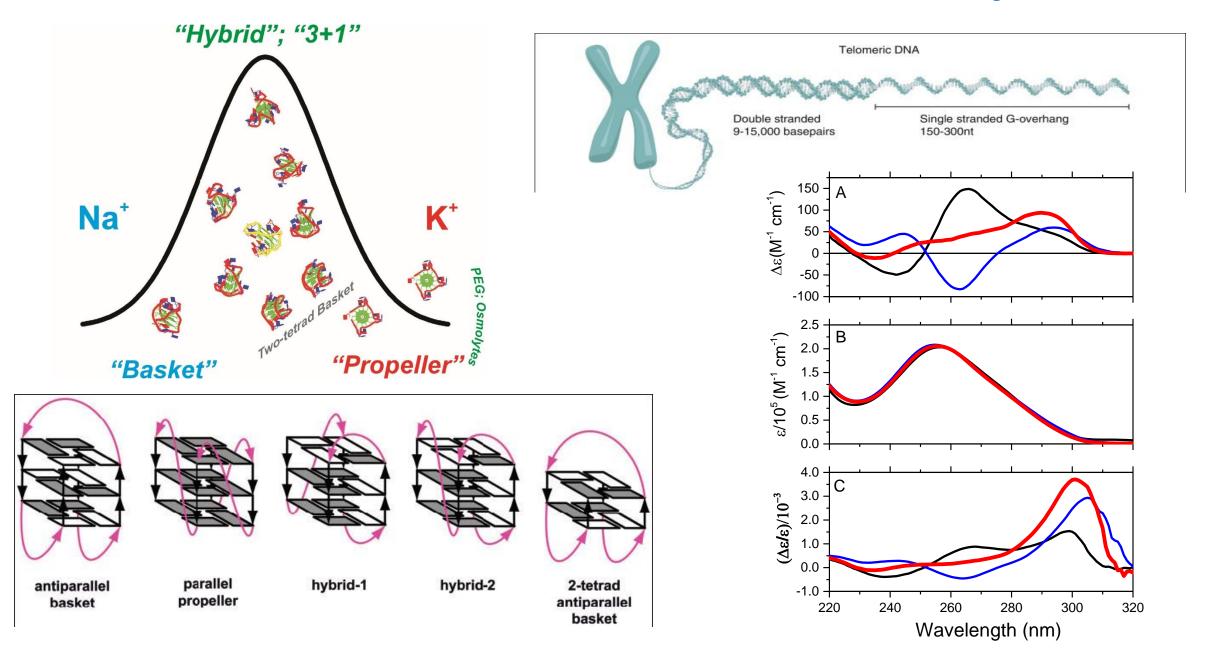
How to biomolecules fold? G4 is DNA acting like proteins and RNA

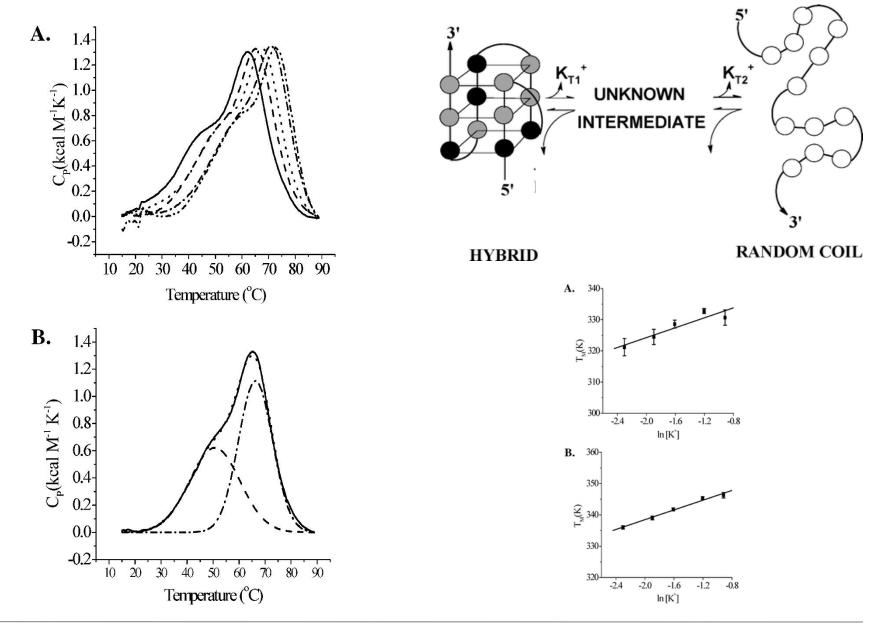




- D. Thirumalai and and Changbong Hyeon Biochemistry 2005 44 (13), 4957-4970 DOI: 10.1021/bi047314+
- D. Thirumalai* and and S. A. Woodson Accounts of Chemical Research 1996 29 (9), 433-439

Human telomere G-quadruplex: 5'-XGGG(TTAGG)₃Y-3'



