

Synthetic life

(continuation of „The molecular origins of life” SoSe 2021)



NaturalNews.com

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Zbigniew Pianowski

Overview of the course

artificial ribozymes and aptamers for efficient catalysis and recognition (SELEX, DNAzymes, foldamers);

unnatural base pairing – expansion of the genetic alphabet;

Artificial genetic polymers and oligonucleotide analogues (XNA);

biosynthetic incorporation of **unnatural aminoacids (UAAs)** into proteins;

enzyme engineering – production of enzymes with unknown or unnatural properties, *ab initio* protein design, directed evolution, theozymes;

Artificial lipid vesicles as models for protocell multiplication;

design of artificial organisms

CHAPTER 1



OLIGONUCLEOTIDES

The less common side of RNA

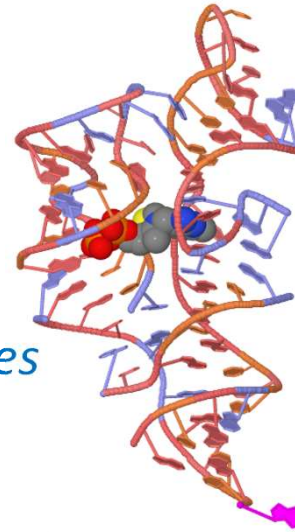
Non-standard functions of RNA

Ribozymes – Ribonucleic acid enzymes

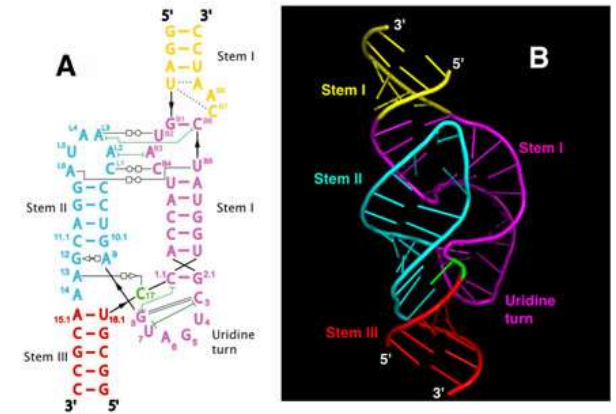
Riboswitches - RNA-based genetic regulatory elements

Aptamers - oligonucleotide or peptide molecules that bind to a specific target molecule.

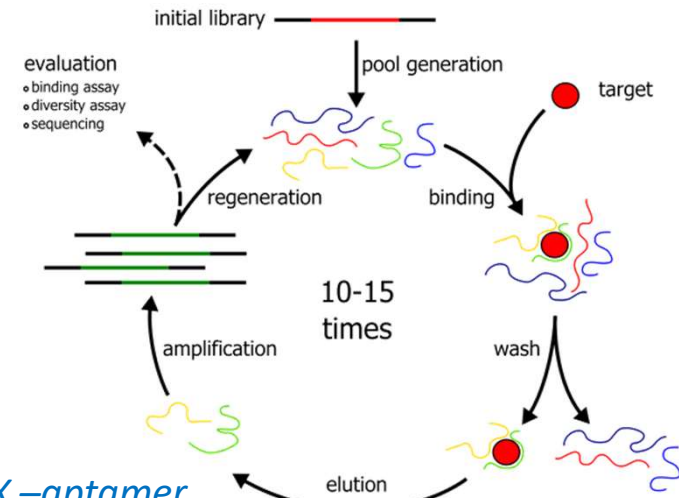
Viroids - subviral pathogens – short (246 to 467 nt), circular, single-stranded, and non-coding RNA without a protein coat



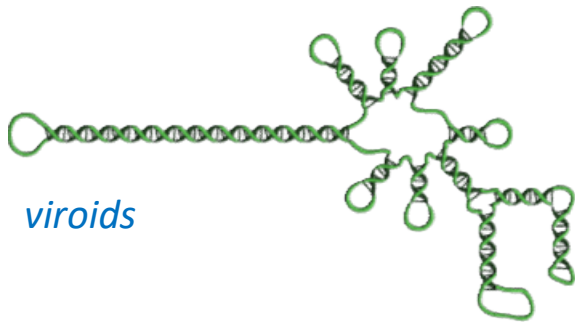
TPP riboswitch



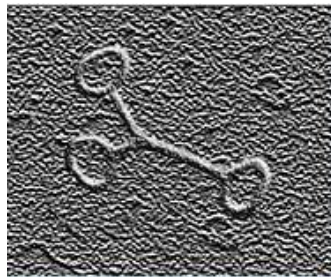
Hammerhead ribozyme



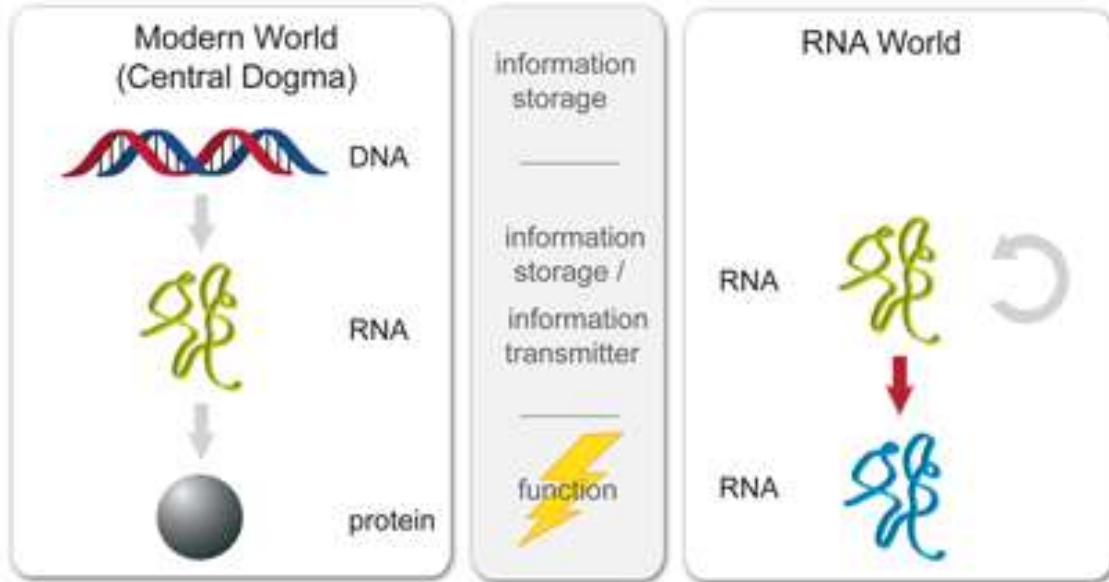
SELEX – aptamer selection



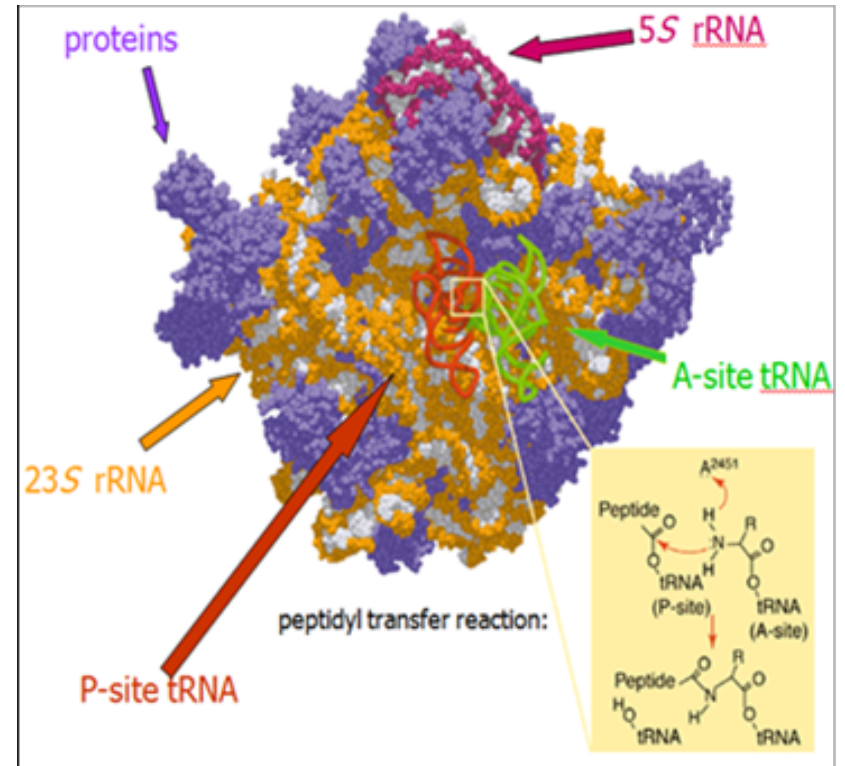
viroids



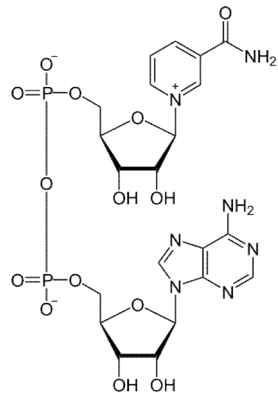
The RNA world



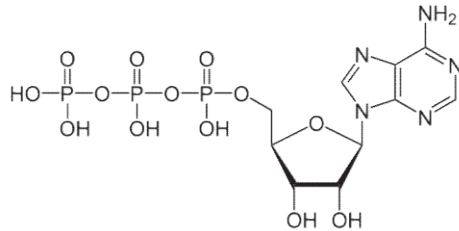
*Living relics of the RNA world:
Ribozymes, riboswitches, viroids,
co-enzymes, structure of the ribosome*



proteins play a structural role, but
DO NOT CATALYZE THE ACYL TRANSFER PROCESS



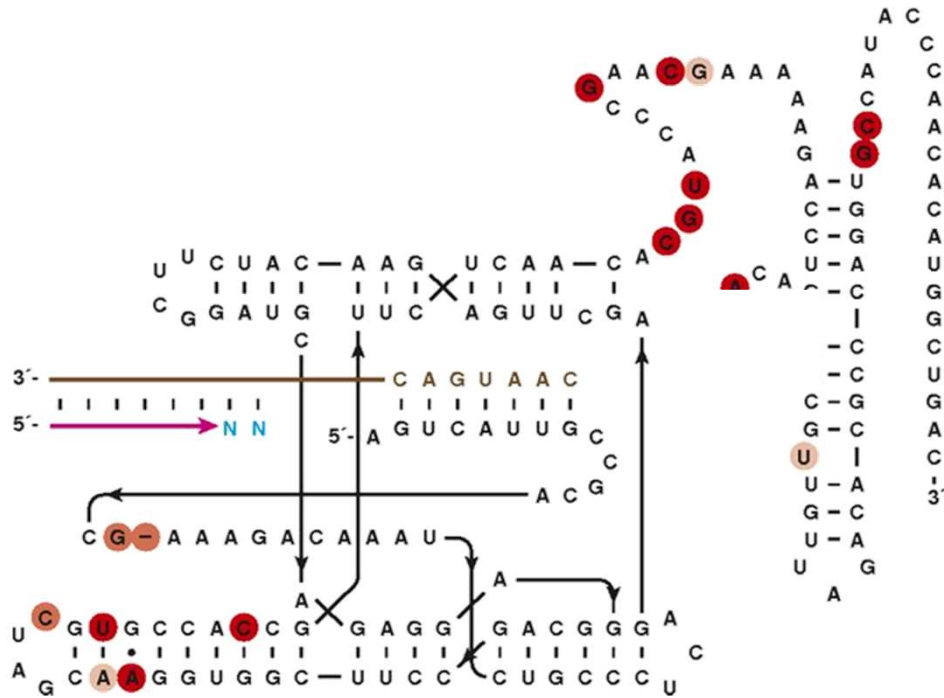
Nicotinamide adenine dinucleotide (NAD⁺)



Adenosine triphosphate (ATP)

The RNA world

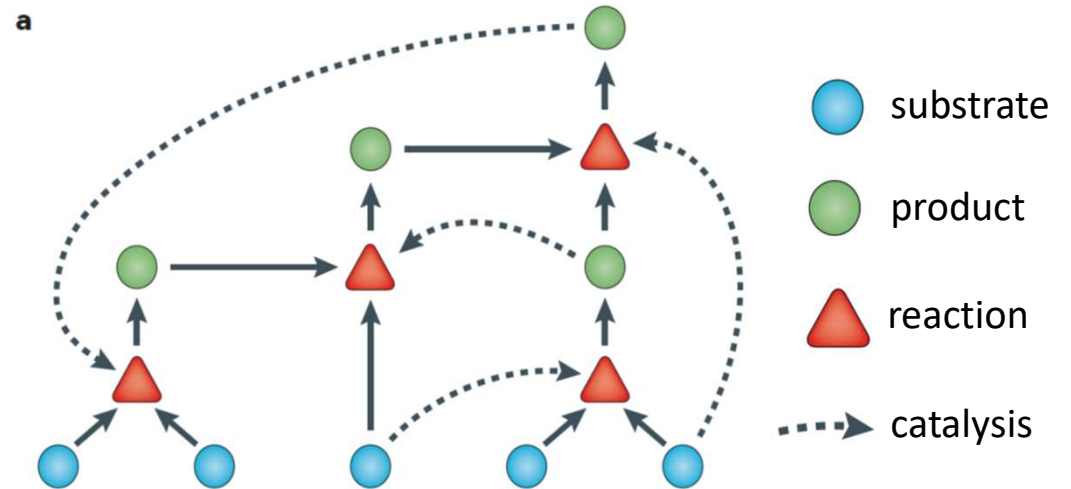
RNA-dependent RNA polymerase ribozyme – Replicase



Replicase - problem

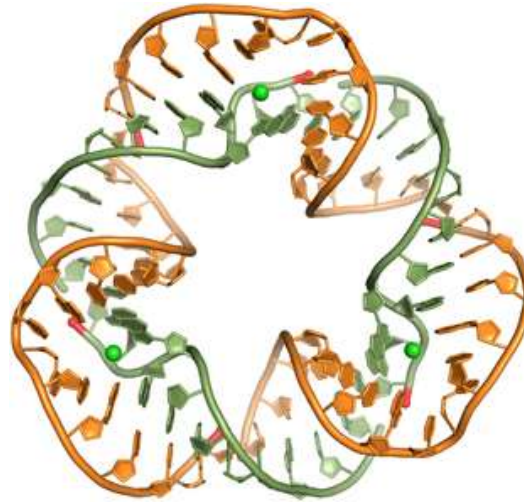
The replicase most likely needs to be long (> 200 nt) for the efficient replication – How could such long functional RNA be spontaneously generated?

Possible solution – autocatalytic networks



No component can replicate without all the others

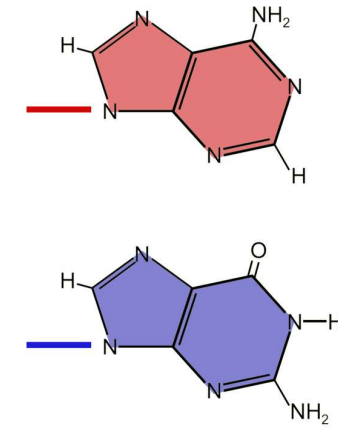
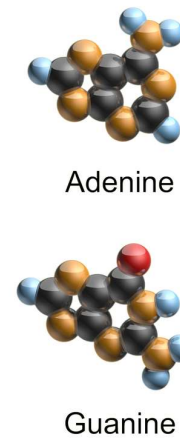
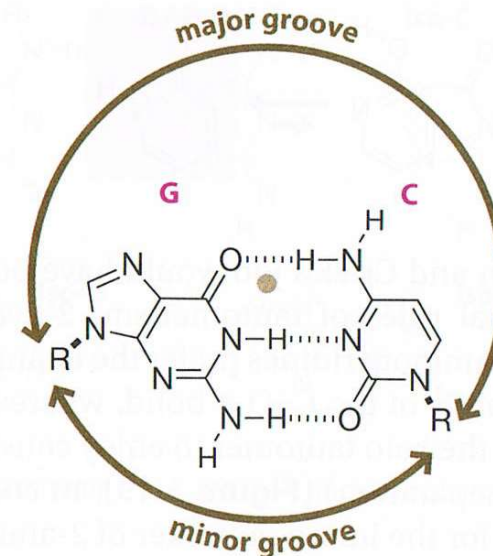
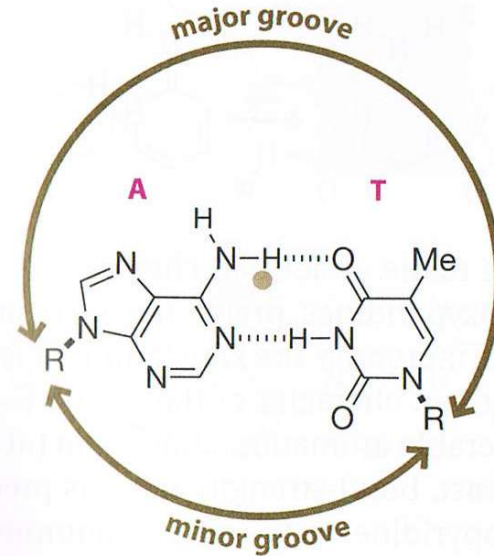
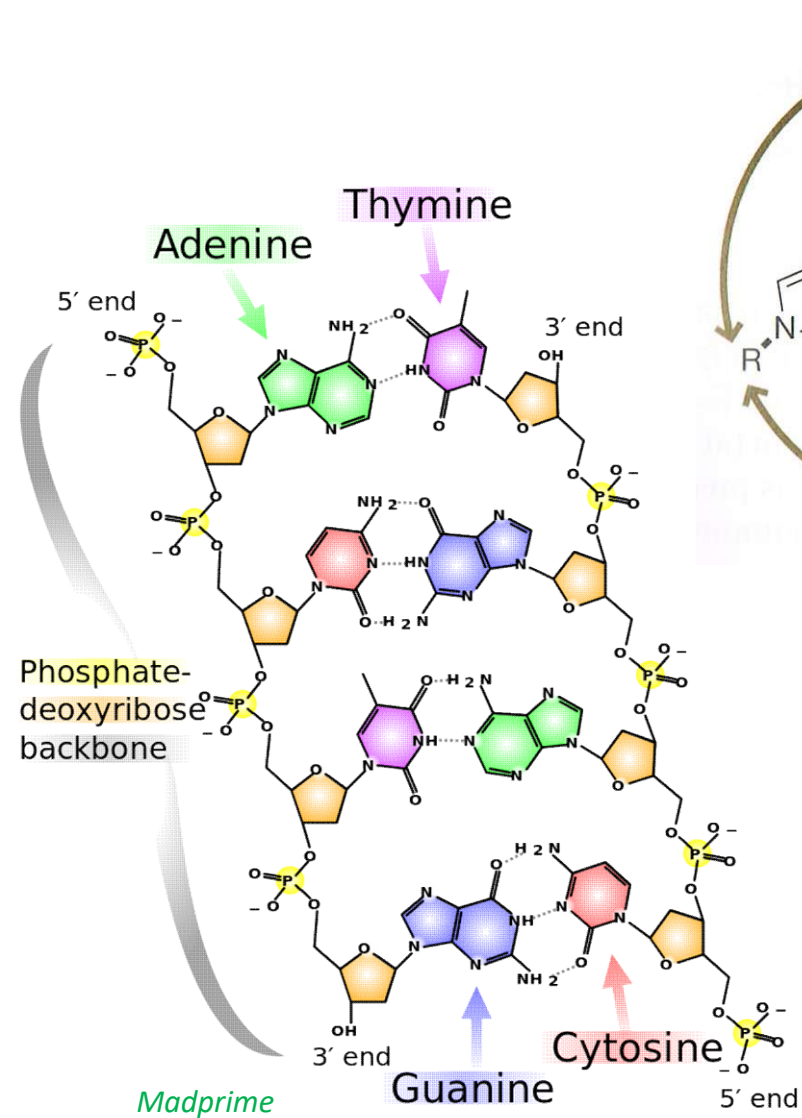
CHAPTER 1



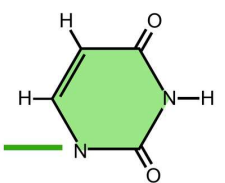
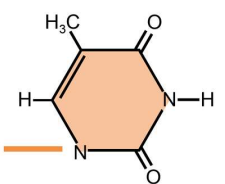
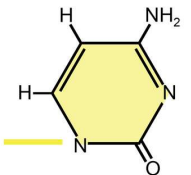
OLIGONUCLEOTIDES

Topic 3 – modified canonical nucleobases

Canonical nucleobases and Watson-Crick pairing in DNA



Purines

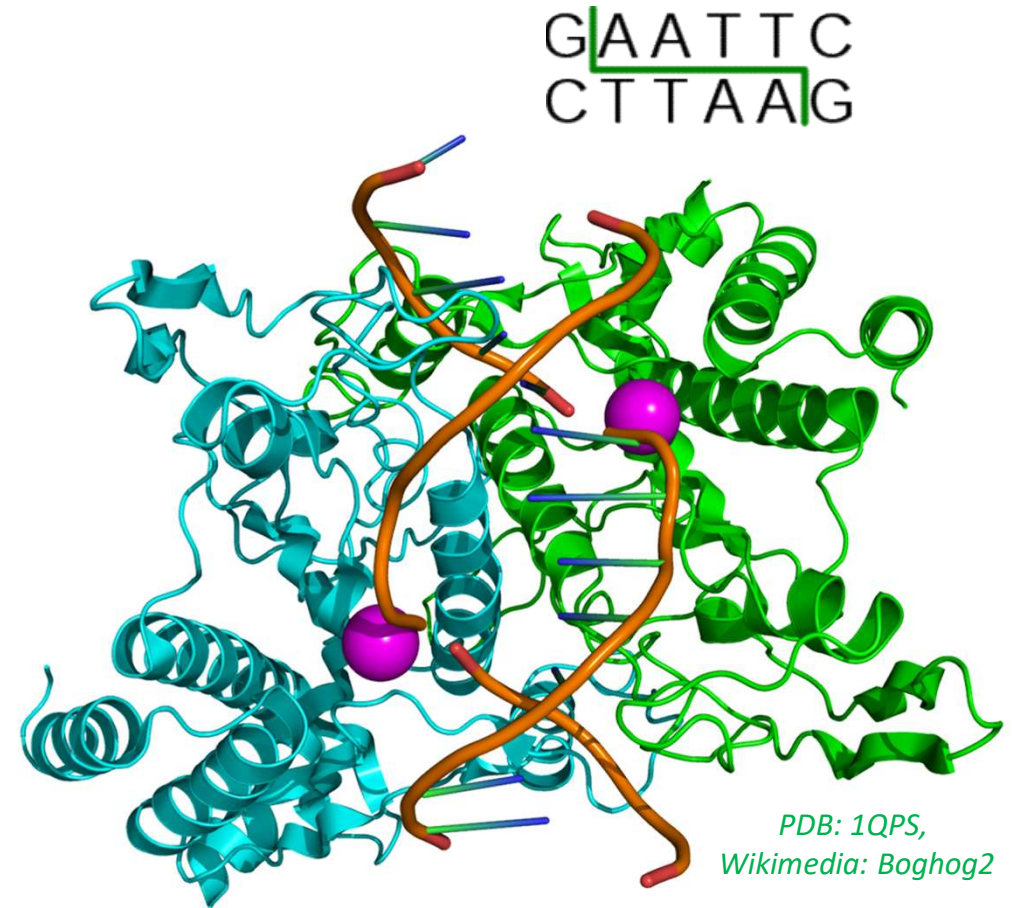
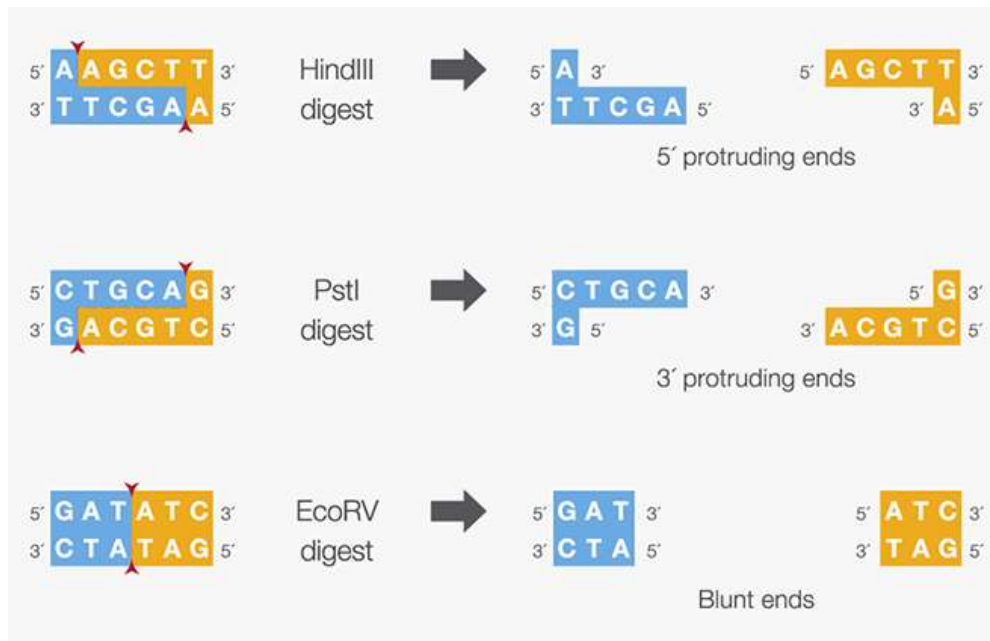


Pyrimidines

Bruce Blaus

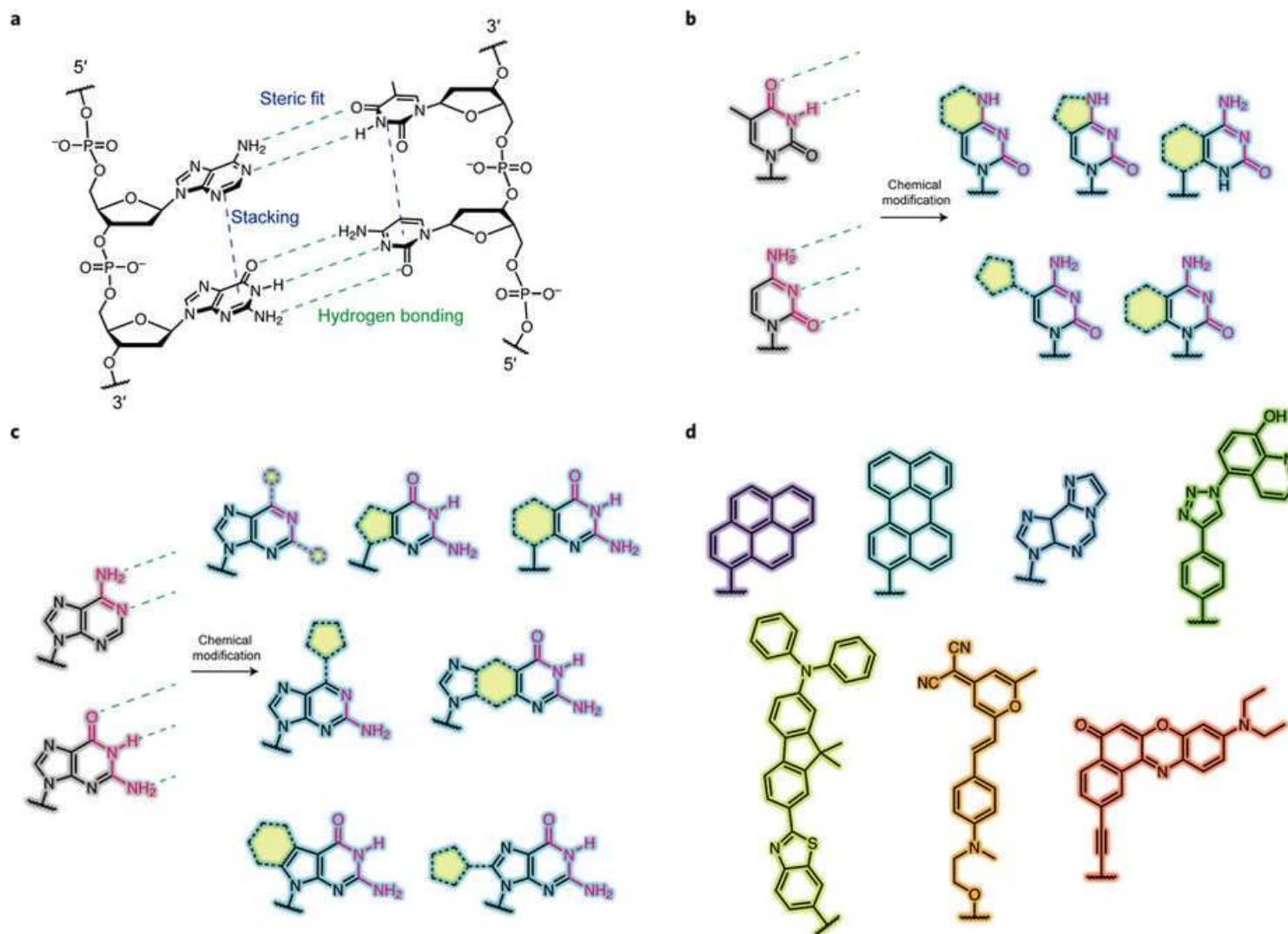
EcoI – a typical restriction enzyme

Products of restriction enzymes

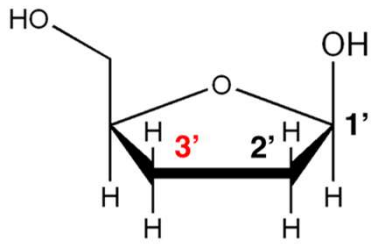


Structure of the homodimeric restriction enzyme EcoRI (cyan and green cartoon diagram) bound to double stranded DNA (brown tubes). Two catalytic magnesium ions (one from each monomer) are shown as magenta spheres and are adjacent to the cleaved sites in the DNA made by the enzyme (depicted as gaps in the DNA backbone).

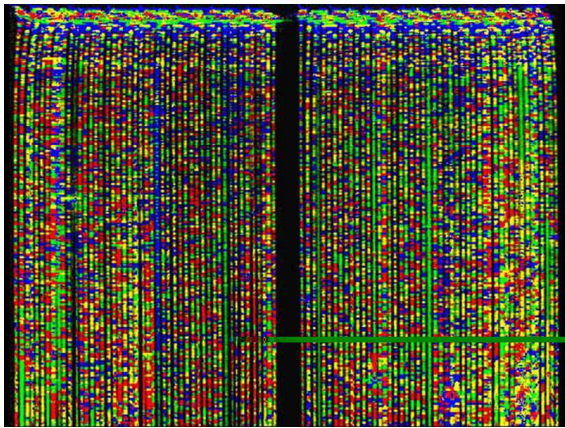
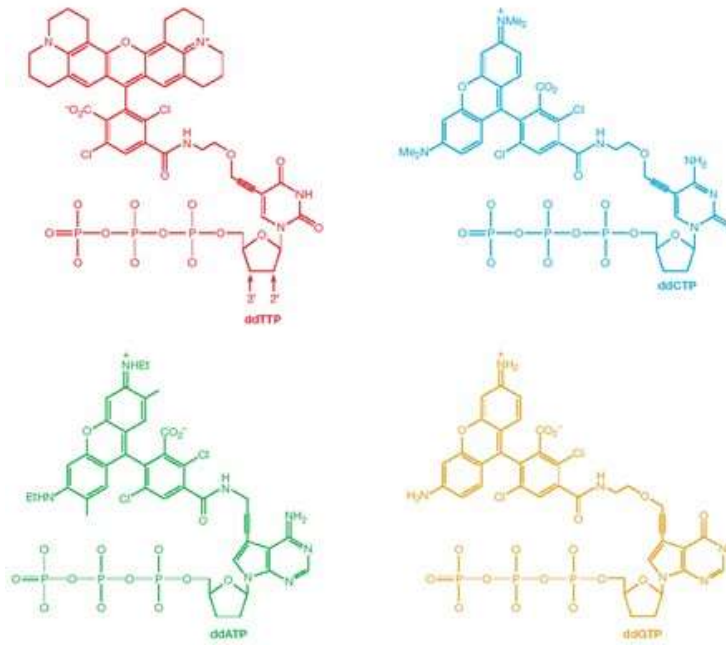
Non-canonical fluorescent nucleobases



W. Xu, K. M. Chan, E. T. Kool *Nature Chem.* **2017**, *9*, 1043-1055



Sanger sequencing



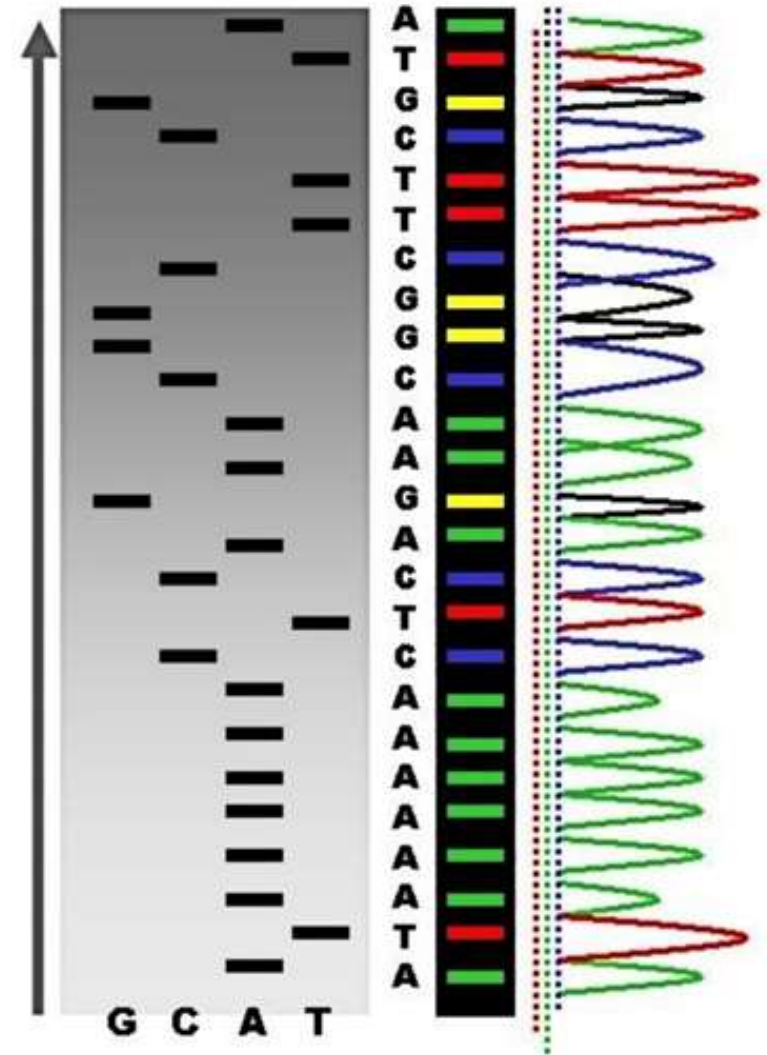
TACGTA****
ATGCATTAGGGCCTGGCTCTTT

TACGTA****
ATGCATTAGGGCCTGGCTCTTT

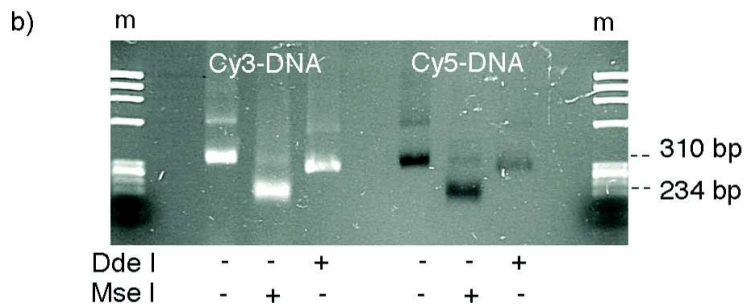
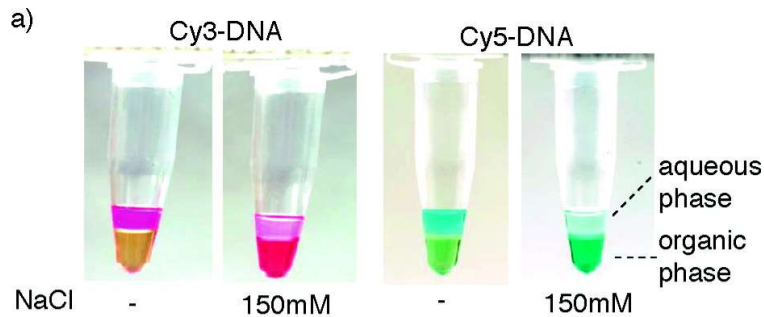
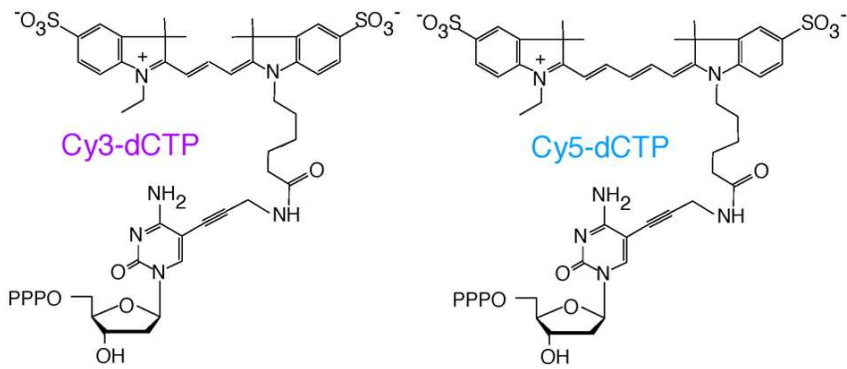
TACGTA**ATCCCG**A****
ATGCATTAGGGCCTGGCTCTTT

TACGTA**ATCCCG**A**CC**G****
ATGCATTAGGGCCTGGCTCTTT

Sequencing Gel



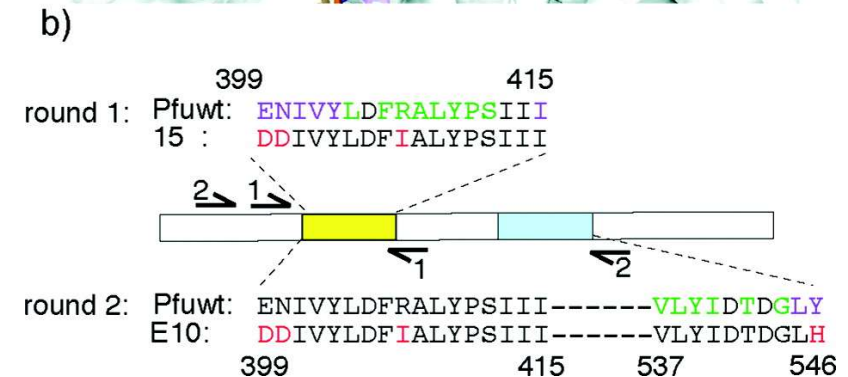
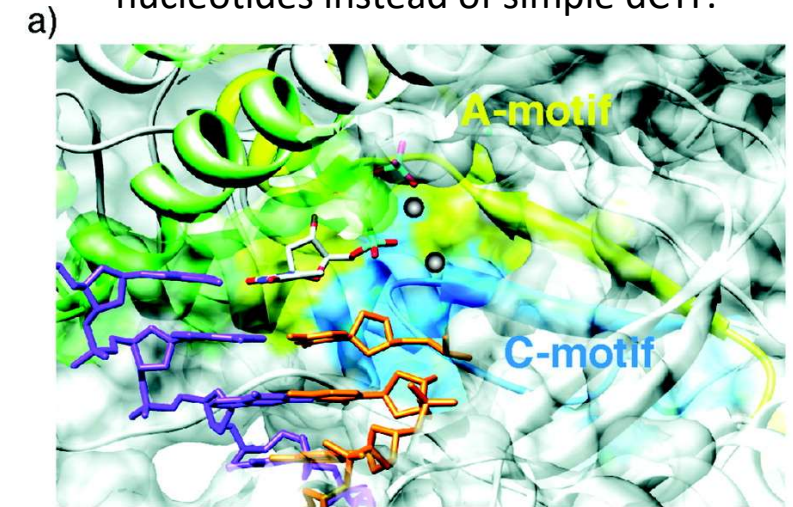
CyDNA – synthesis and replication of highly fluorescently-labelled DNA



Fulvio314

Pyrococcus furiosus
– an extremophilic
Archaeon from
marine sediments
Optimal life
temperature 100°C

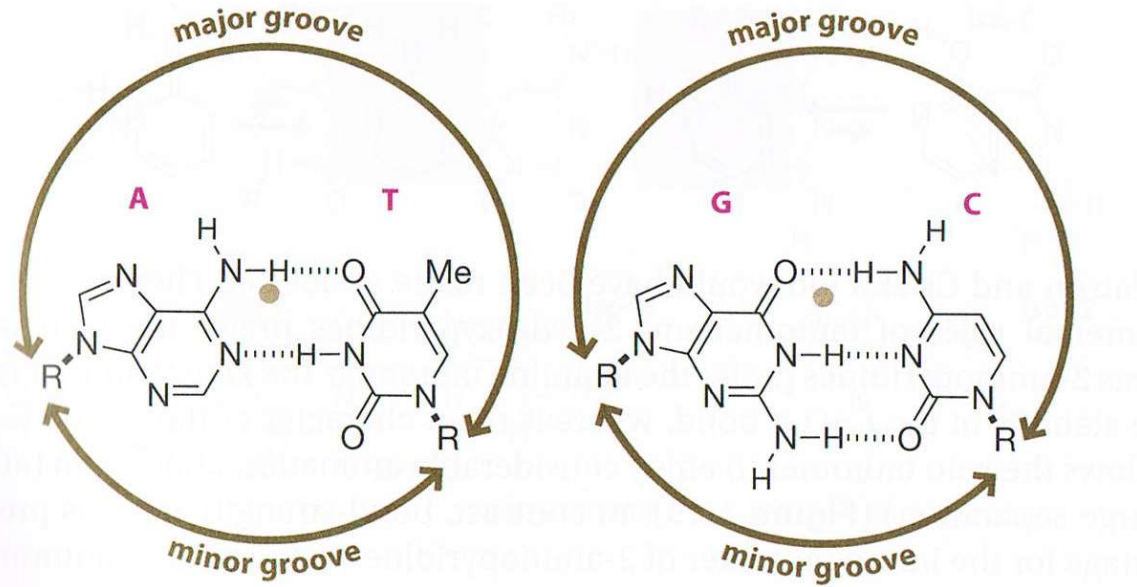
DNA Polymerase is evolutionarily optimized by mutagenesis to accept fluorescent Cy3 or Cy5 nucleotides instead of simple dCTP.