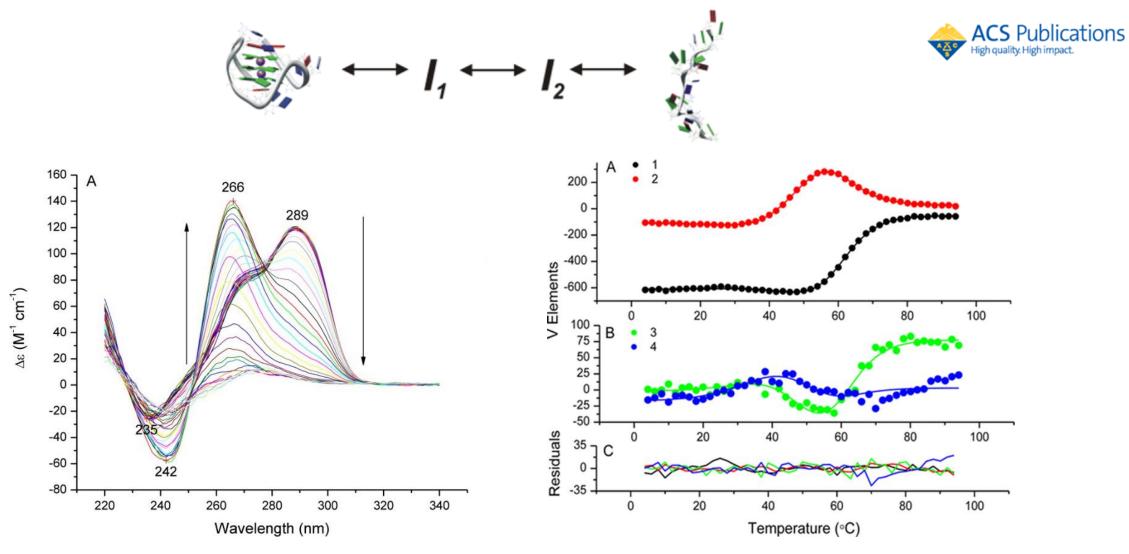


Published in: Cosimo Antonacci; Jonathan B. Chaires; Richard D. Sheardy; *Biochemistry* **2007**, 46, 4654-4660.

DOI: 10.1021/bi602511p

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Singular Value Decomposition

Gray RD, Chaires JB Analysis of multidimensional G-quadruplex melting curves. *Curr Protoc Nucleic Acid Chem.* 2011 Jun; Chapter 17:Unit17.4. doi: 10.1002/0471142700.nc1704s45.

Published in: Robert D. Gray; Robert Buscaglia; Jonathan B. Chaires; J. Am. Chem. Soc. 2012, 134, 16834-16844.

DOI: 10.1021/ja307543z

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- 1) $F \rightleftharpoons U$
- $2) F_1 \rightleftharpoons U \rightleftharpoons F_2$
- 3) $F \rightleftharpoons I \rightleftharpoons U$
- 4) $F \rightleftharpoons I_1 \rightleftharpoons I_2 \rightleftharpoons U$
- 5) $F_1 \rightleftharpoons I \rightleftharpoons U$ $\downarrow F_2$

F = folded state(s)
I = intermediate state(s)
U = unfolded ensemble

Table 3. Model-dependent fitting statistics for thermal unfolding of Tel22 in 25 mM KCl monitored by CD

Model	Model	χ^2	AIC Value		
Single Transition	1	720265. 5	1544.1		
Two Transitions	2	15235.4	846.6		
Parallel Transitions	3	15235.4	846.6		
Three Transitions	4	7759.5	734.5		
Parallel Intermediate Transitions	5	7757.3	734.4		



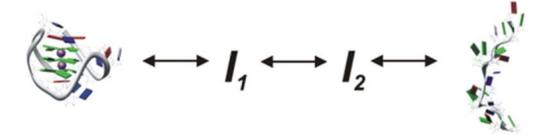


Table 4. Optimal values of thermodynamic parameters for folding Tel22 in 25 mM KCl^a

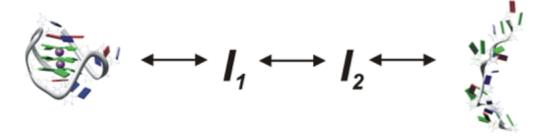
Model 4 Model 5 -21.9 ± 4.7^{b} ΔH_1 -25.3 35.2 ± 5.3 48.4 T_{m1} ΔH_2 -33.4 ± 4.2 -54.6 T_{m2} 47.6 ± 1.6 42.8 ΔH_3 -45.3 ± 4.2 -43.6 61.4 ± 1.0 60.7 T_{m3} ΔG_1 -1.1 ±0.4 -2.2 ΔG_2 -2.9 ± 0.4 -3.9 ΔG_3 -5.6 ± 0.6 -5.3 $\Delta \textbf{G}_{\text{Total}}$ -9.5 ± 0.7 -11.5

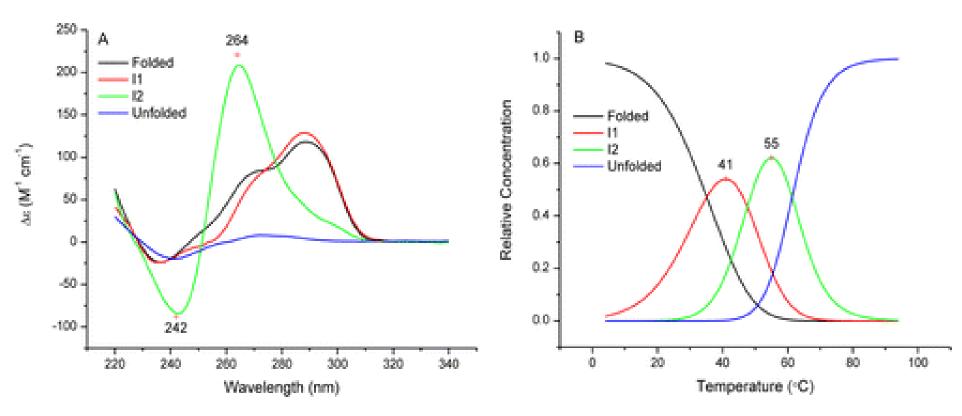
Greenfield, N. J. (2007) Using circular dichroism collected as a function of temperature to determine the thermodynamics of protein unfolding and binding interactions. *Nat. Protocols* 1, 2527-2535.