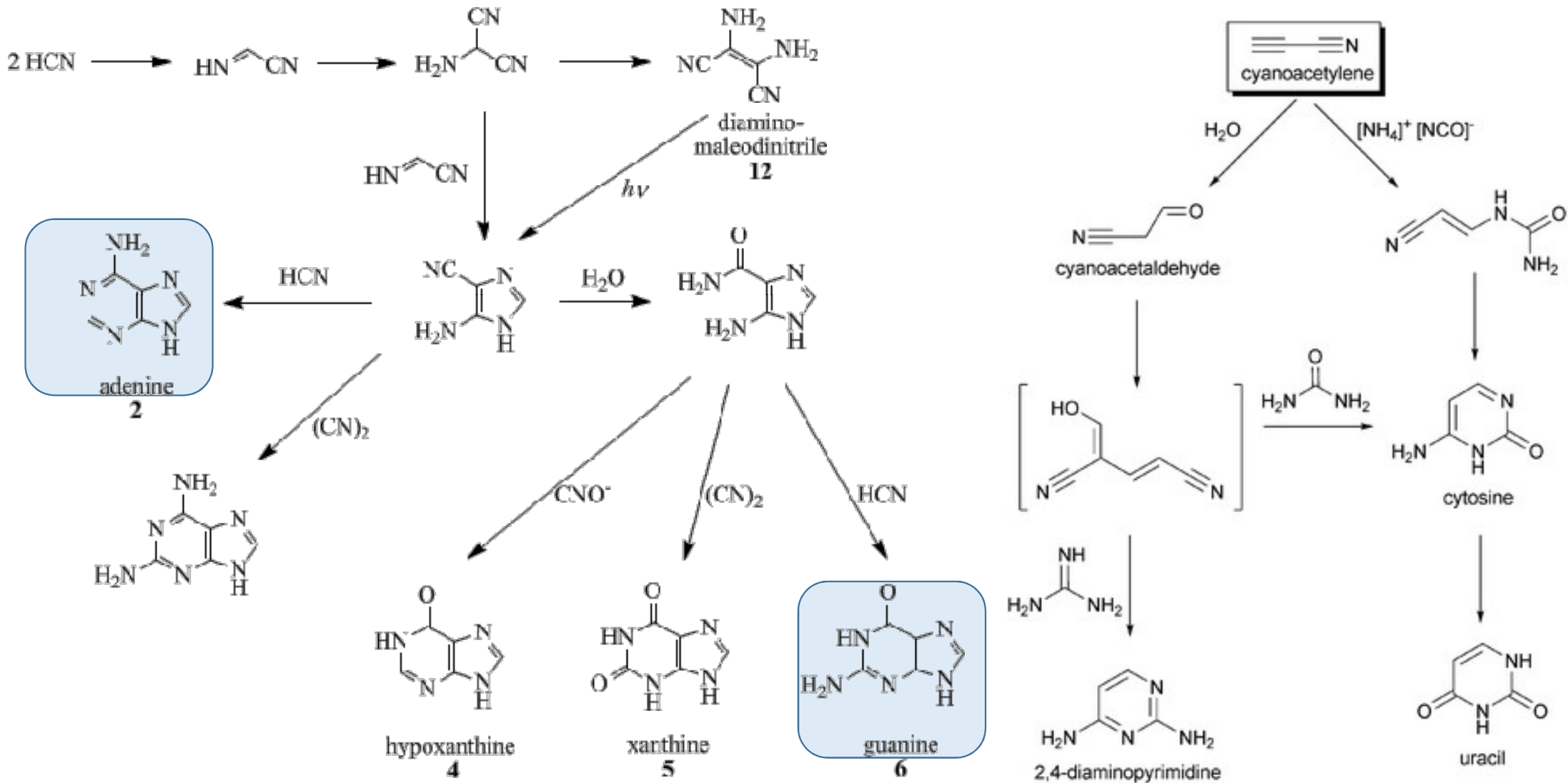
P. Holliger et al. *J. Am. Chem. Soc.* 2010, 132, 5096-5104

Why are A, C, G and T the letters of genetic alphabet.

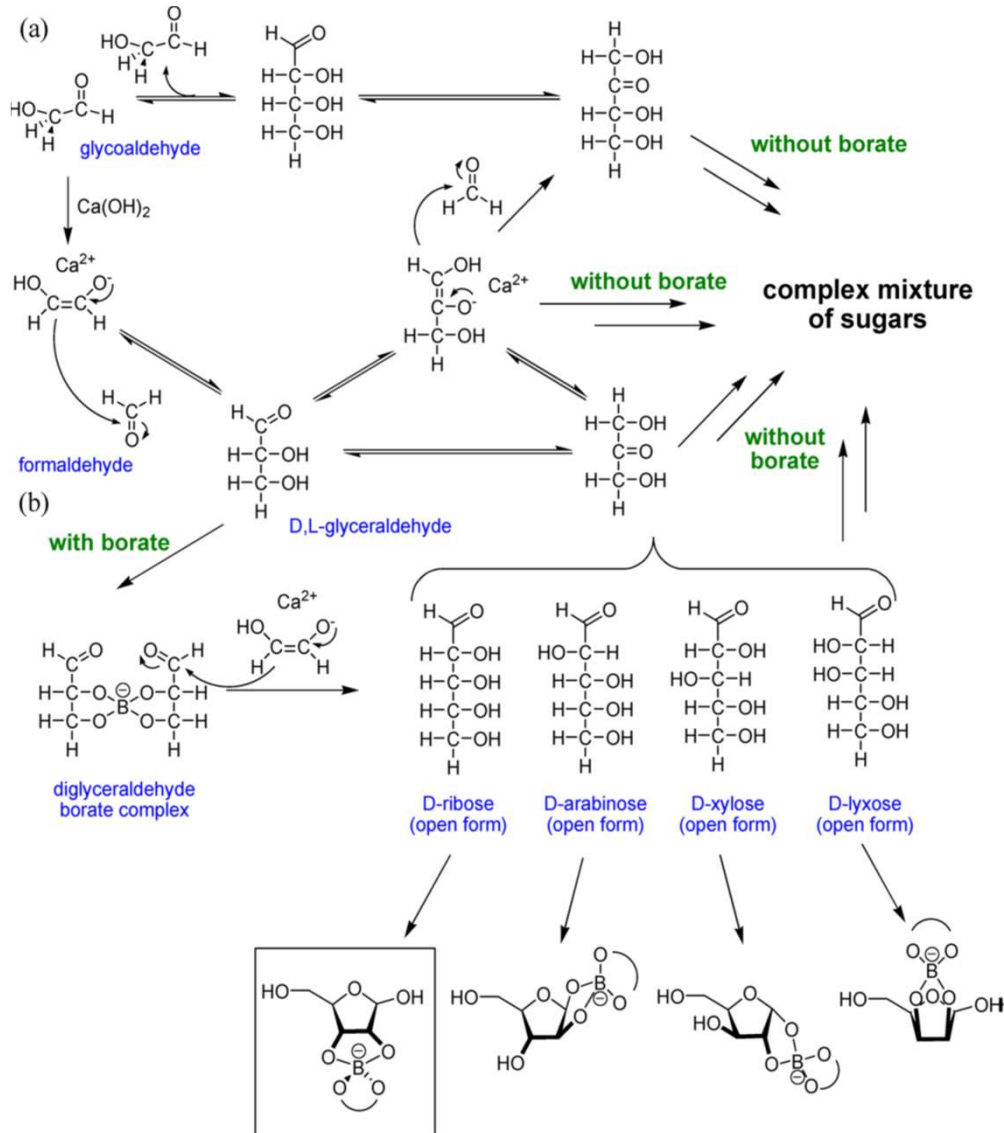
	common amine base	cytosine	thymine	adenine	guanine
pK_a	10.8	4.2	0.5	4.2	3.3
relative basicity of conj. base	4,000,000	1	0.0002	1	0.1



Prebiotic synthesis of nucleobases



Formose reaction in presence of borates

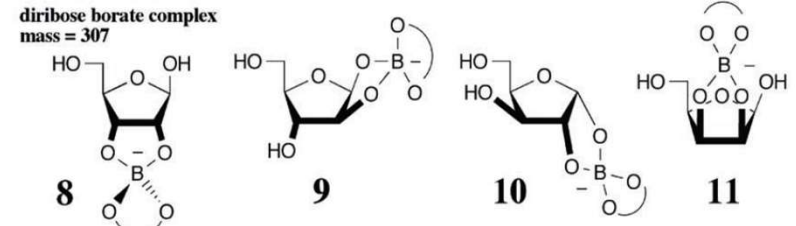


Pentose formation in the presence of borate

With borate (left)
Without borate (right)
Colemanite (background)



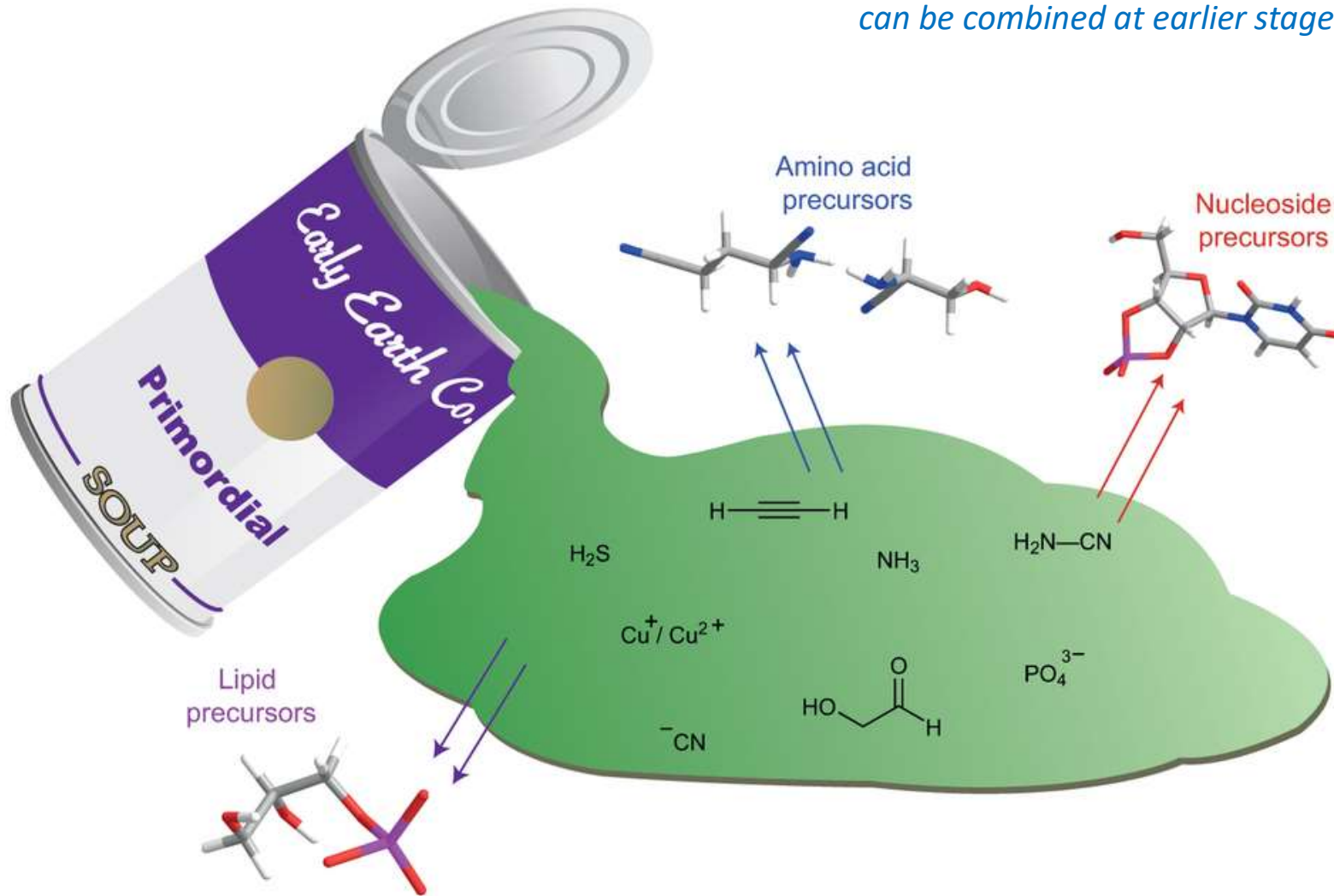
By NMR, the ribose borate complex **8** has the structure shown; cyclic structures for other pentoses are speculative.



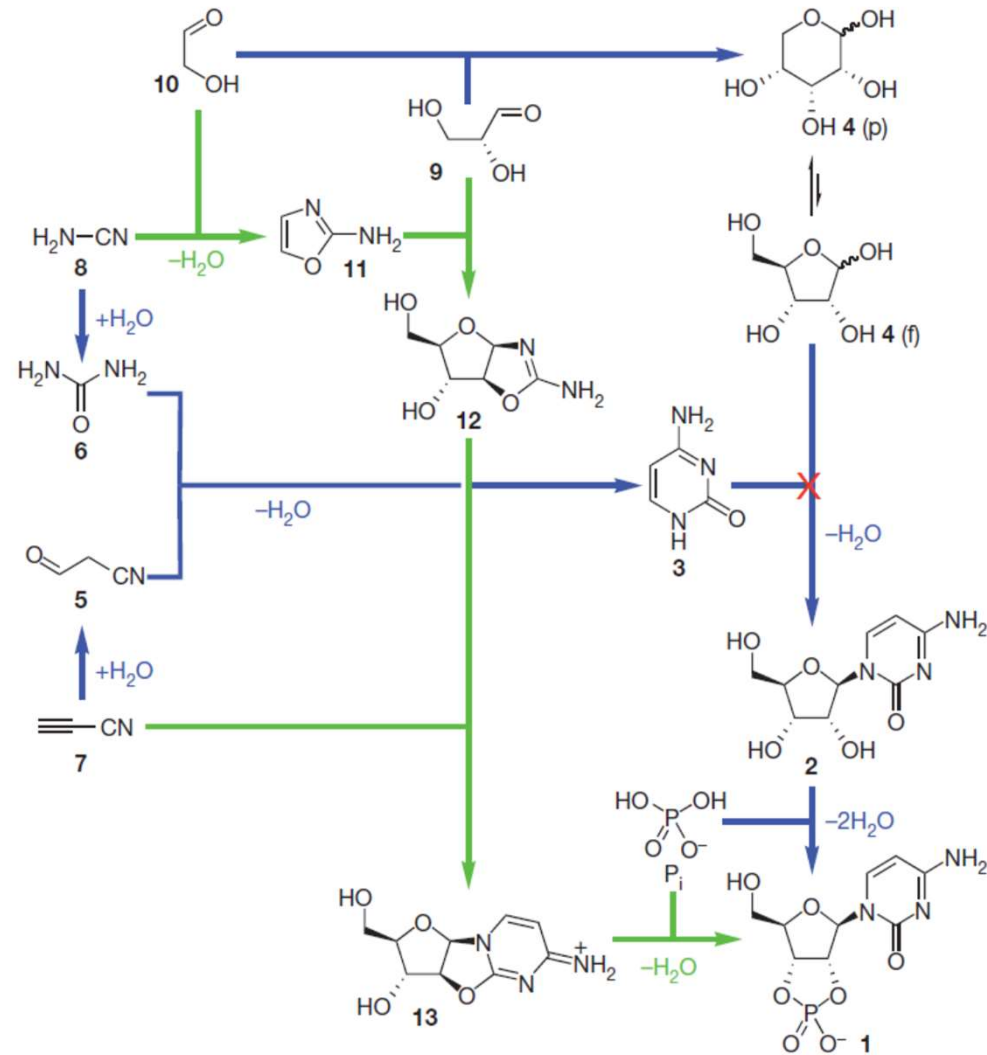
A. Ricardo, M. A. Carrigan, A. N. Olcott, S. A. Benner
Science **2004**, 303, 196

Cyanosulfidic chemistry

The aldol chemistry of sugars and cyanide chemistry of nucleobases can be combined at earlier stages than glycosylation.

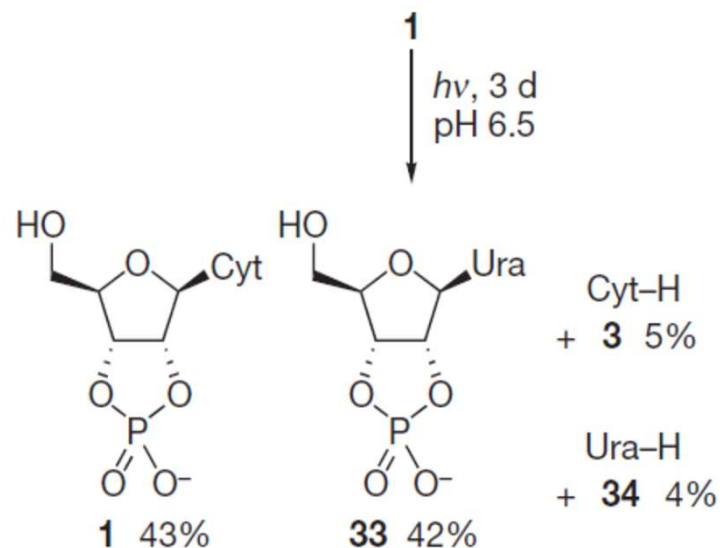


Cyanosulfidic chemistry



M. W. Powner, B. Gerland, J. D. Sutherland, *Nature* **2009**, *459*, 239–242

Cyanosulfidic chemistry



Photochemistry of *beta*-ribocytidine-2',3'-cyclic phosphate **1**. Under conditions of irradiation that destroy most other pyrimidine nucleosides and nucleotides, **1** undergoes partial hydrolysis and slight nucleobase loss. Ura, N1-linked uracil; Cyt-H, cytosine; Ura-H, uracil.

M. W. Powner, B. Gerland, J. D. Sutherland, *Nature* **2009**, *459*, 239–242

J. D. Sutherland, *Angew. Chem. Int. Ed.* **2016**, *55*, 104-121.

B. H. Patel, C. Percivalle, D. J. Ritson, C. D. Duffy, J. D. Sutherland, *Nat. Chem.* **2015**, *7*, 301–307.

J. D. Sutherland, *et al. Nat. Chem.* **2013**, *5*, 383–389.

CHAPTER 1



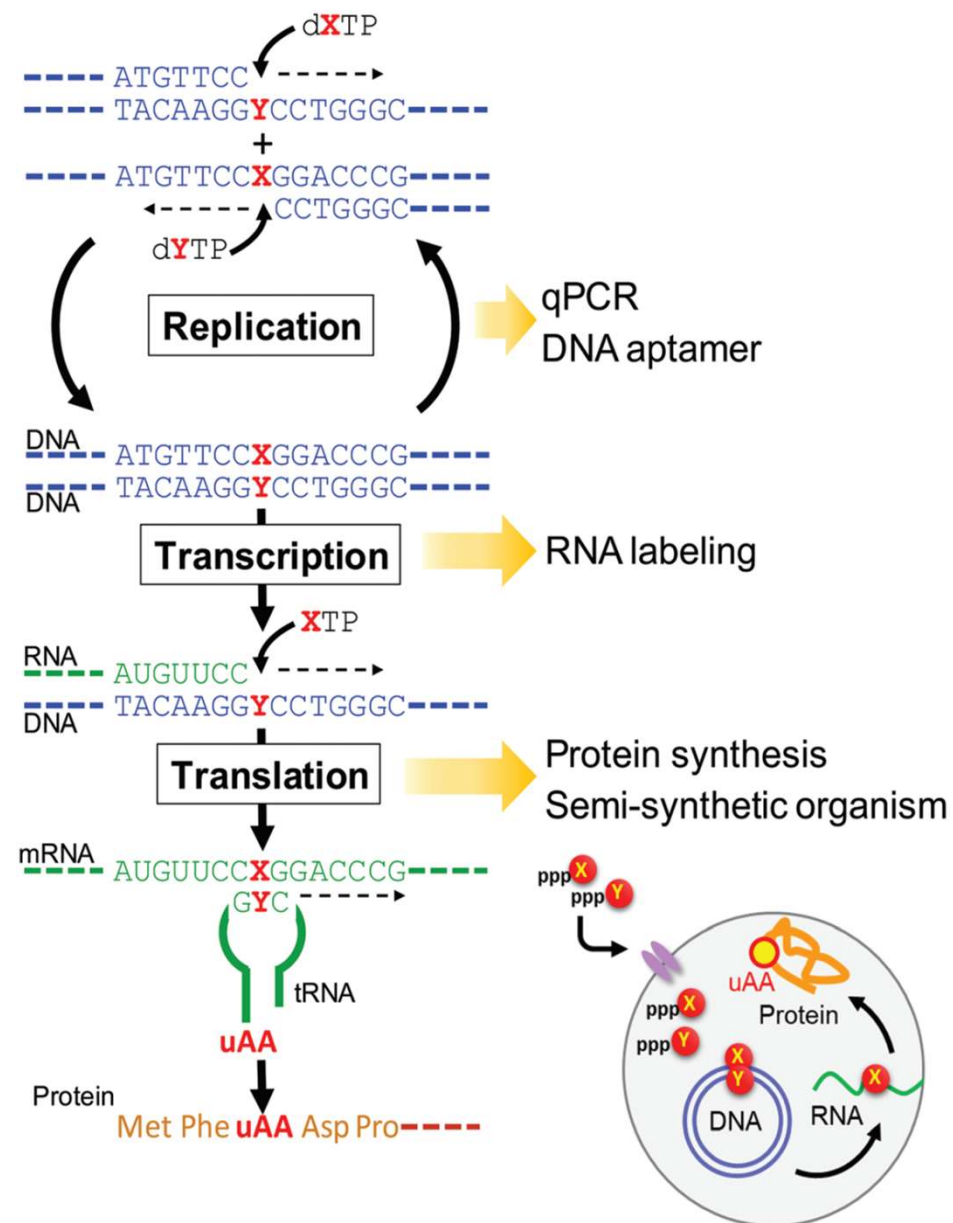
OLIGONUCLEOTIDES

Topic 4 – expansion of the genetic alphabet

Expansion of the genetic alphabet

Expansion of the genetic alphabet and code by creating an unnatural base pair (UBP) as a third pair.

The creation of a UBP (i.e., X–Y) that functions in replication, transcription, and translation as a third base pair with the natural A–T(U) and G–C pairs allows the storage and retrieval of the expanded genetic information in vitro and in vivo, enabling a variety of applications using biopolymers with increased functionalities



Tautomeric instability in non-canonical nucleobases

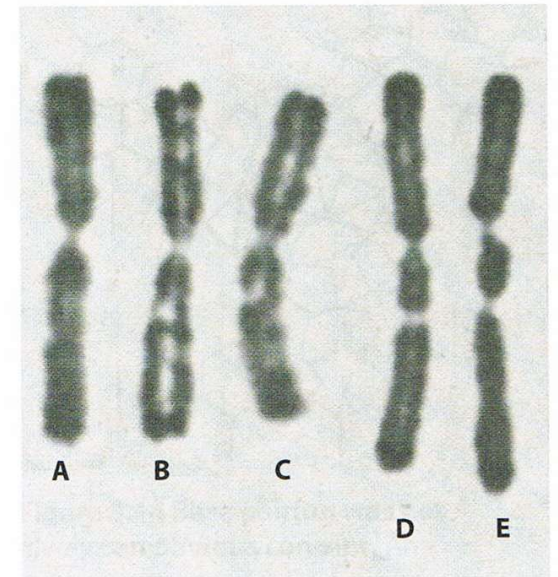
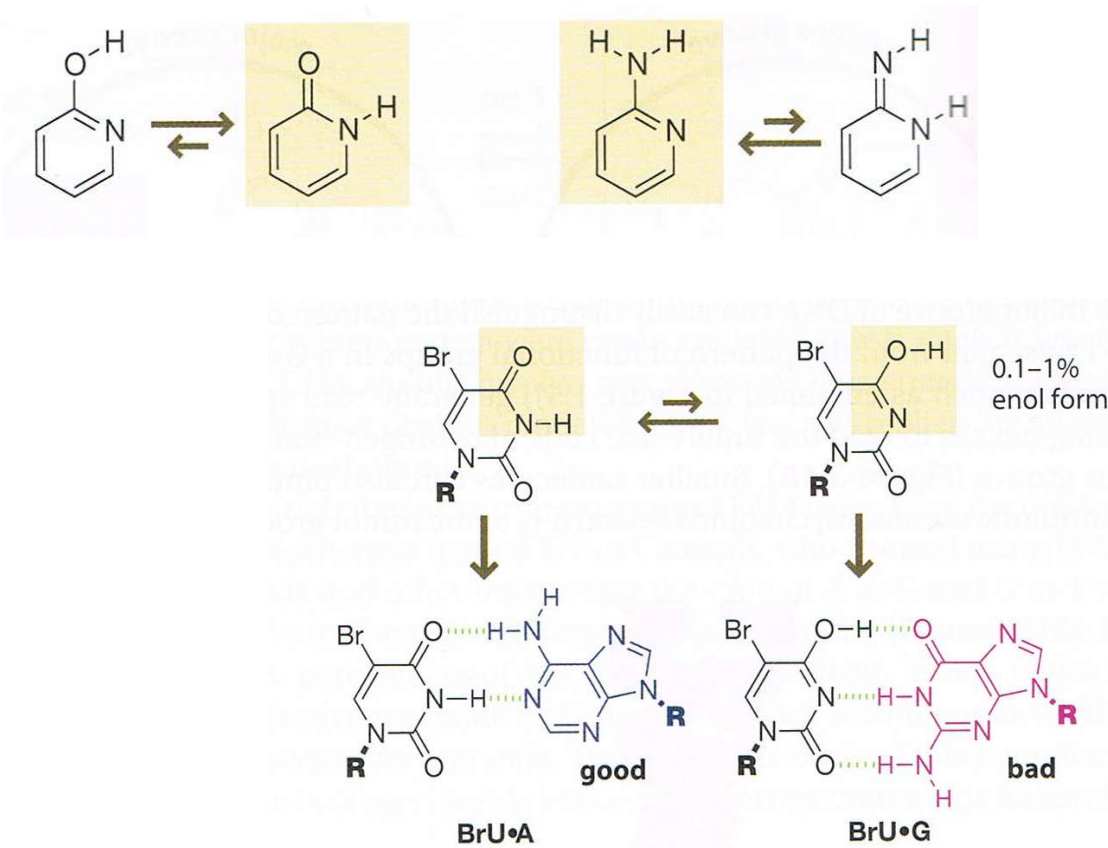
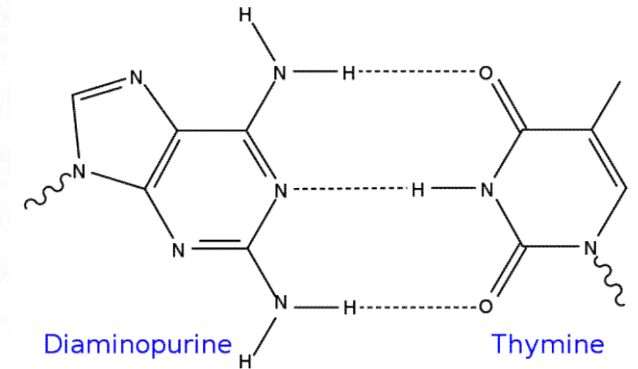
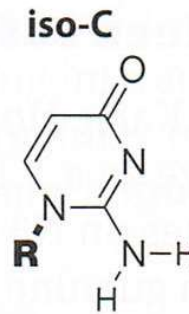
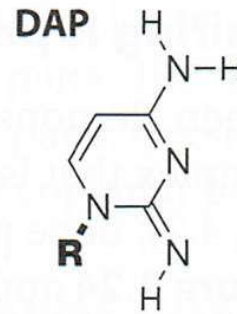
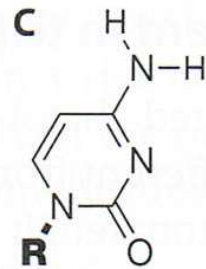
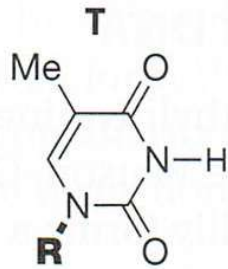


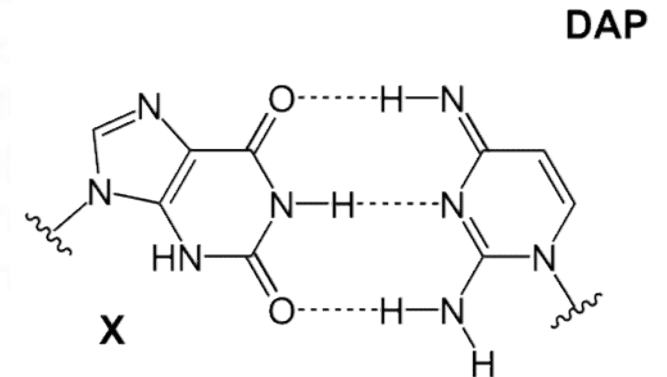
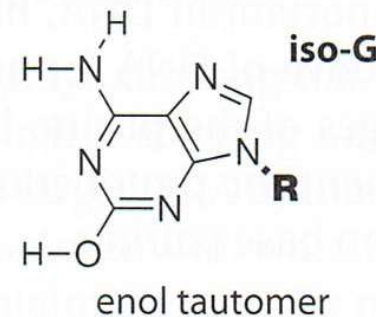
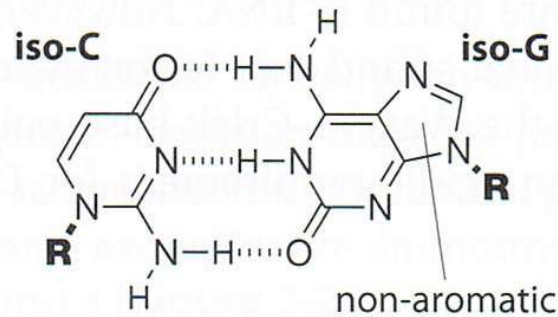
Figure 3.20 Chromosome 1 from hamster cells exposed to bromodeoxyuridine. (A) Normal chromosome. (B–E) Aberrant chromosomes. (From T.C. Hsu and C.E. Somers, *Proc. Natl. Acad. Sci. USA* 47: 396–403, 1961. With permission from the MD Anderson Cancer Center.)

Alternative base pairs – synthetic biology

Cyanophage S-2L uses diaminopurine instead of adenine (3 H-bonds!)



why not a third type of base pair?

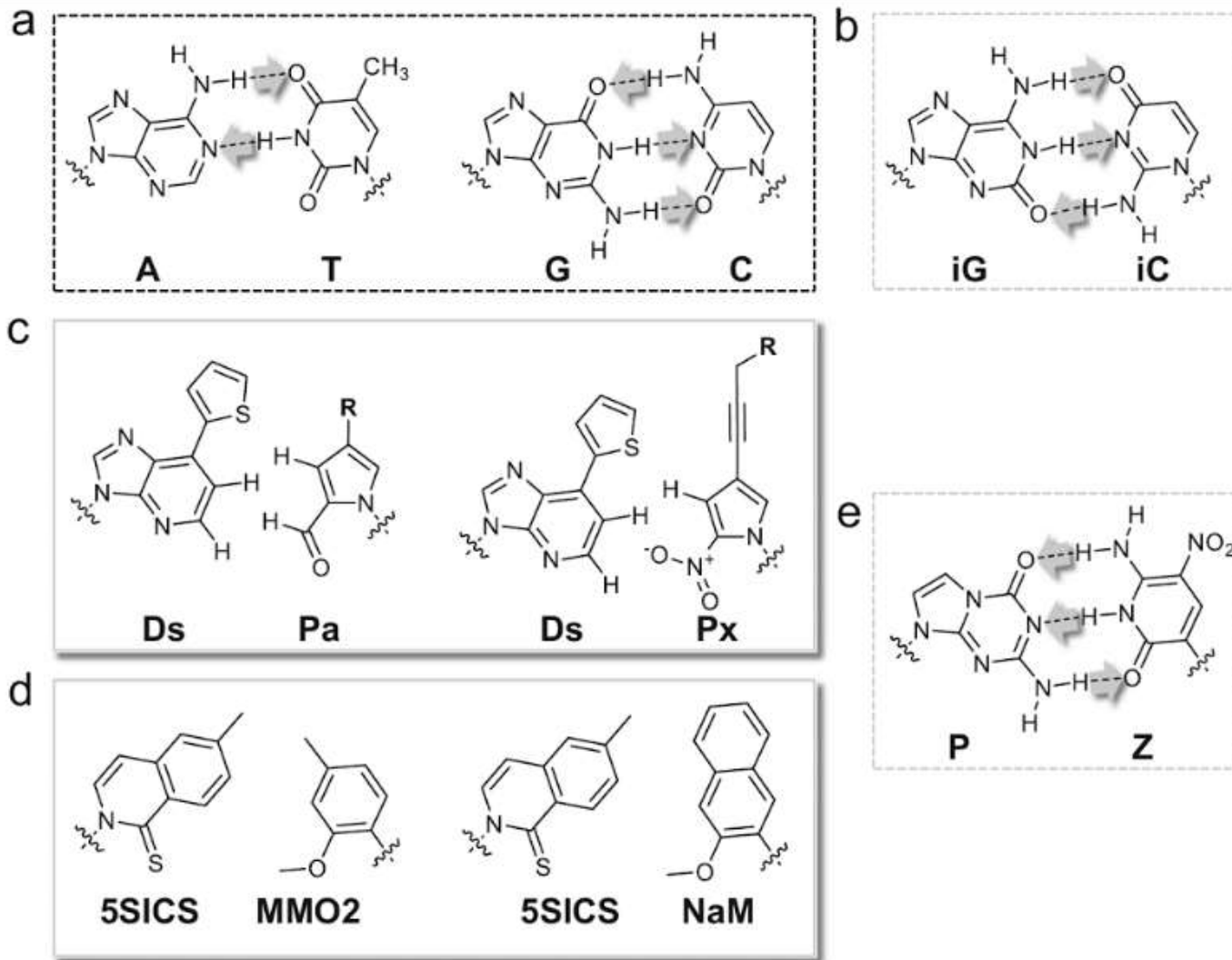


DAP – one tautomer forms a base pair with guanine

iso-C/iso-G

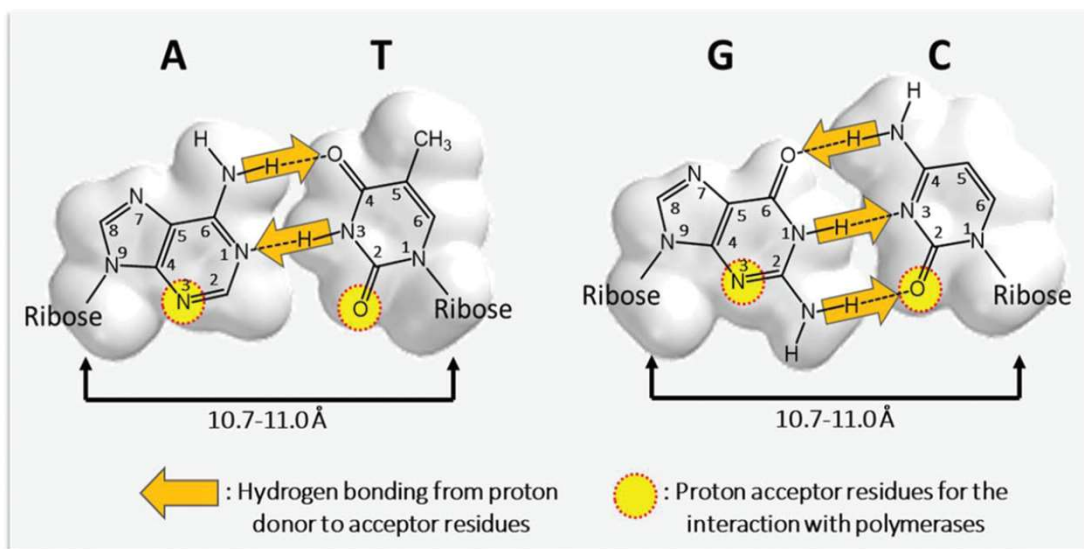
- specificity (the enol tautomer of iso-G, stabilized by aromatization, complementary to thymine)
- the 2-amino group of iso-C hydrolyses easily to uracil

Natural and non-natural base pairs that function in polymerase reactions



Unnatural base pair (UBP) design rules:

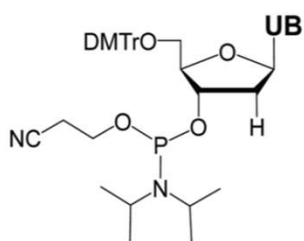
Design



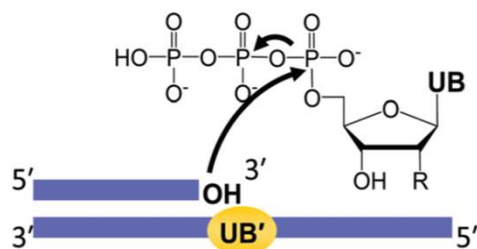
- Distance of 10.7-11.0 Å between the glycosidic bonds of the pair
- no mispairing with natural bases
- Reasonable hydrophobicity
- Chemical stability (phosphoramidite chemistry)
- Recognition by DNA and RNA polymerases (fidelity, efficiency)