Published in: Robert D. Gray; Robert Buscaglia; Jonathan B. Chaires; J. Am. Chem. Soc. 2012, 134, 16834-16844.

DOI: 10.1021/ja307543z







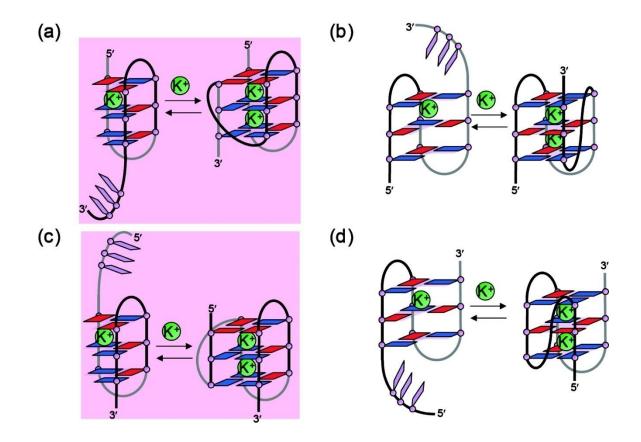
Published in: Robert D. Gray; Robert Buscaglia; Jonathan B. Chaires; *J. Am. Chem. Soc.* **2012,** 134, 16834-16844.

DOI: 10.1021/ja307543z

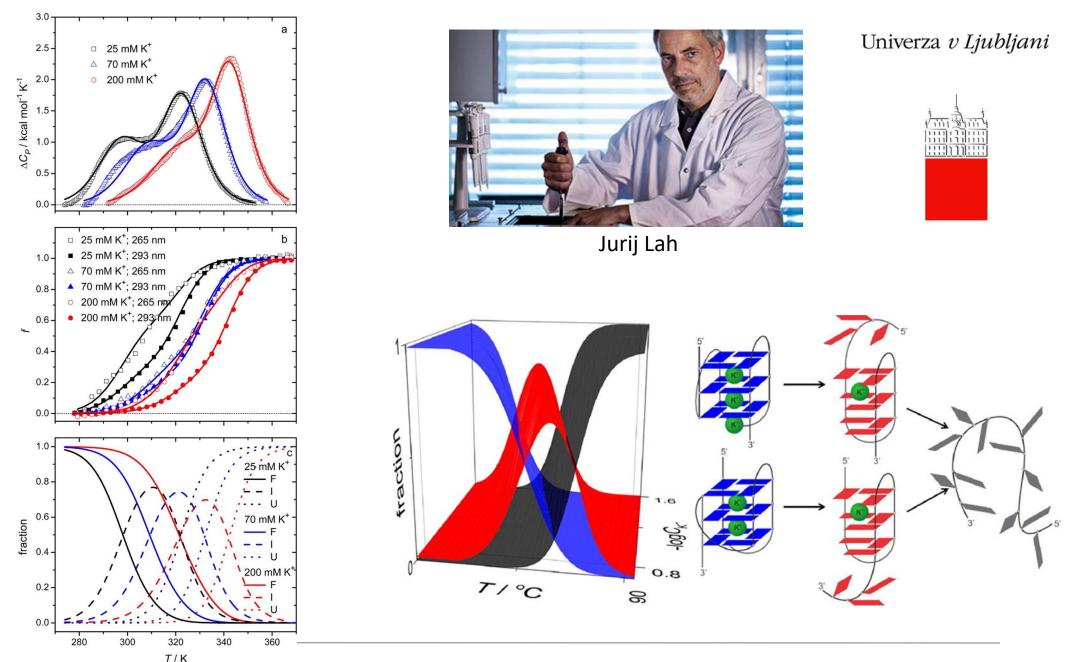
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What is it?





Models of the predicted stable triplexes with four syn conformation of deoxyguanosine and their quadruplex folding. Triplex (a) was formed from hairpin1–2. This structure is the same as triplex (d) in Figure 6. In the same way, triplexes (b) and (c) were formed from hairpin2–3. These structures are the same as triplexes (e) and (l) in Figure 6, respectively. Triplex (d) was formed from hairpin3–4. This structure is the same as triplex (m) in Figure 6. The pink background indicates the stable G-quadruplex structures.



T/K
Published in: Matjaž Bončina; Jurij Lah; Iztok Prislan; Gorazd Vesnaver; *J. Am. Chem. Soc.* **2012,** 134, 9657-9663. DOI: 10.1021/ja300605n

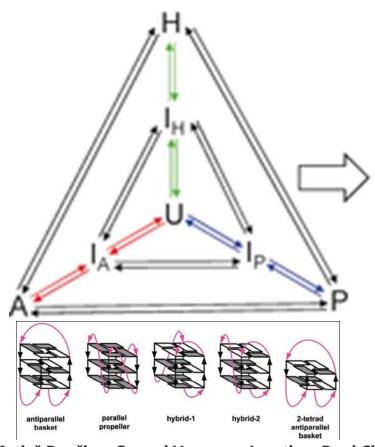
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"Collaboration is more fun than competition"