Chemical synthesis

Phosphoramidite reagents for DNA chemical synthesis

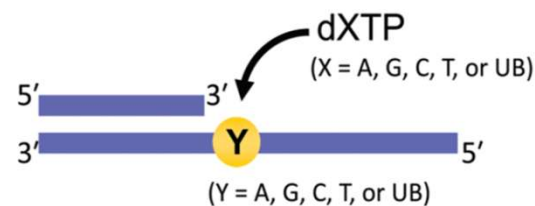


Nucleoside triphosphates (R = H: d(UB)TP, R = OH: (UB)TP)

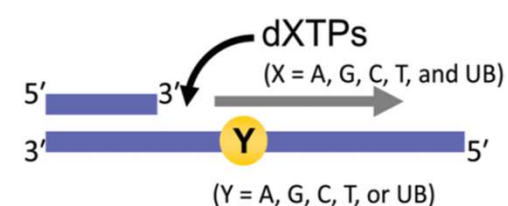


Polymerase reaction tests

Single-nucleotide insertion

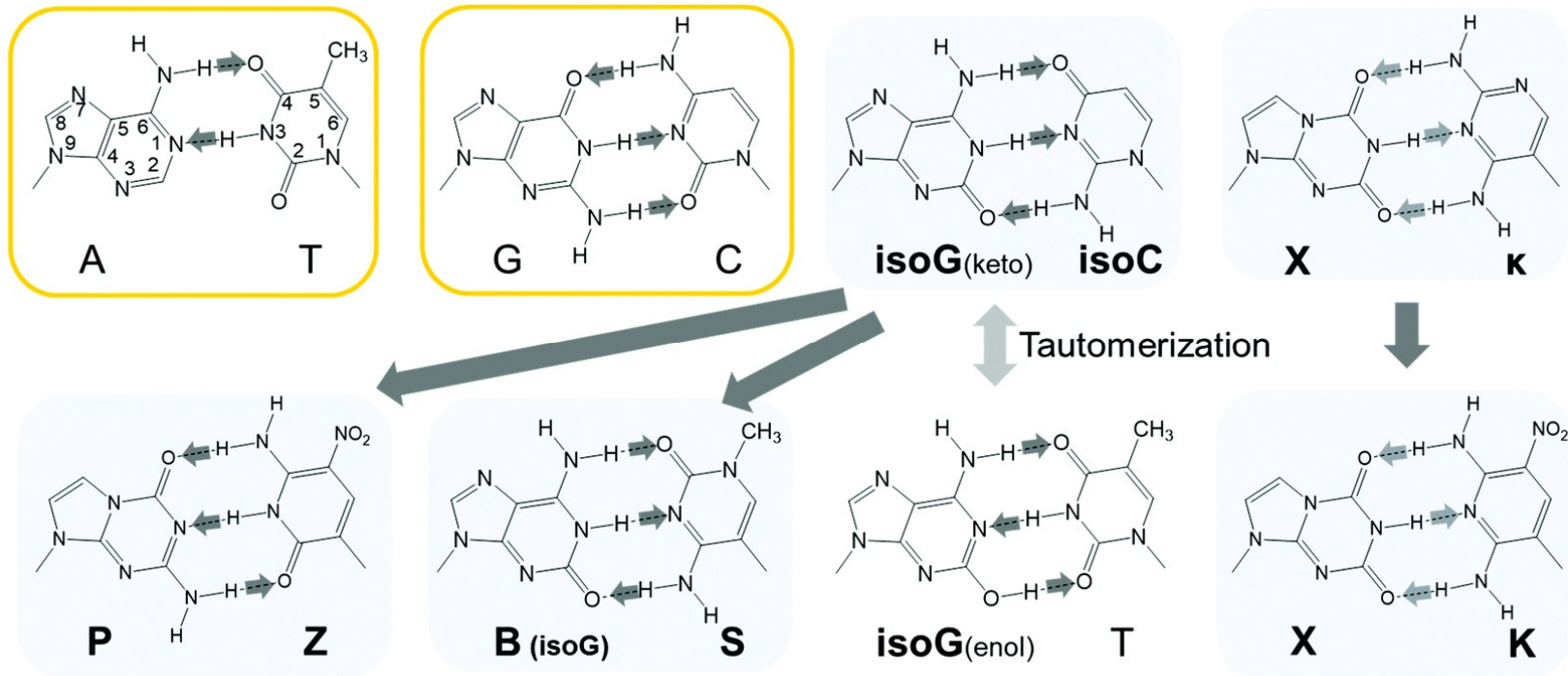


Primer extension



M. Kimoto, I. Hirao *Chem. Soc. Rev.* **2020**, *49*, 7602-7626

Non-natural nucleobases compatible with polymerases



Alexander Rich (1962): isoG–isoC pair

Steven Benner (1989-95): the artificially expanded genetic information system (AEGIS) including the isoG–isoC and X–κ pairs → *in vitro* replication, transcription, and translation systems.

Benner and Prudent (2004): new quantitative PCR (qPCR) methods, such as Plexor, using the isoG–isoC pair

Benner (2007): Z-P pair - the P base by removing the hydrogen at position 1 of G to exclude the keto–enol tautomerism, by introducing the nitro group into Z, the chemical stability of the nucleoside was improved;

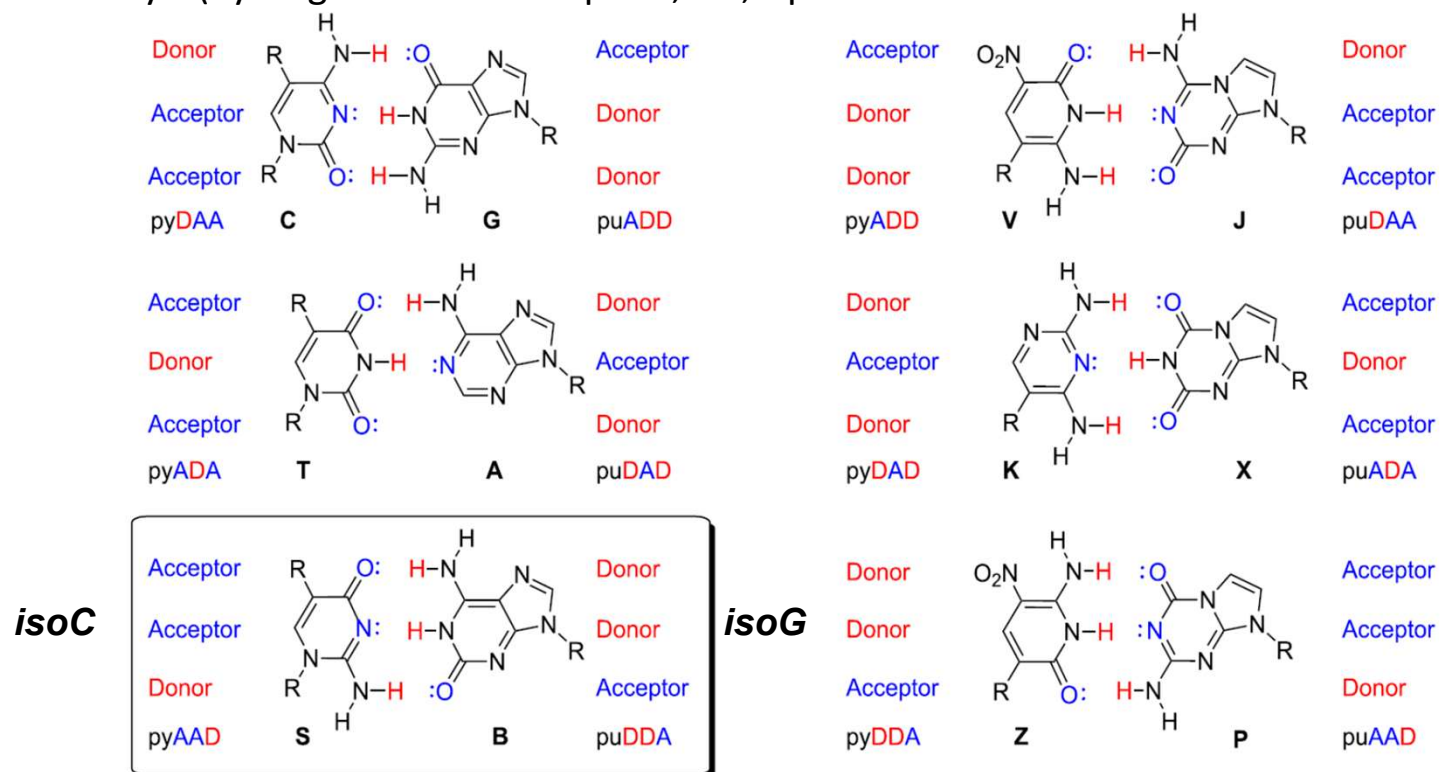
With the same strategy, they also developed the B–S and X–κ pairs from isoG–isoC and X–κ pairs, respectively

AEGIS – Artificially Expanded Genetic Information System

Watson–Crick pairing rules:

(a) size complementarity - large purines pair with small pyrimidines

(b) hydrogen-bonding complementarity (hydrogen-bond acceptors, A, pair with hydrogen-bond donors, D).



Rearranging donor and acceptor groups on the nucleobases, while not changing the geometry of the Watson–Crick pair, creates an artificially expanded genetic information system (AEGIS). AEGIS components add information density to DNA strands built from them.

S. Benner *et al.*, *Beilstein J. Org. Chem.* **2014**, *10*, 2348–2360. doi:10.3762/bjoc.10.245

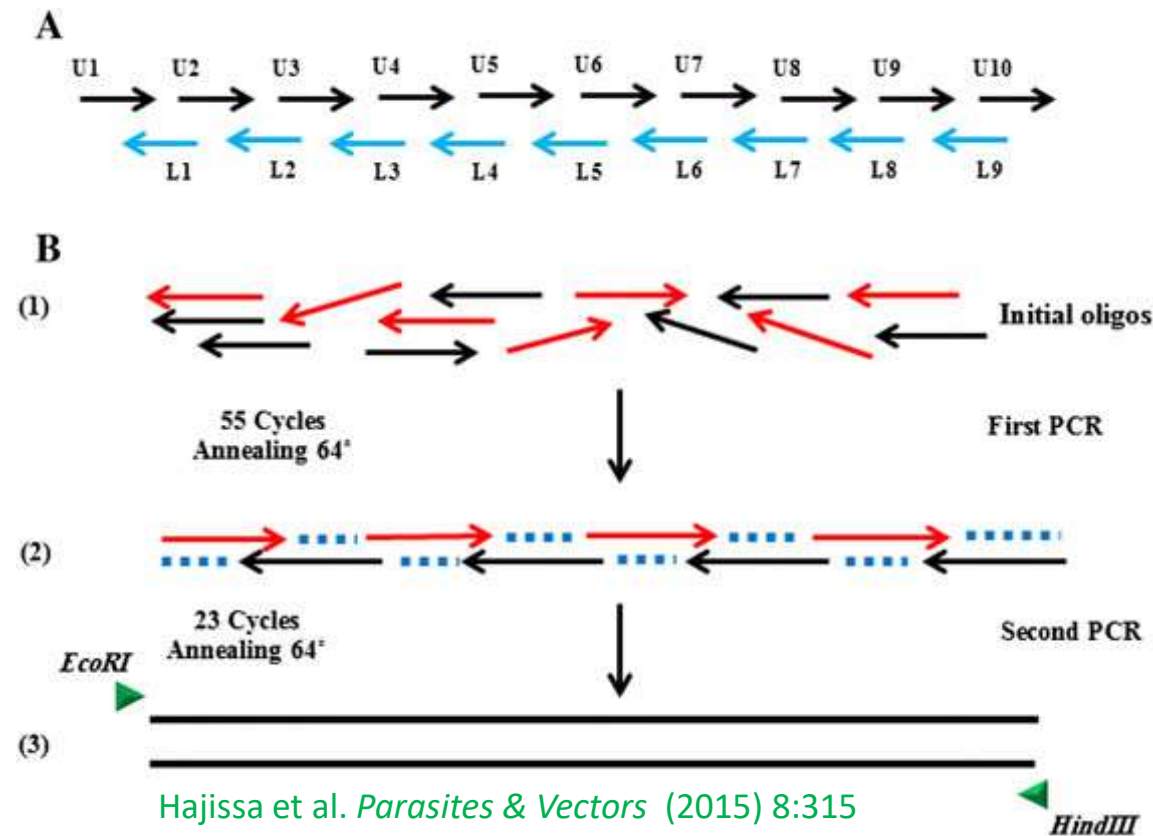
Artificial Gene Synthesis

Artificial gene synthesis (DNA printing) - method in synthetic biology to create artificial genes in the laboratory:

- currently based on solid-phase DNA synthesis,
- the user does not have to begin with preexisting DNA sequences.
- Therefore, it is possible to make a completely synthetic double-stranded DNA molecule with no apparent limits on either nucleotide sequence or size.

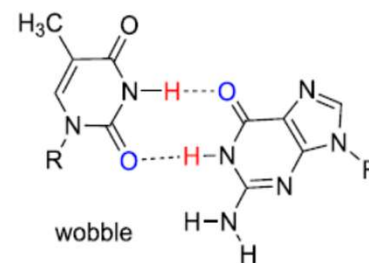
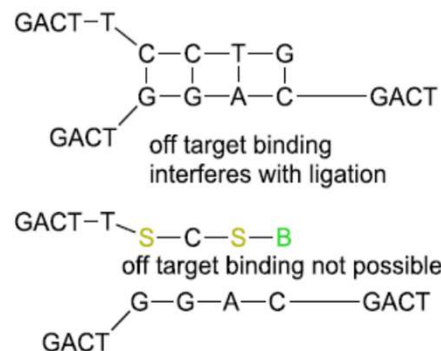
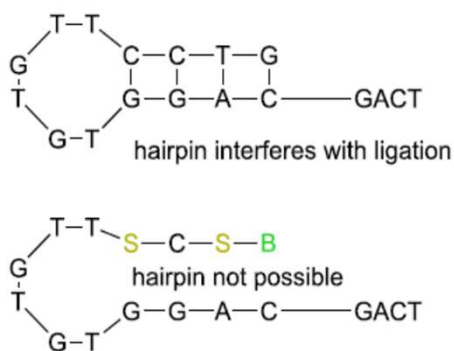
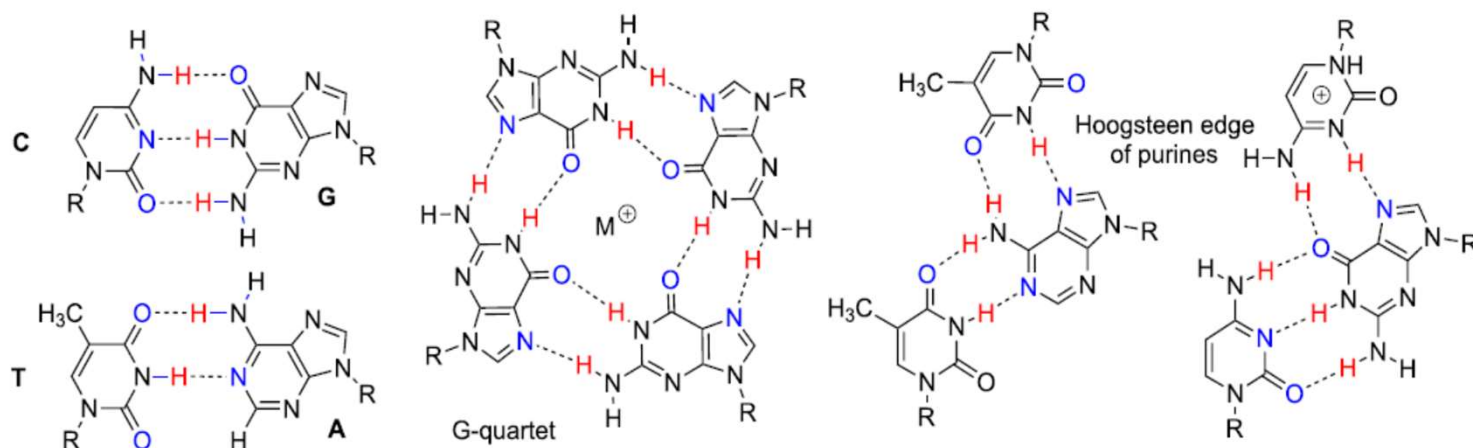
Applications:

- recombinant DNA technology including heterologous gene expression, vaccine development, gene therapy and molecular engineering.
- The synthesis of nucleic acid sequences can be more economical than classical cloning and mutagenesis procedures
- the ability to safely obtain genes for vaccine research without the need to grow the full pathogens.
- to optimize protein expression in a particular host, or to remove non-functional DNA segments
- For DNA digital data storage and computing
- For synthetic biological circuits



Self-assembly of whole genes and DNA nanostructures

Limitations of DNA puzzle assembly: unequal A:T vs. G:C strength, insufficient ACGT information density, higher-order structures

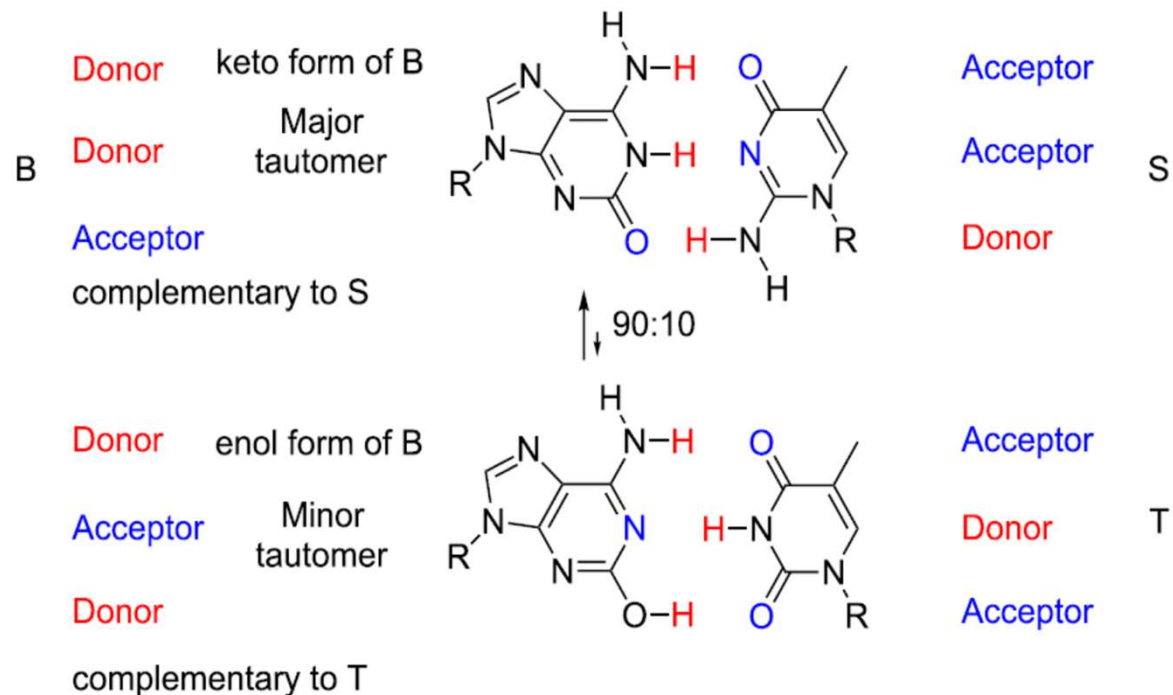


S. Benner *et al.*, *Beilstein J. Org. Chem.* **2014**, *10*, 2348–2360. doi:10.3762/bjoc.10.245

Self-assembly of whole genes and DNA nanostructures

Solution: an orthogonal pair from the AEGIS system, that can be removed from the product, yielding native DNA structures