Unravelling the Thermodynamics of the Folding and Interconversion of Human Telomere G-Quadruplexes

$$\Delta G_{(T,K,Na,PEG)} = \Delta G_{(T)} - RT \left(n_K \ln[K^+] + n_{Na} \ln[Na^+] + m_1 [PEG] + m_2 [PEG]^2 \right)$$



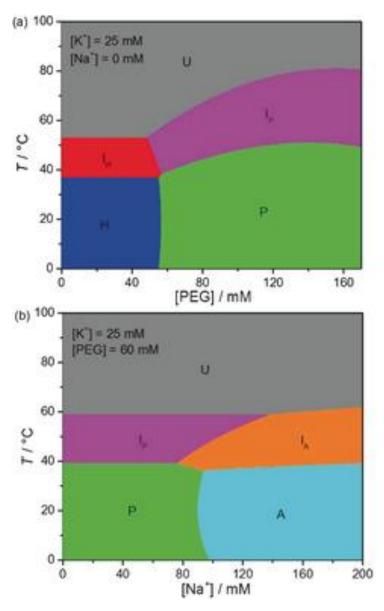
	U→P	U→H°	U→Aª	U→I _P	U→I _H ª	U→I _A ª
$\Delta G_{(T_0)}$ / kcal mol $^{ ext{-}1}$	−3.5±0.1	-8.0±0.1	-6.2±0.1	-2.6±0.1	-5.6±0.1	-4.9±0.1
$\Delta H_{(T_0)}$ / kcal mol ⁻¹	-45.0±0.3	-46.0±0.6	-45.5±1.0	-19.3±0.3	-23.6±0.6	-25.4±1.0
$T\Delta S_{(T_0)}$ / kcal mol ⁻¹	-41.5±0.3	-38.0±0.6	-39.3±1.0	-16.7±0.3	-18.0±0.6	-20.5±1.0
ΔC_P / cal mol ⁻¹ K ⁻¹	-280±20	-420±30	-390±30	-280±20	-420±20	-390±30
n _K	-2.1±0.2ª	-2.1±0.2	0	-1.4±0.1 ^a	-1.4±0.1	0
n _{Na}	0	0	-1.8±0.1	0	0	-1.4±0.1
m_1 / L mol ⁻¹	-166±4	/	/	-101±2	1	/
m_2 / L ² mol ⁻²	554±10	1	1	322±5	1	1
25 mM K ⁺ and/or Na ^{+b}						
$\Delta G_{(T_0,X)}$ / kcal mol $^{-1}$	1.1±0.1	-3.4±0.1	-2.4±0.1	0.5±0.1	−2.5±0.1	-2.0±0.1
$T\Delta S_{(T_0,X)}$ / kcal mol ⁻¹	-46.1±0.3	-42.6±0.6	-43.1±1.0	-19.8±0.3	-21.1±0.6	-23.4±1.0

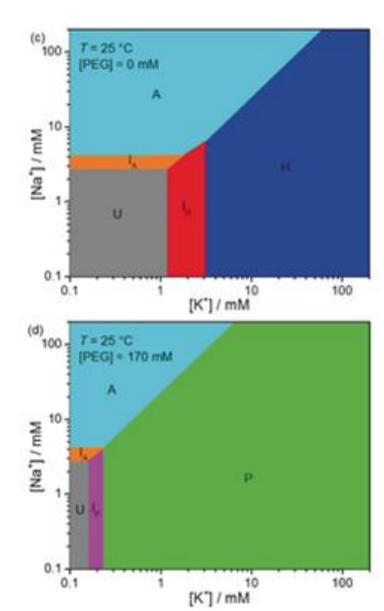
Matjaž Bončina, Gorazd Vesnaver, Jonathan Brad Chaires, Jurij Lah

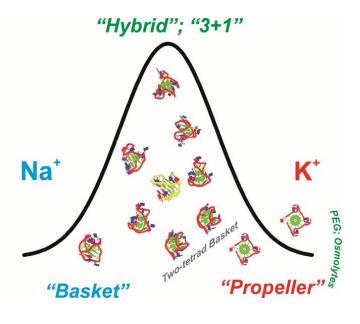
Angewandte Chemie International Edition
Volume 55, Issue 35_pages 10340-10344, 3 AUG 2016 DOI: 10.1002/anie.201605350
http://onlinelibrary.wiley.com/doi/10.1002/anie.201605350/full#anie201605350-fig-0003



Unravelling the Thermodynamics of the Folding and Interconversion of Human Telomere G-Quadruplexes

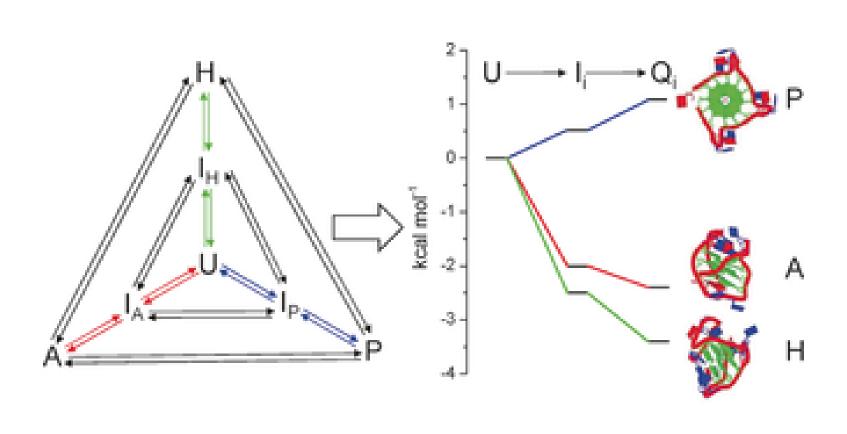


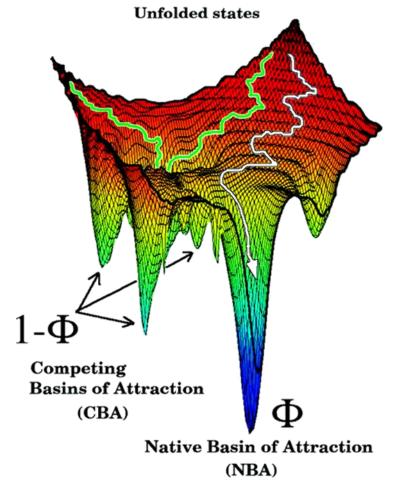




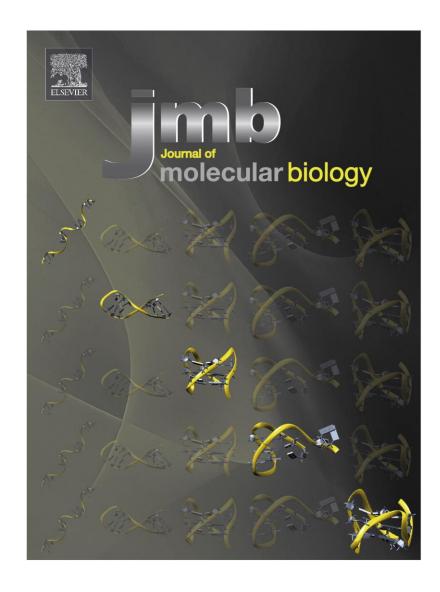


Unraveling the Thermodynamics of the Folding and Interconversion of Human Telomere G-Quadruplexes