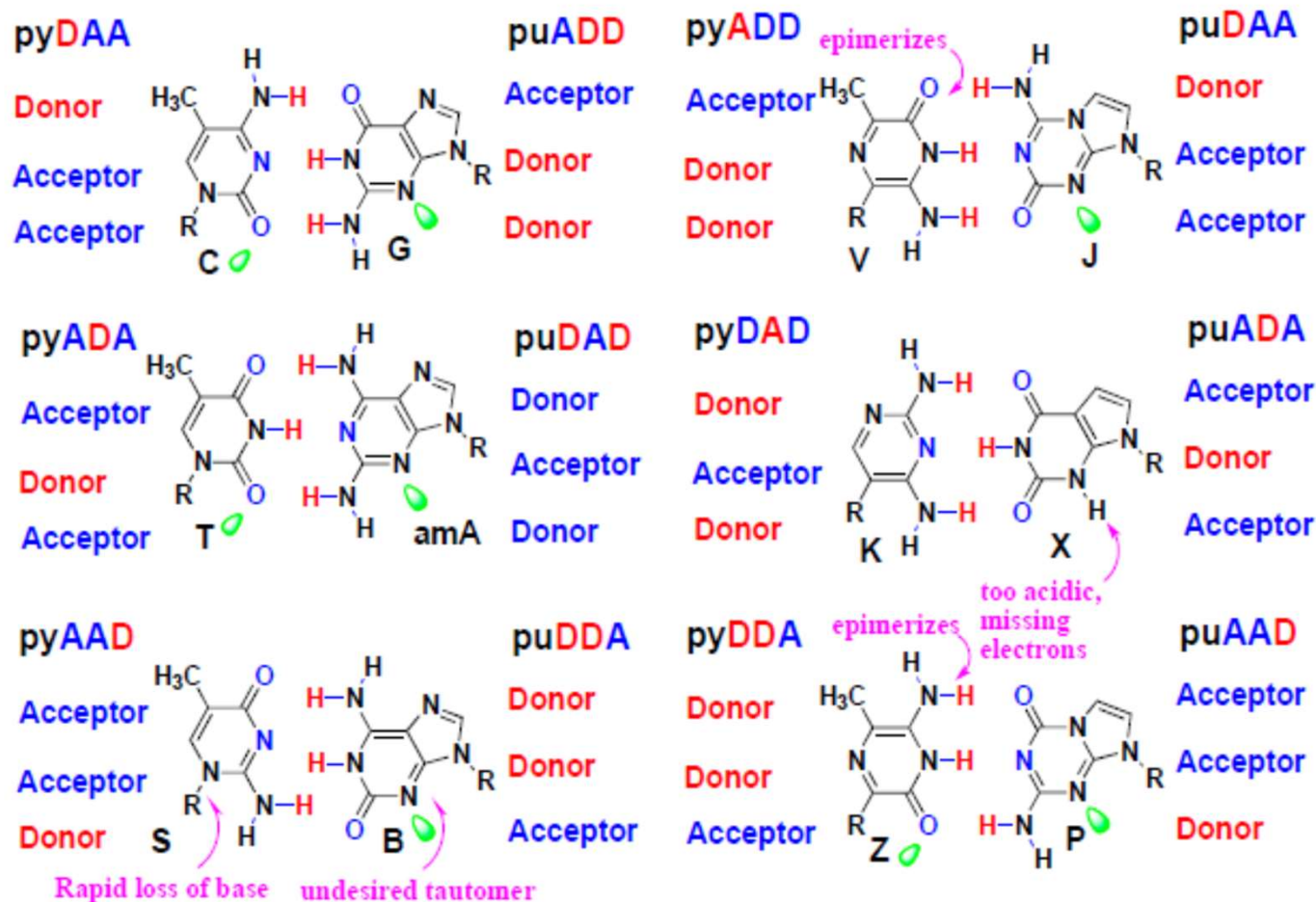
Conversion occurs when polymerases are forced to mismatch a standard nucleotide opposite an AEGIS nucleotide by
(a) not being provided the complementary AEGIS triphosphate and
(b) exploiting a chemical feature of the AEGIS nucleotide that directs a specific mismatch.



B in its major tautomeric form pairs with **S**; in its minor tautomeric form, **B** pairs with standard **T**. Assembly of the target gene/DNA nanostructure is followed by conversion of the **S:B** pairs to **T:A** pairs after two cycles of PCR: **B** → **A** via an intermediate **B:T** mispairing, **S** → **T** (intermediate **S:B** followed by a second **B:T** mispairing).

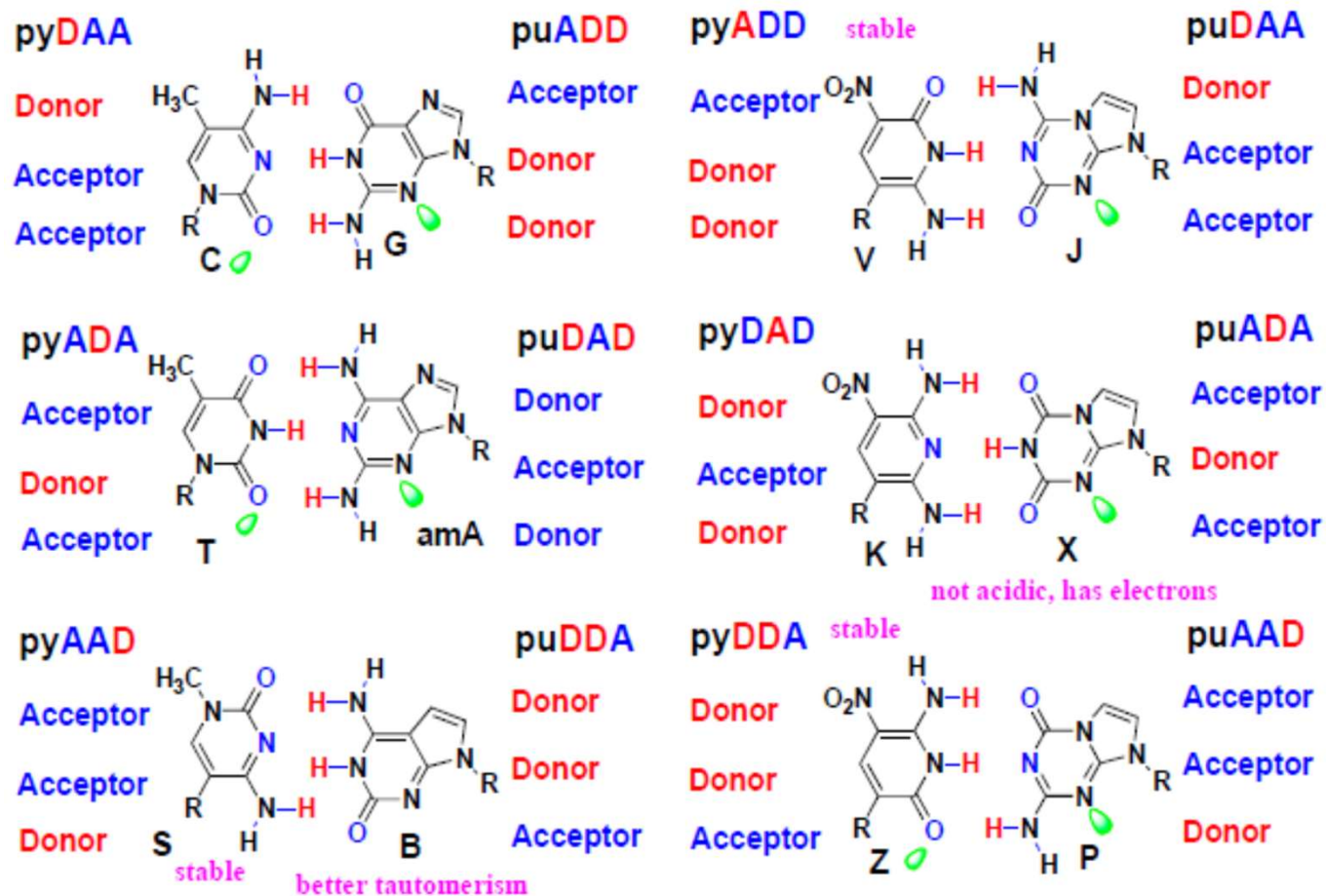
AEGIS – Artificially Expanded Genetic Information System

First Generation AEGIS

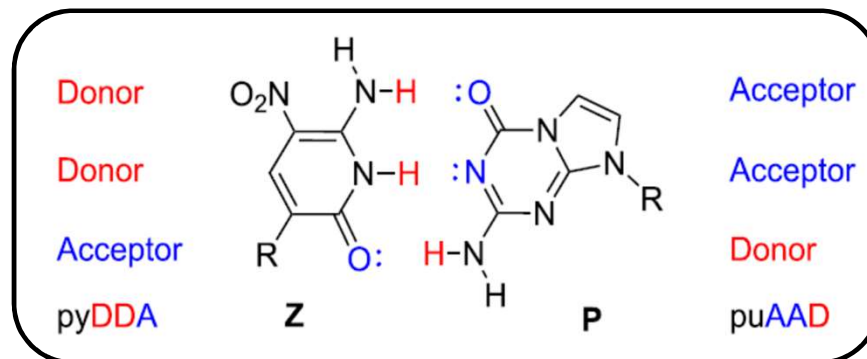
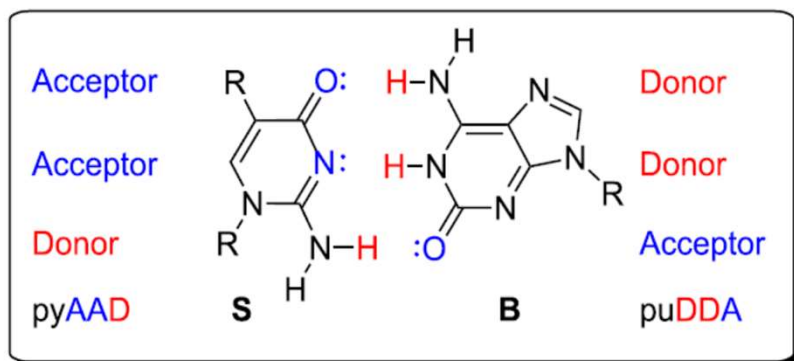
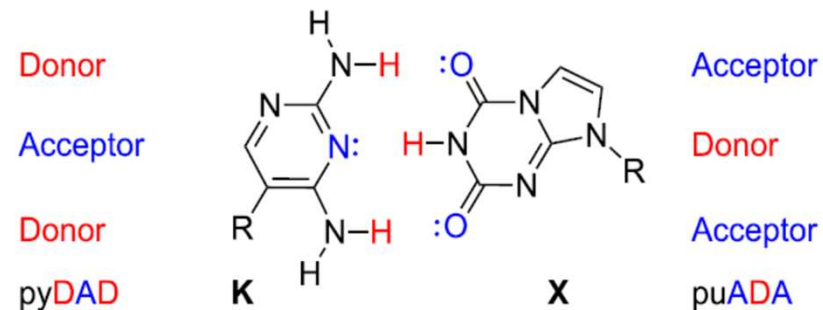
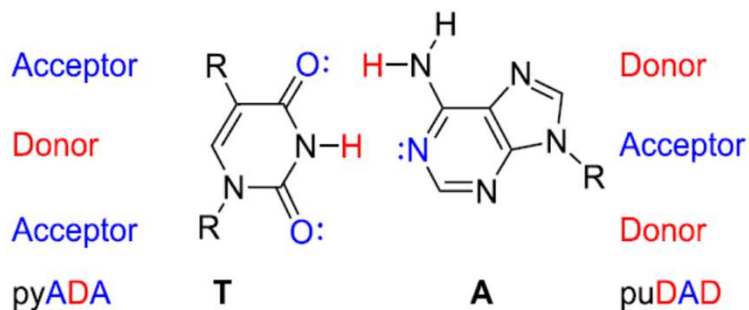
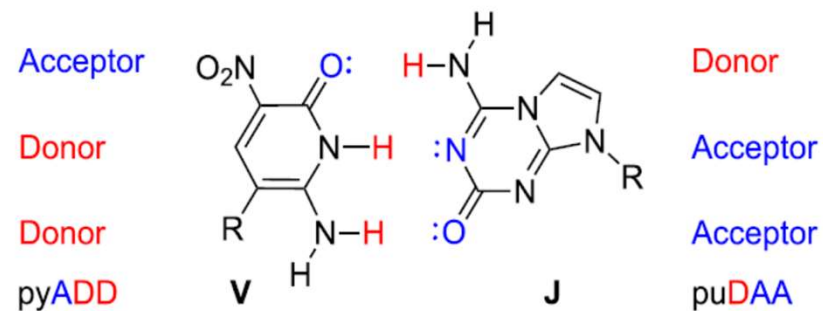
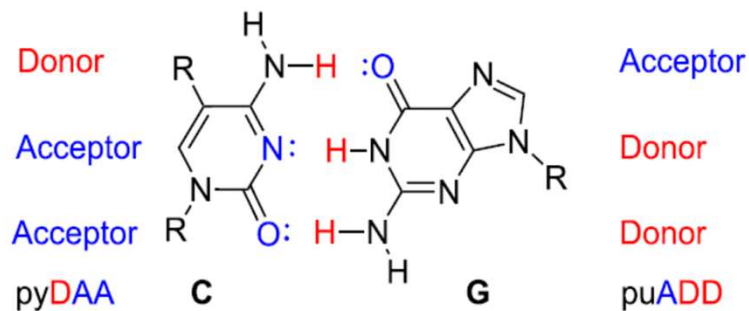


AEGIS – Artificially Expanded Genetic Information System

Second Generation AEGIS

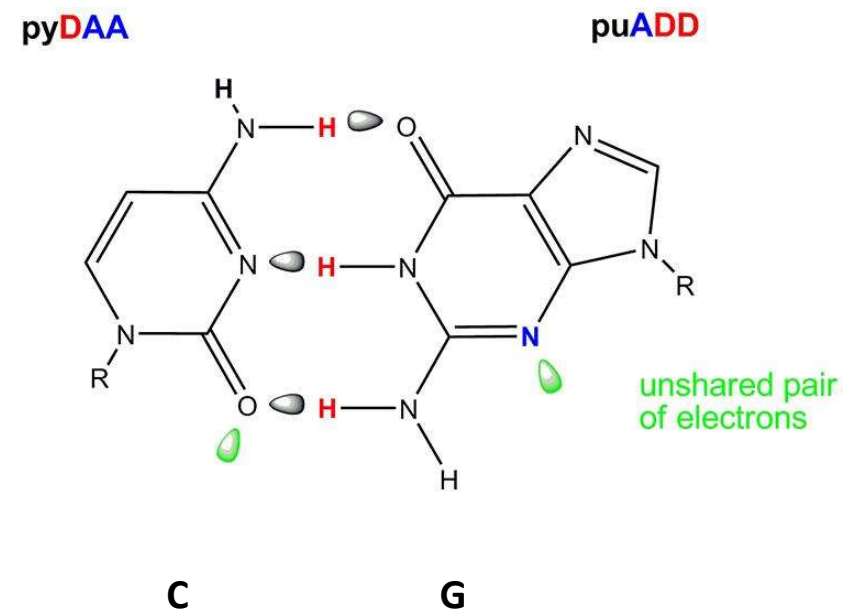
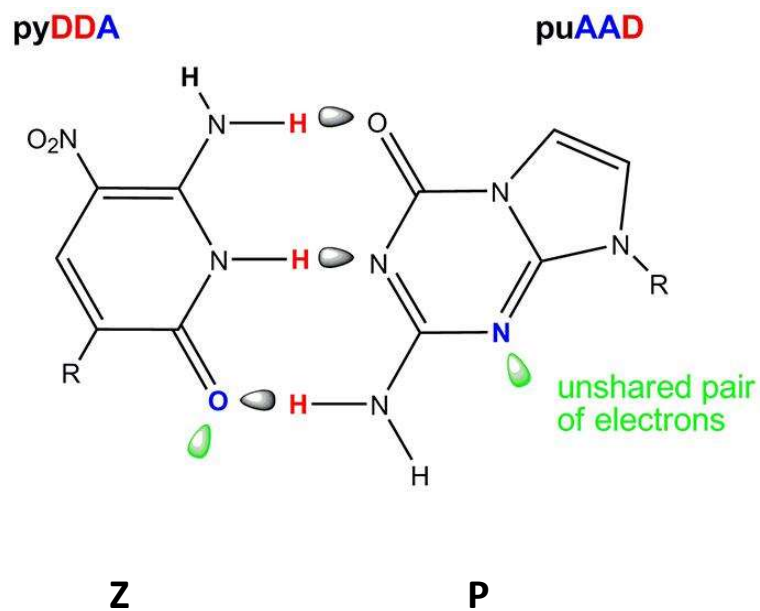
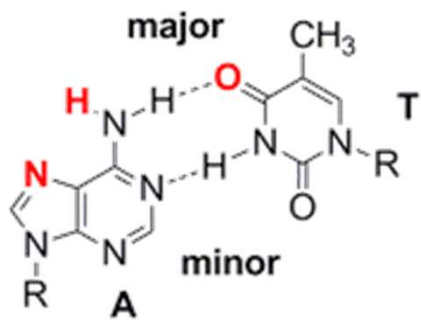
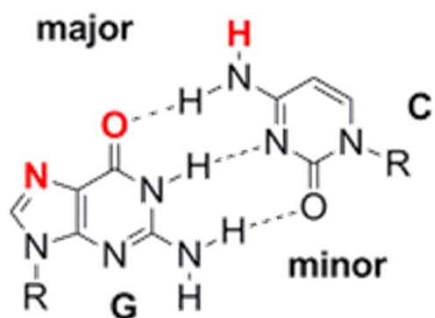


AEGIS – Artificially Expanded Genetic Information System



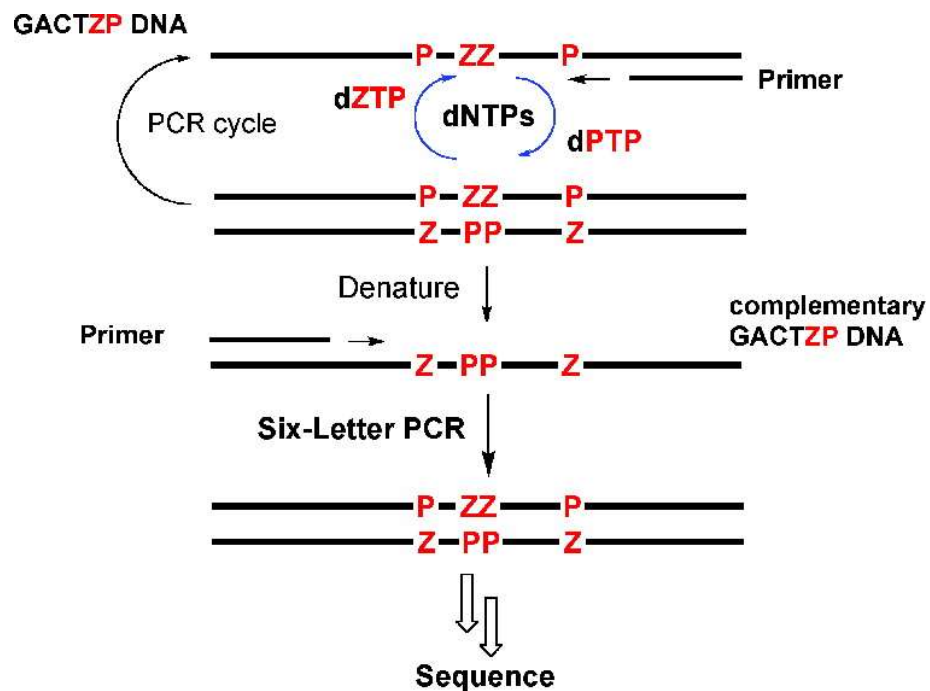
S. Benner *et al.*, *Beilstein J. Org. Chem.* **2014**, *10*, 2348–2360. doi:10.3762/bjoc.10.245

AEGIS – Artificially Expanded Genetic Information System

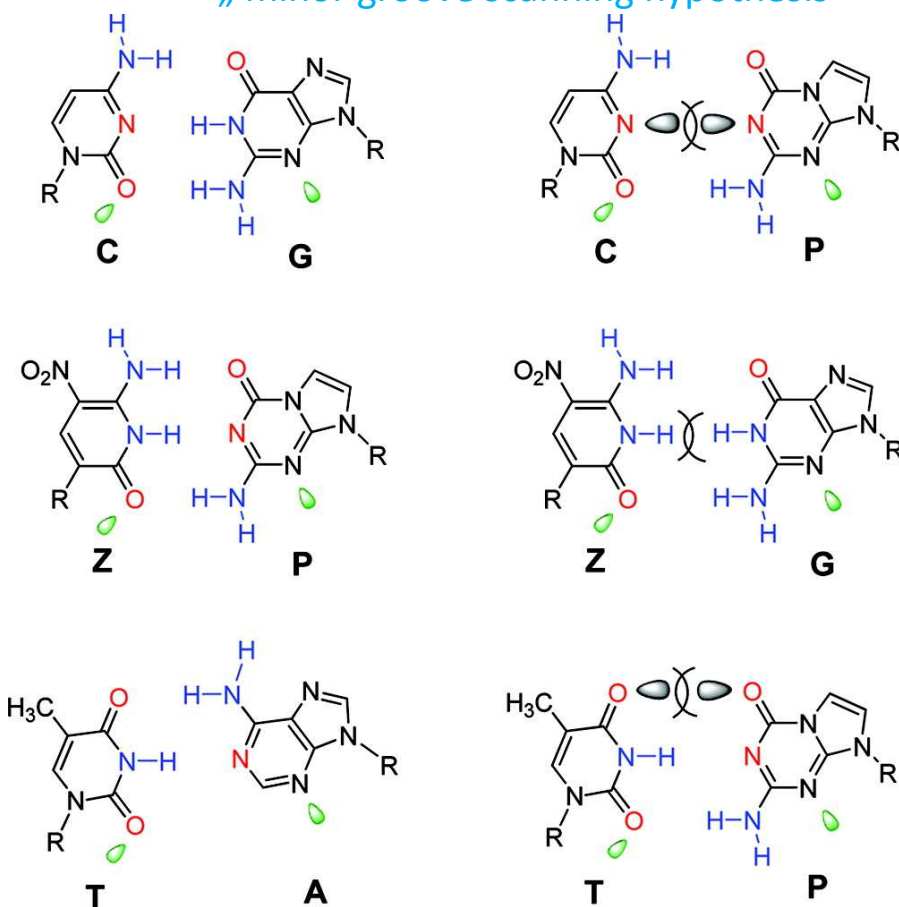


S. Benner *et al.*, *J. Am. Chem. Soc.*, **2011**, *133* (38), pp 15105–15112

AEGIS – Permanent orthogonal nucleobases surviving PCR



Electron density presented to the minor groove
 → recognition site by polymerases
 „minor groove scanning hypothesis”

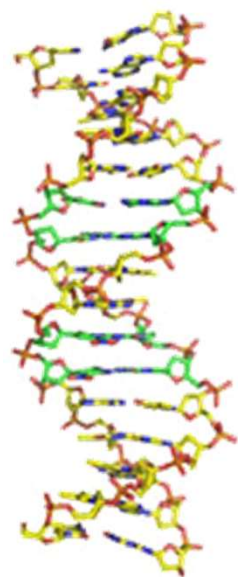


Error rate 0,2% per a PCR cycle – both removal and incorporation of **Z** and **P** → the artificial genetic system capable to evolve.