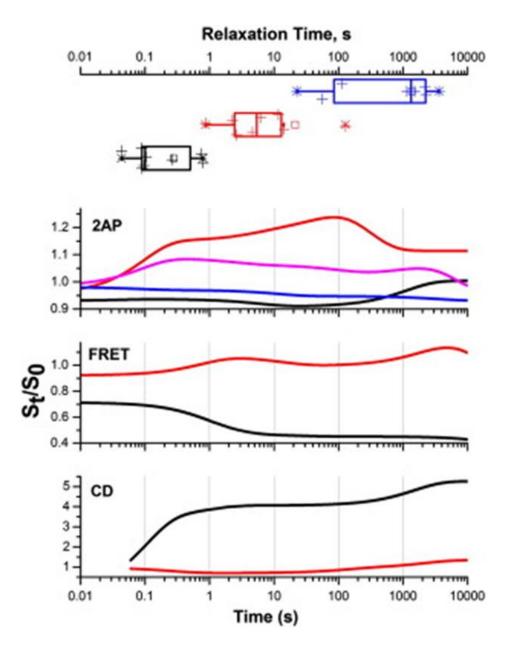




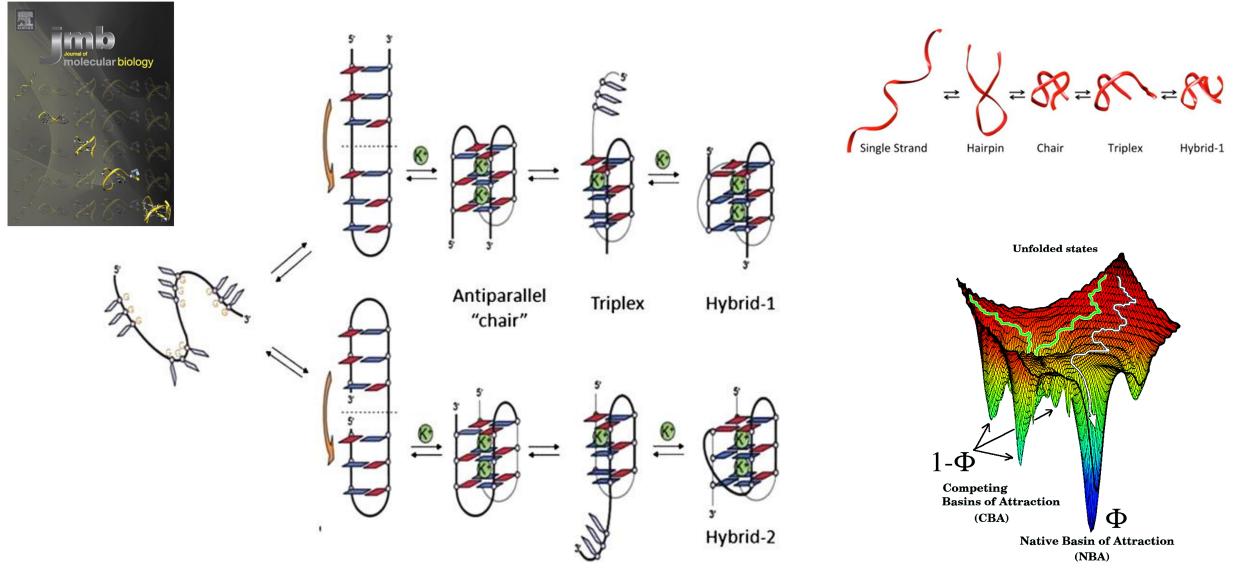




Stopped-flow KCI jump experiments



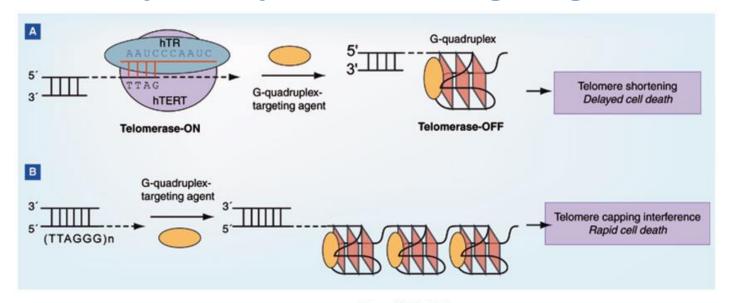
RD Gray, JO Trent & JB Chaires Journal of Molecular Biology Volume 426, Issue 8, 17 April 2014, Pages 1629-1650



(Movies available online a JMB website)

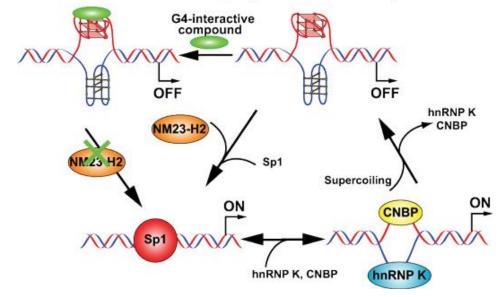
G-quadruplexes as drug targets

At telomeres:



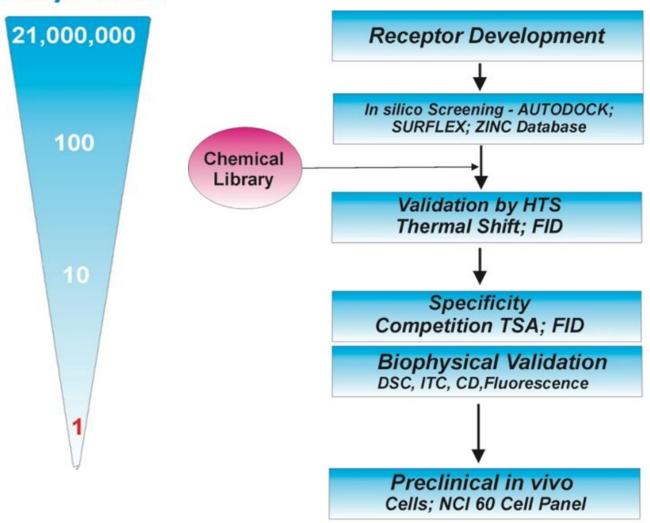
c-Myc NHE III1 (G-quadruplex/i-motif)

In gene promoters:



Drug Discovery at the JGBCC

Number of Compounds



Drug Discovery

Clinical

CHAPTER 4

Thermal Denaturation of Drug-DNA Complexes
JONATHAN B. CHAIRES
Chemical Biology No. 7
DNA-targeting Molecules as Therapeutic Agents
Edited by Michael J. Waring
The Royal Society of Chemistry 2018
Published by the Royal Society of Chemistry
www.rsc.org

Calorimetry and thermodynamics in drug discovery Annu. Rev. Biophys. 2008. 37:135–51

Dock to unique G4 binding sites...

Hybrid 1 (2HY9) Hybrid 2 (2JPZ) Propeller (1KF1)

ThermoFluor®:

High Throughput Thermodynamic Assay

Plate-based Protein Unfolding

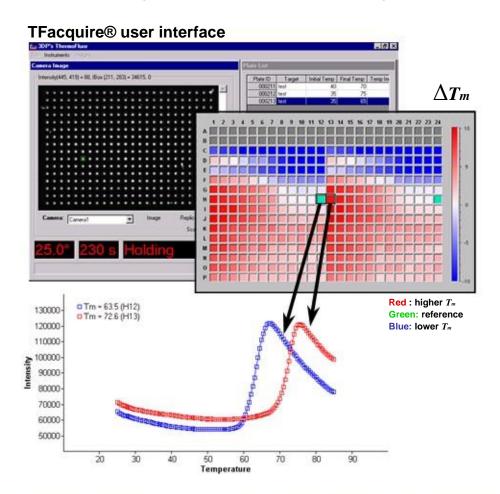
- § 384-well assay plate; high throughput characterization and screening of proteins.
- § Low volume, 3 μl, small-scale reactions, ~1 μM protein; typically < 200 ng well.
- § Each well comprises an individual protein unfolding assay.
- § Compound binding free energy adds to protein stability shifts stability curve to higher temperature.

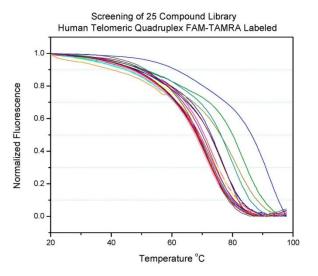
Optimization for HTS is an optimization of protein stability and signal intensity.