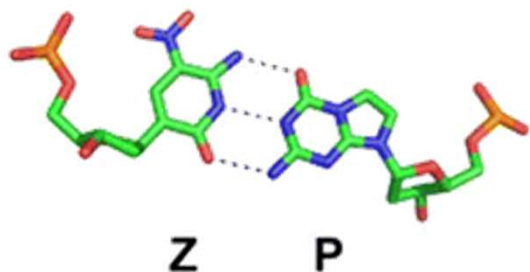
Pol: Deep Vent – 2 Z/P, Taq/Phu – 3-4 Z/P
 dZTP (deprotonated) at higher pH pairs slightly with G
 → loss of some **Z**, but also gain of some new **Z** mutants.

S. Benner *et al.*, *J. Am. Chem. Soc.*, **2011**, *133* (38), pp 15105–15112

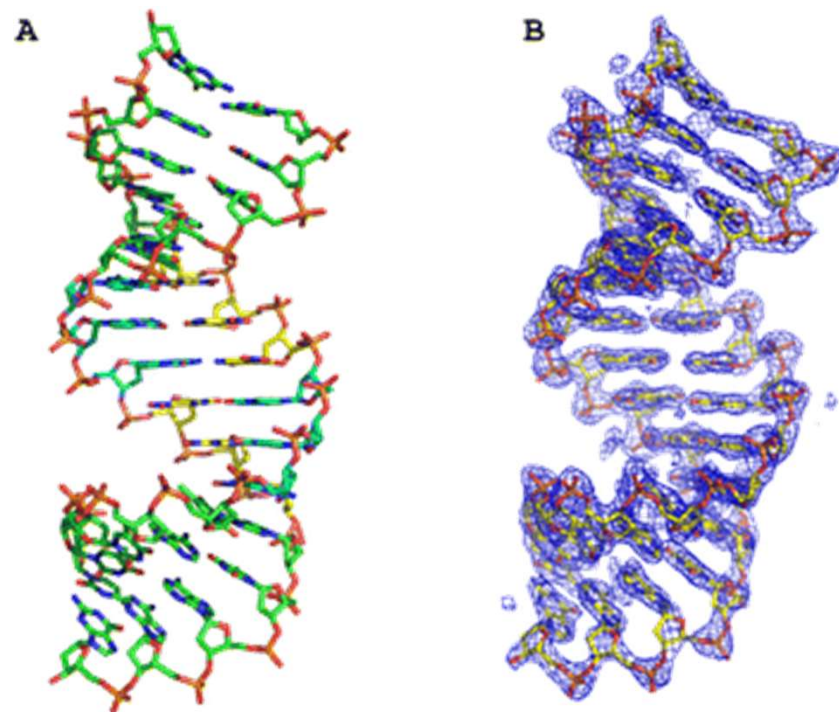
ACGTZP-DNA crystal structures



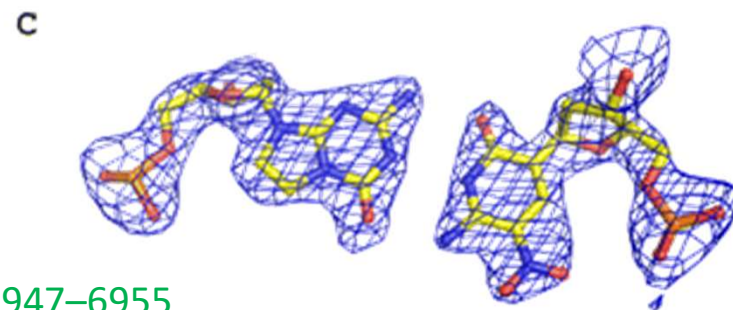
B-DNA



A-DNA



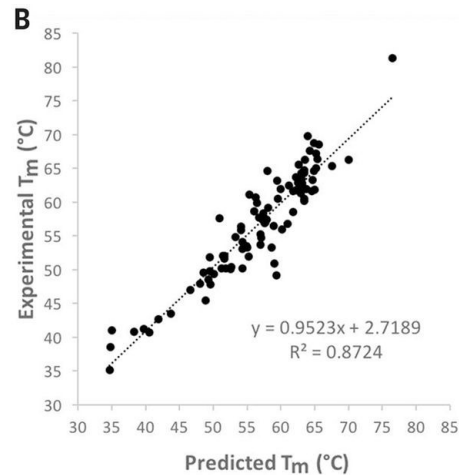
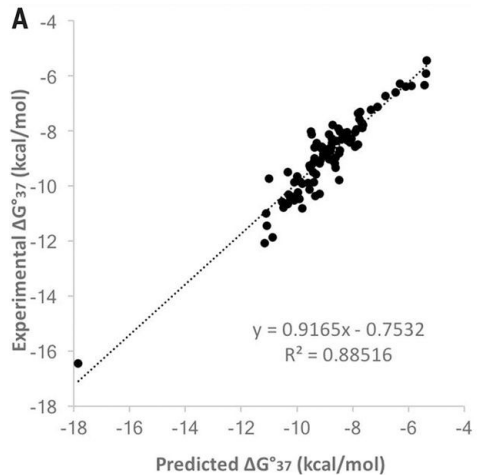
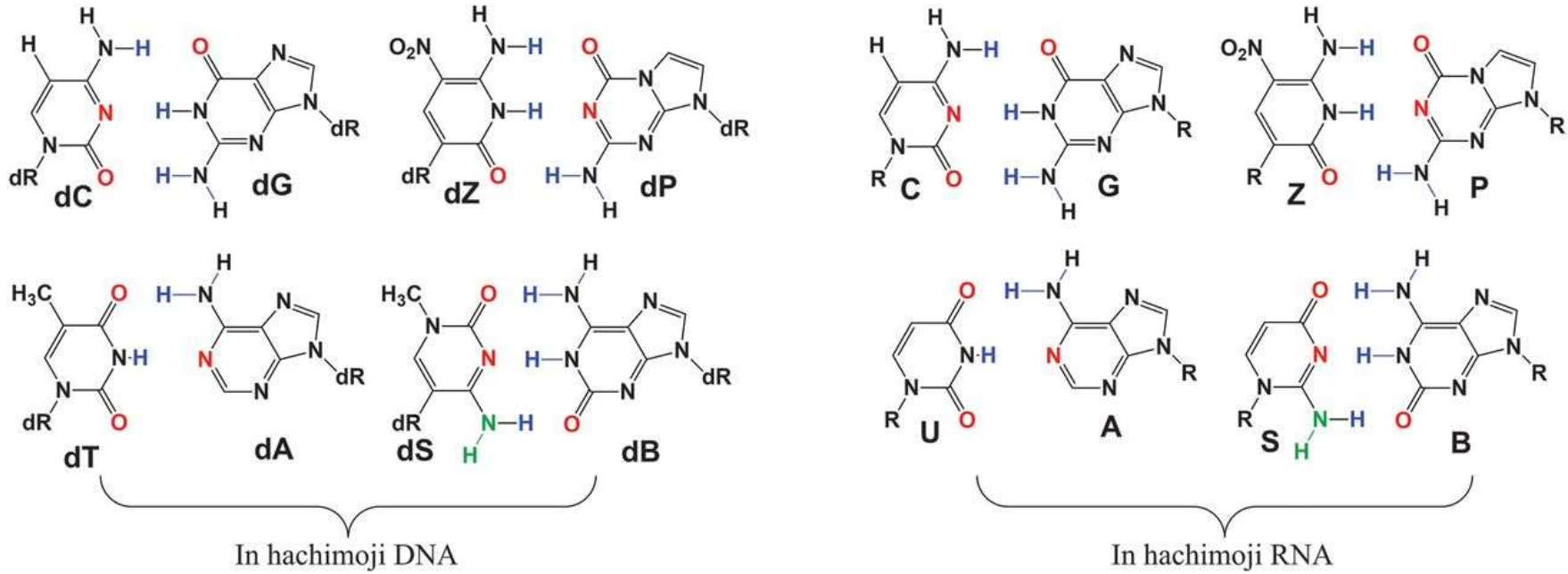
A 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
 5' -CTTATPPPZZZATAAG-3'
 3' -GAATAZZZPPPTATTC-5'
 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 B



18-mers: 2+2 **Z:P** pairs → B-DNA
 6 consecutive **Z:P** → A-DNA
 0,1 nm wider, but otherwise alike **G:C** pairs

S. Benner et al., *J. Am. Chem. Soc.*, **2015**, 137, pp 6947–6955

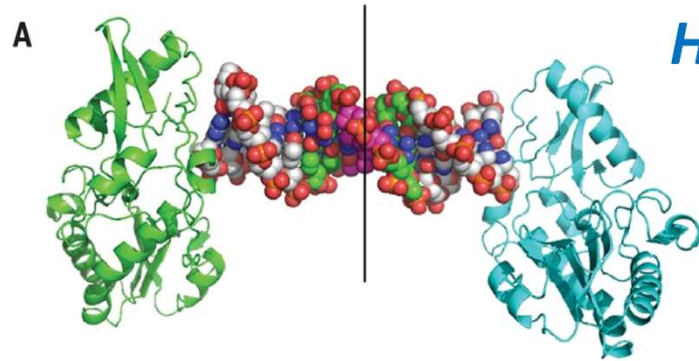
Hachimoji DNA and RNA – a genetic system with eight (Jap.- Hachi) letters



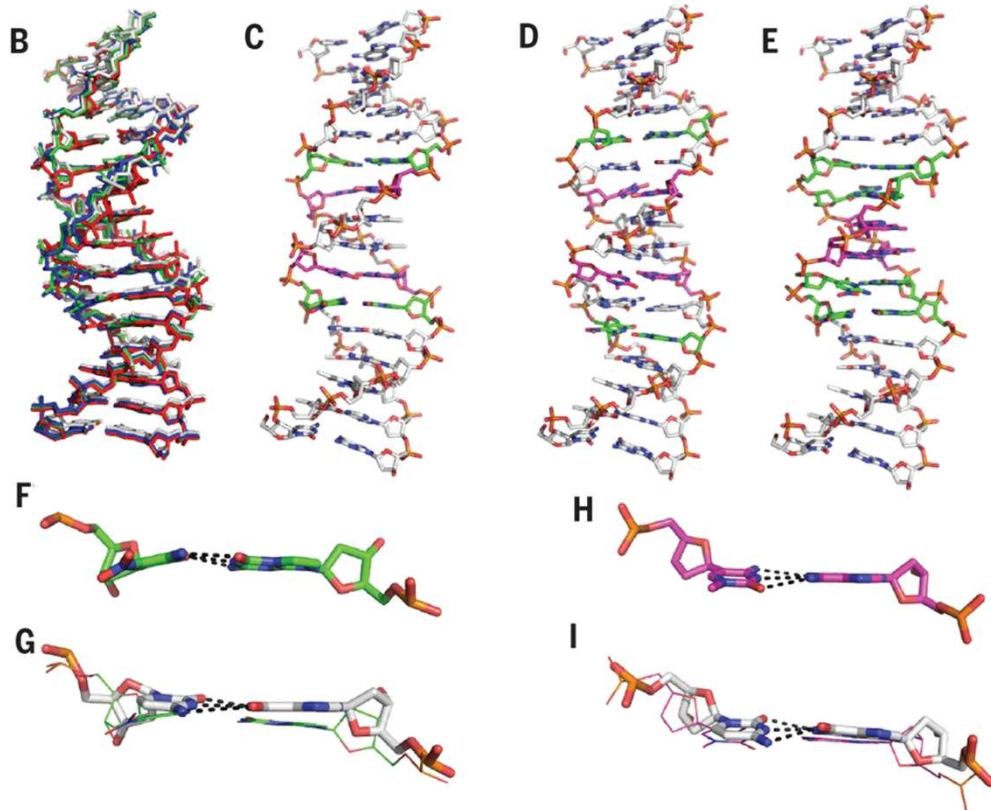
Plots of experimental versus predicted **(A)** free energy changes (ΔG°_{37}) and **(B)** melting temperatures T_m for 94 SBZP-containing hachimoji DNA duplexes.

Hachimoji DNA and RNA

Crystal structures of hachimoji DNA.



(A) The host-guest complex with two N-terminal fragments from Moloney murine leukemia virus reverse transcriptase bound to a 16-mer PP hachimoji DNA; Z:P pairs are green and S:B pairs are magenta.



(B) Hachimoji DNA structures PB (green), PC (red), and PP (blue) are superimposed with GC DNA (gray).

(C) Structure of hachimoji DNA with self-complementary duplex 5'-CTTATPBTASZATAAG ("PB").

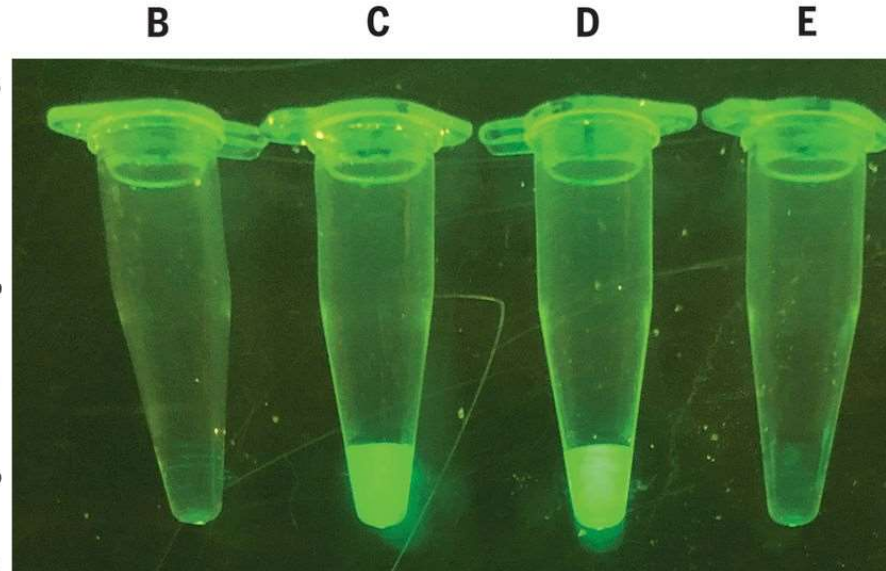
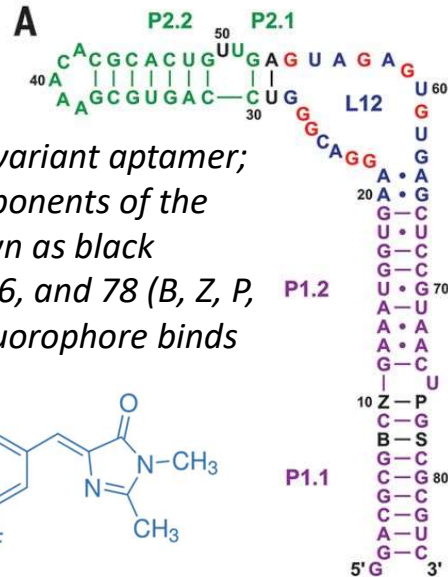
(D) Structure of hachimoji DNA with self-complementary duplex 5'-CTTAPCBTASGZTAAG ("PC").

(E) Structure of hachimoji DNA with self-complementary duplex with six consecutive nonstandard 5'-CTTATPPSBZZATAAG (PP) components.

(F to I) Examples of largest differences in detailed structures. The Z:P pair from the PB structure (F) is more buckled than the corresponding G:C pair (G). The S:B pair from the PB structure (H) exhibits a propeller angle similar to that in the corresponding G:C pair (I).

Hachimoji RNA aptamer

T7 RNA polymerase incorporates ZTP, PTP, and BTP, but not STP opposite to dP, dZ, dS, and dB, respectively. A mutant of T7 RNA Pol (Y639F H784A P266L, “FAL”) incorporated also STP – full DNA→RNA conversion possible



The hachimoji variant of the spinach fluorescent RNA aptamer. In its standard form, spinach folds and binds **3,5-difluoro-4-hydroxybenzylidene imidazolinone**, which fluoresces green when bound.

(B) Control with fluorophore only, lacking RNA.

(C) Hachimoji spinach with the sequence shown in (A).

(D) Native spinach aptamer with fluorophore.