M. W. Pantoliano et al. (2001) J. Biomol. Screen. 6: 429

M. J. Todd & F. R. Salemme (2003) Gen. Eng. News 23

D. Matulis et al. (2005) Biochemistry 44: 5258



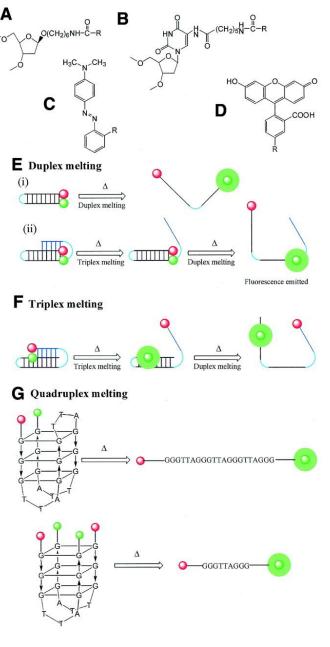


Mergny, JL; Maurizot, JC Fluorescence resonance energy transfer as a probe for G-quartet formation by a telomeric repeat.

CHEMBIOCHEM Volume: 2 Issue: 2 Pages: 124-132 DOI: 10.1002/1439-7633(20010202)2:2<124

Richard A. J. Darby, Matthieu Sollogoub, Catherine McKeen, Lynda Brown, Antonina Risitano, Nicholas Brown, Christopher Barton, Tom Brown, and Keith R. Fox High throughput measurement of duplex, triplex and quadruplex melting curves using molecular beacons and a LightCycler Nucl. Acids Res. (2002)

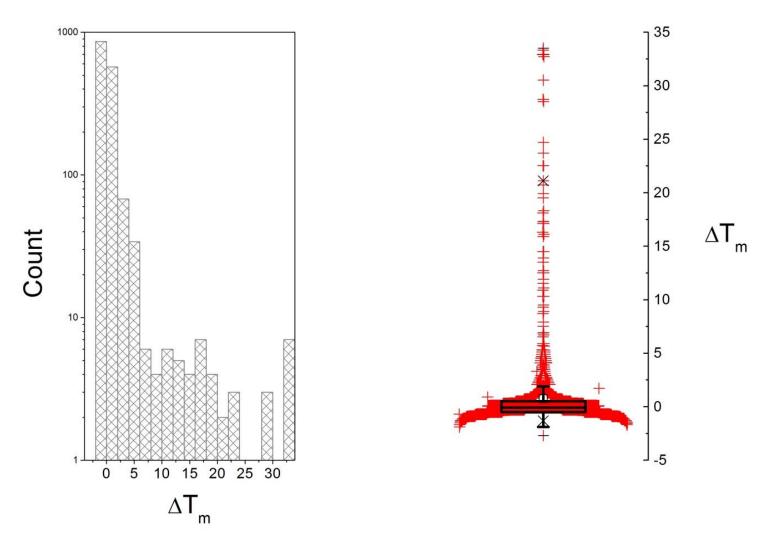
De Cian, A; Guittat, L Kaiser, M; Sacca, B; Amrane, S; Bourdoncle, A; Alberti, P; Teulade-Fichou, MP; Lacroix, L; Mergny, JL Fluorescence-based melting assays for studying quadruplex ligands. METHODS Volume: 42 Issue: 2 Pages: 183-195 DOI: 10.1016/j.ymeth.2006.10.004 Published: JUN 2007



Darby R A J et al. Nucl. Acids Res. 2002;30:e39-e39

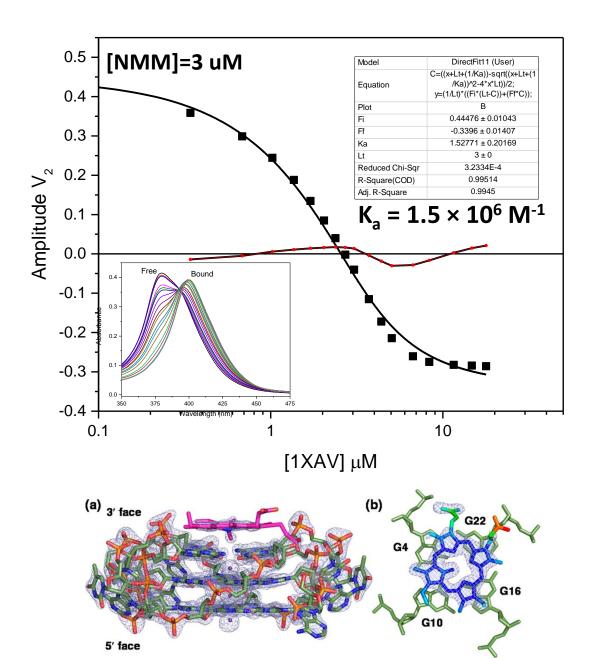
Results from HTS of NCI Diversity Set III

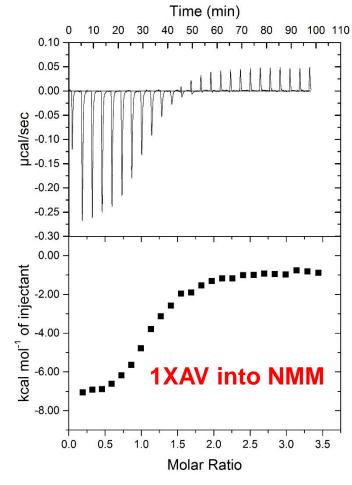
The NCI Diversity Set III of 1596 compounds is available on Greiner 650201 96-well PP U-bottom plates. Compounds are arrayed at 20 uL /10 mM in DMSO



Binding to human telomere quadruplex in K⁺

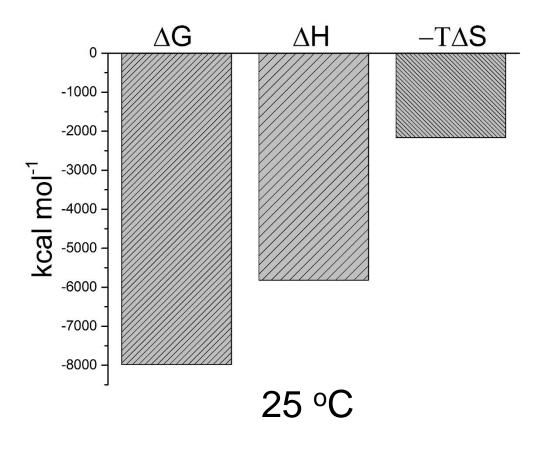
Binding measured by Isothermal Titration Calorimetry

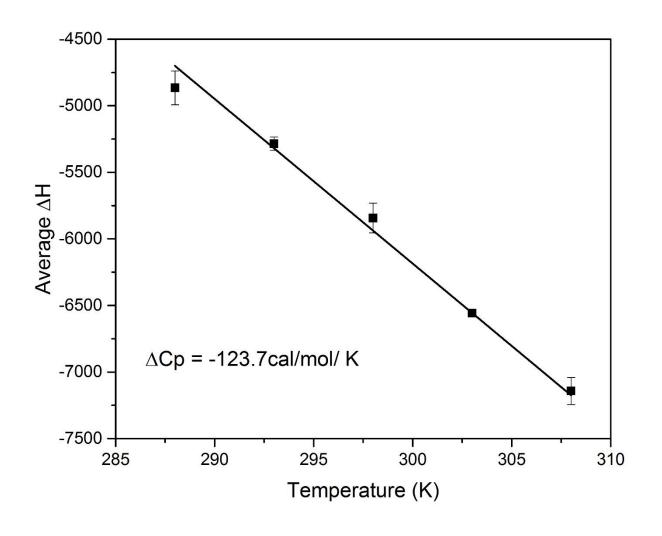




n	1.1
Ка	$2.1 \times 10^6 \mathrm{M}^{-1}$
ΔН	-5.7 kcal mol ⁻¹
ΔH _{dil}	+0.8 kcal mol ⁻¹

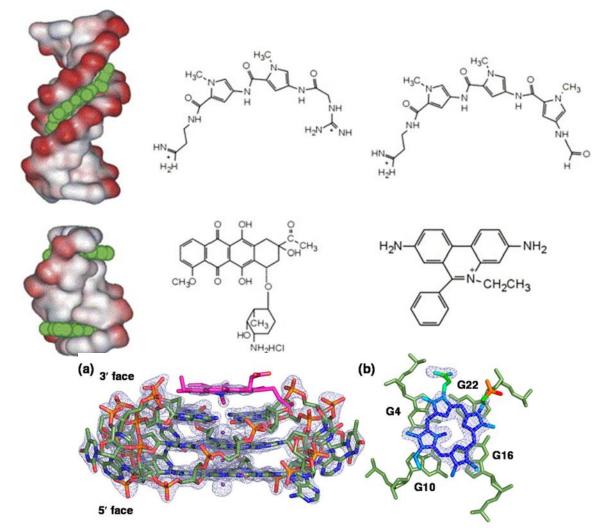
Thermodynamic Profile for NMM Binding to 1XAV – Enthalpy Driven $\Delta G = \Delta H - T\Delta S$





10 **NMM** ∆H, kcal mol⁻¹ -20 -25 -30 -35 -40 -T∆S, kcal mol⁻¹

The NMM binding profile is at the interface between intercalators and groove-binders!



Jonathan B. Chaires **A thermodynamic signature for drug–DNA binding mode** *Archives of Biochemistry and Biophysics* Volume 453, Issue 1, 2006, 26–31

A Biophysical Core Facility for the James Graham Brown Cancer Center University of Louisville Health Science Center

Dr. J. Brad Chaires, Director
Dr. Nichola Garbett, Assistant Director & Manager

\$1 million+ invested in 2004



Operates as a fee-for-service facility providing the tools necessary for detailed thermodynamic and kinetic studies for:

- drug-macromolecule interactions
- macromolecular association reactions
- macromolecule stability
- long-term collaborative interactions
- preliminary studies for grant proposals

Will do experiments using samples provided, or will train personnel to use instruments

Available to University community

Will provide services to nonuniversity companies or Academics

Expected to be at least 50% self-sufficient; subsidized by Departments, Centers, training and program project grants

Nonprofit

Techniques Available

Calorimetry:

❖ Microcal VP DSC

(with Pressure Perturbation)

❖ Microcal VP ITC

Microcal Capillary VP DSC ("High-throughput")

Spectroscopy:

> Jasco J-800 CD

Jasco Fluorescence

> UV/Vis

Biacore SPR

➤ OLIS Rapid Scan Stoppedflow

Analytical Ultracentrifuge

What I learned...

- Don't set up a biophysics core facility in a medical school not enough users
- "Nonprofit" is the operative word it is hard to even break even
- Deciding appropriate user fees is almost impossible administrators want "more" but "more" drives users away
- The cost of service contracts will kill you
- Promised subsidies often never appear
- Start up companies sometimes don't pay their bills
- Trained users don't care about instruments as much as you do. Their incompetence can be costly.
- Users rarely listen to good advice, especially about sample purity and quantity
- Don't provide too many techniques. With limited personnel it is hard to provide necessary expertise across too many platforms
- The best, most likely to succeed facility, would probably be focused on a single method (ie AUC or ITC or DSC).