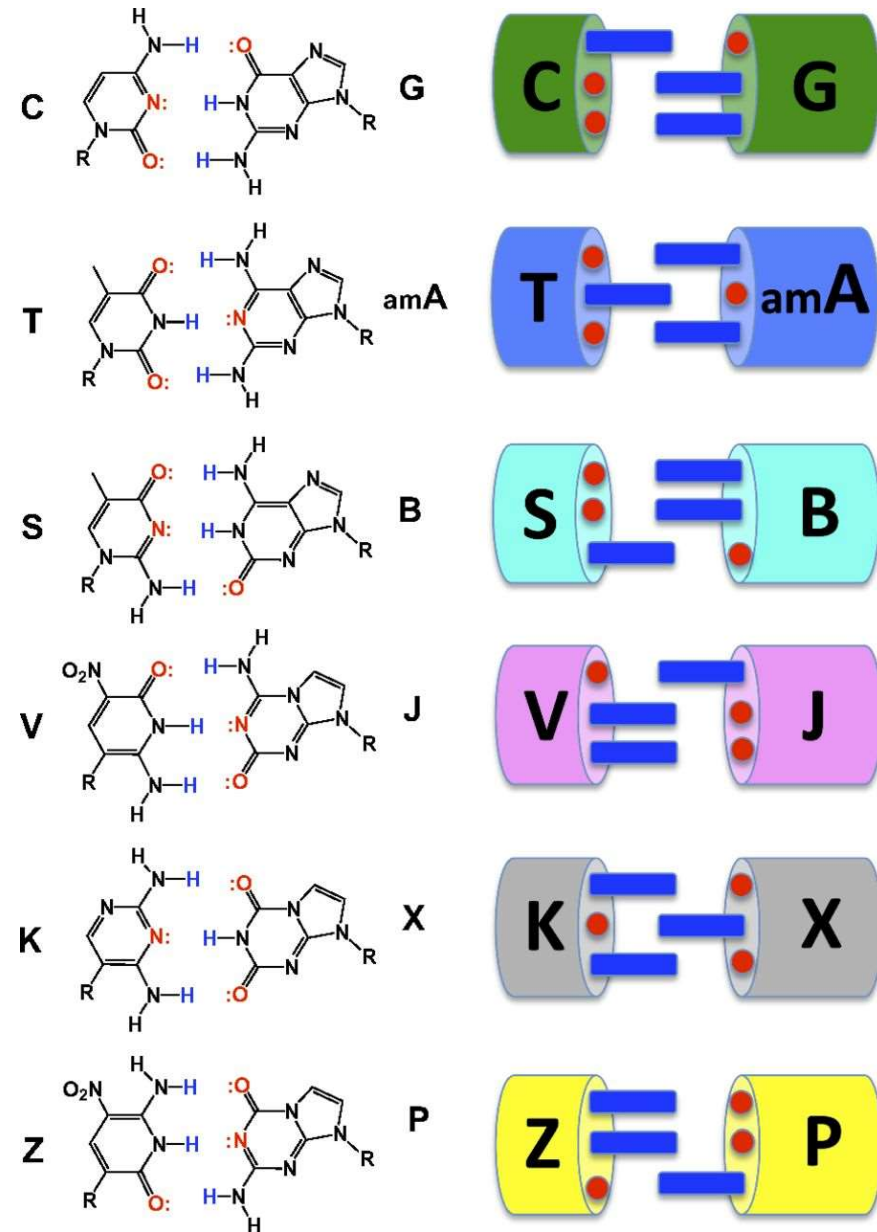
(E) Fluorophore and spinach aptamer containing Z at position 50, replacing the A:U pair at positions 53:29 with G:C to restore the triple observed in the crystal structure. This places the quenching Z chromophore near the fluorophore;

S. Hoshika *et al.*, *Science* **2019**, *363*, 884-887

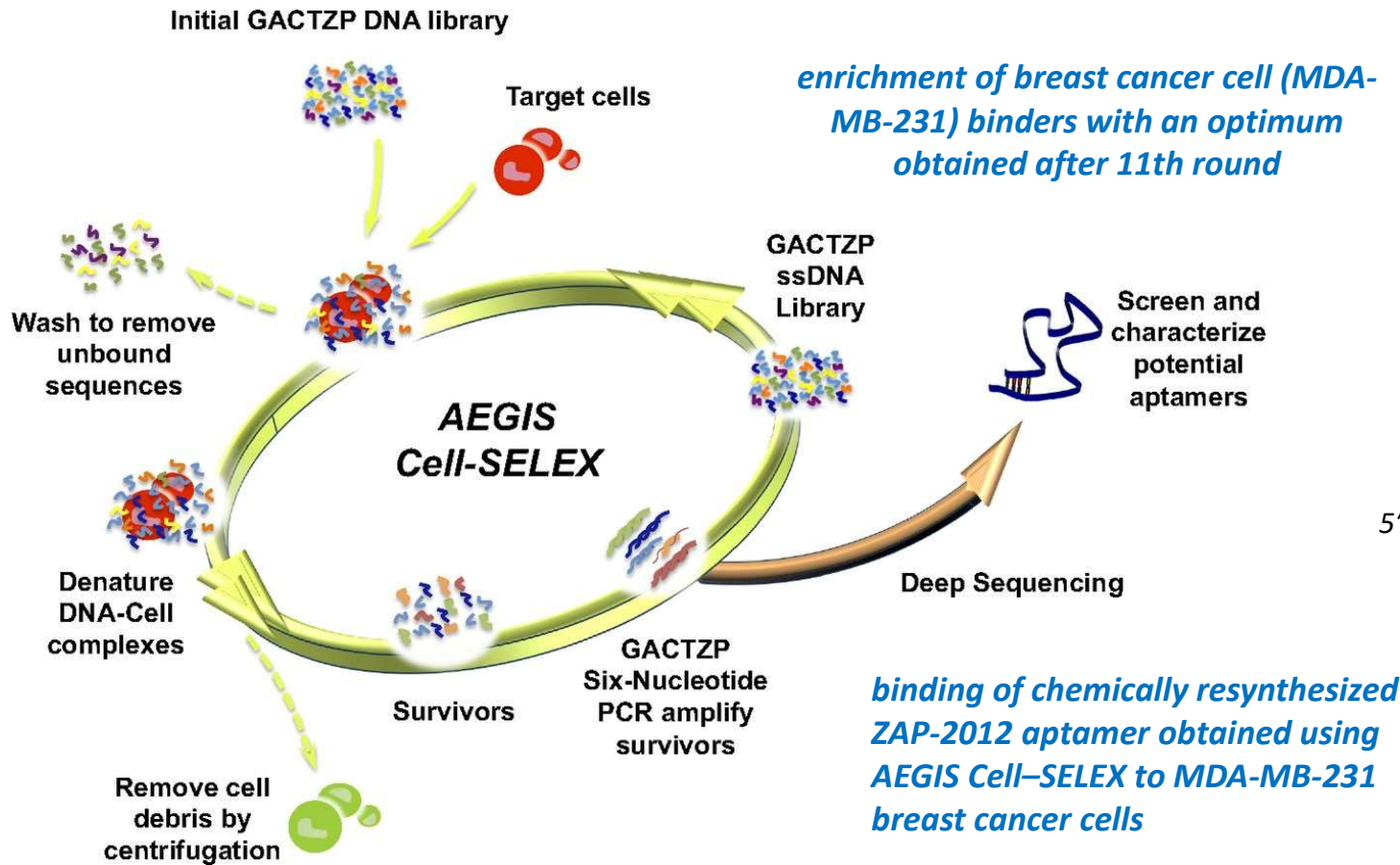
AEGIS – Artificially Expanded Genetic Information System

An **xNA** biopolymer having functionalized AEGIS components may allow SELEX to yield aptamers better than the standard DNA and RNA biopolymers.

K. Sefah *et al.*, *Proc. Natl. Acad. Sci. USA* **2014**, *111* (4), 1449-1454.



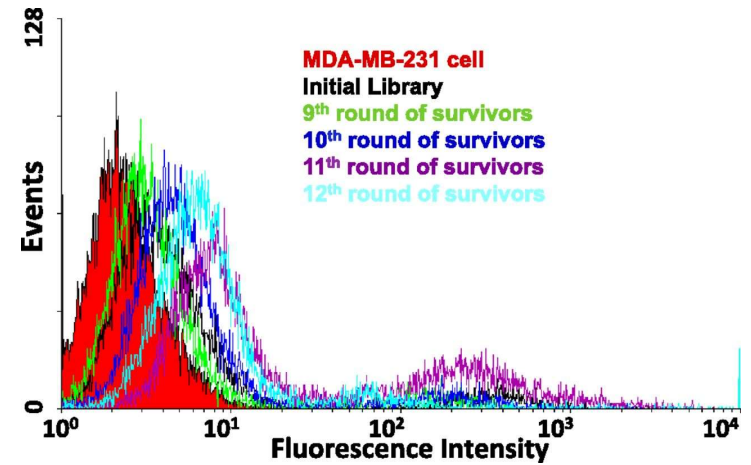
ACGTZP-aptamers



enrichment of breast cancer cell (MDA-MB-231) binders with an optimum obtained after 11th round

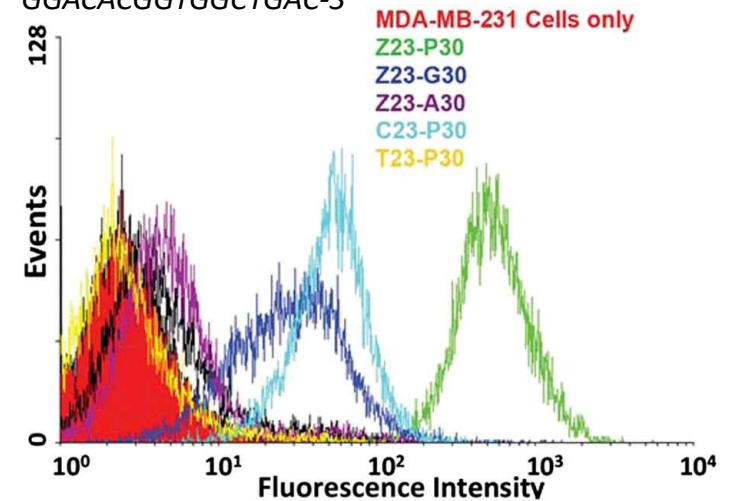
binding of chemically resynthesized ZAP-2012 aptamer obtained using AEGIS Cell-SELEX to MDA-MB-231 breast cancer cells

Where the **Z** or **P** are separately replaced with standard nucleotides, binding affinity is reduced.
Where the **Z** and **P** are both replaced with standard nucleotides, binding affinity is lost (not shown).



ZAP-2012 (Z23-P30) $K_d = 30$ nM

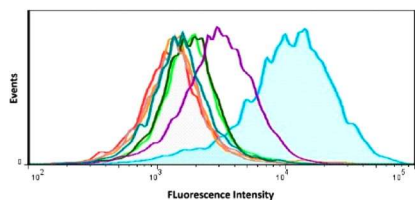
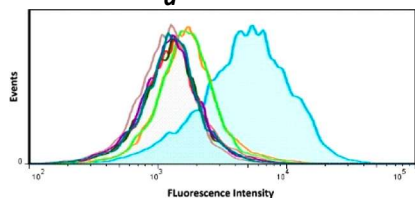
5'-biotin-TCCCGAGTGACGCAGC-
CCCCGGZGGGATT**P**ATCGGT-
GGACACGGTGGCTGAC-3'



K. Sefah *et al.*, *Proc. Natl. Acad. Sci. USA* **2014**, *111* (4), 1449-1454.

ACGTZP-aptamers

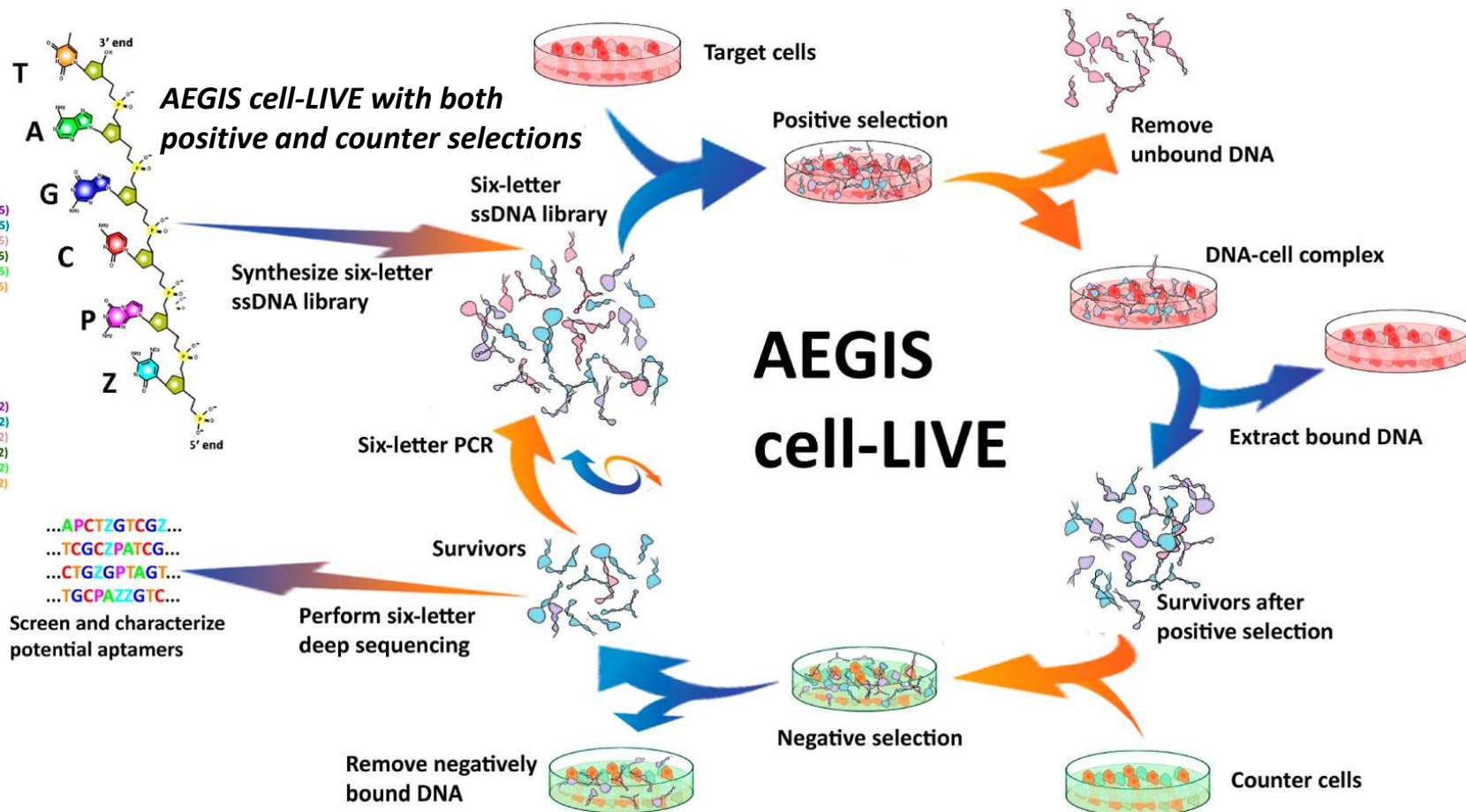
$K_d = 24 \text{ nM}$



$K_d = 55 \text{ nM}$

LZH3 (Z24_P35)
LZH3-5 (Z24_G35)
LZH3-6 (Z24_A35)
LZH3-4 (T24_P35)
LZH3-3 (C24_P35)
LZH3-2 (T24_A35)
LZH3-1 (C24_G35)
Random DNA

LZH7 (P29_Z32)
LZH7-5 (G29_Z32)
LZH7-6 (A29_Z32)
LZH7-4 (P29_T32)
LZH7-3 (P29_C32)
LZH7-2 (A29_T32)
LZH7-1 (G29_C32)
Random DNA

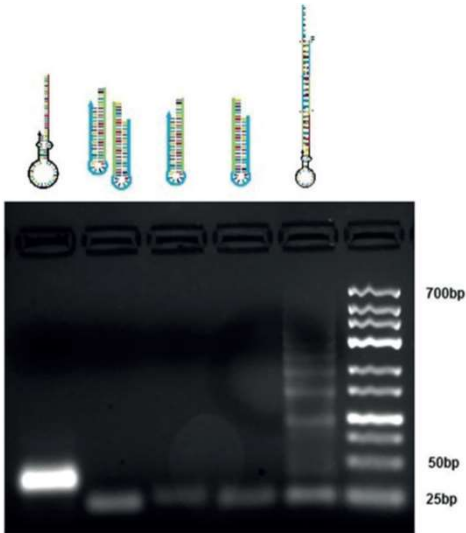


Nucleotides **Z** and **P** were added to a library of oligonucleotides used in a laboratory *in vitro* evolution (LIVE) experiment; the GACTZP library was challenged to deliver molecules that bind selectively to **liver cancer cells**, but not to untransformed **liver cells**. Unlike in classical *in vitro* selection, low levels of mutation allow this system to evolve to create binding molecules not necessarily present in the original library. Over a dozen binding species were recovered. The best had multiple Z and/or P in their sequences.

S. Benner *et al.*, *J. Am. Chem. Soc.*, **2015**, *137*, pp 6734-6737

Aptamer-Nanotrain

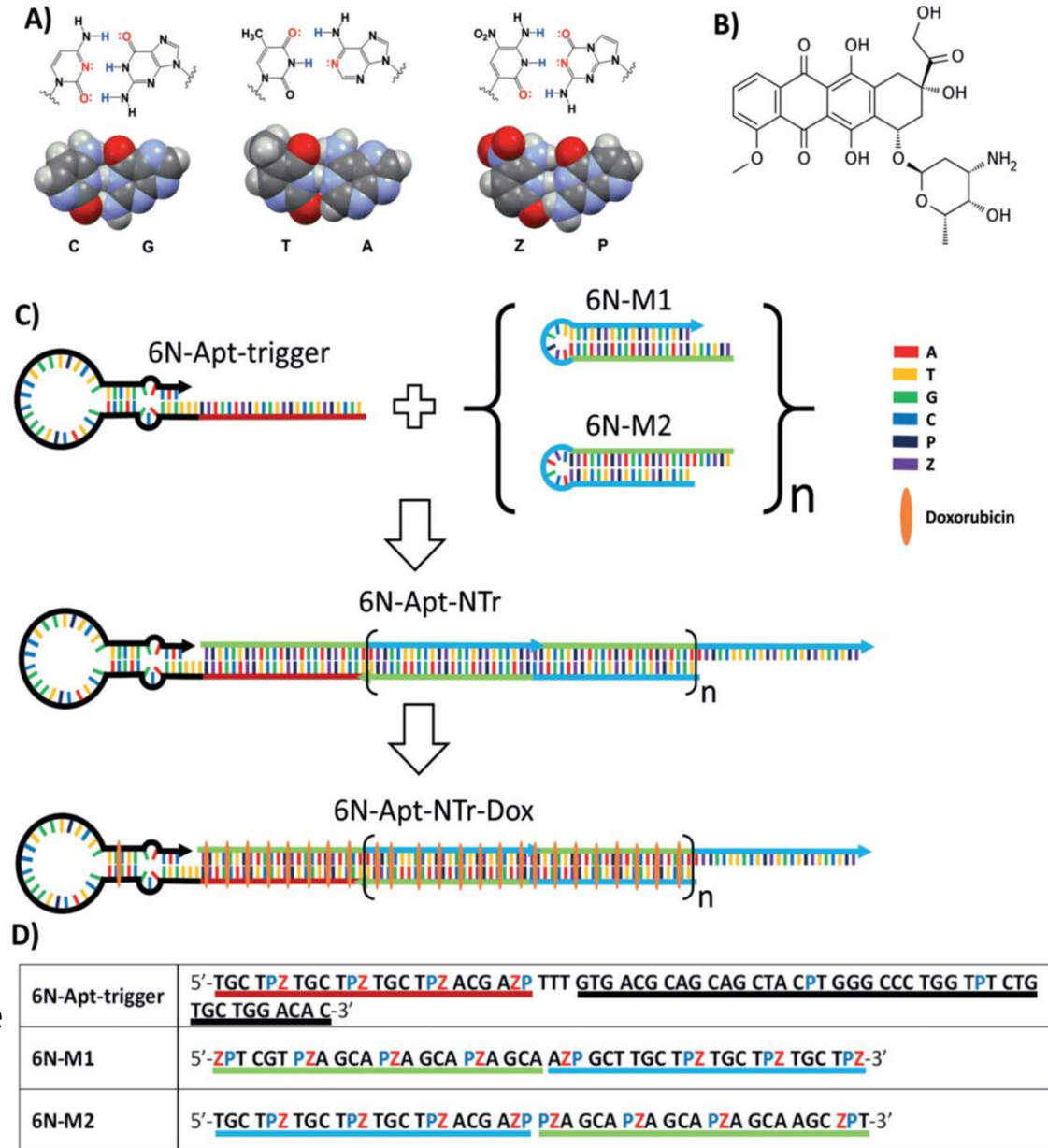
The aptamer-nanotrain assembly, charged with doxorubicin, selectively kills liver cancer cells in culture, as the selectivity of the aptamer binding directs doxorubicin into the aptamer-targeted cells. The assembly does not kill untransformed cells that the aptamer does not bind.



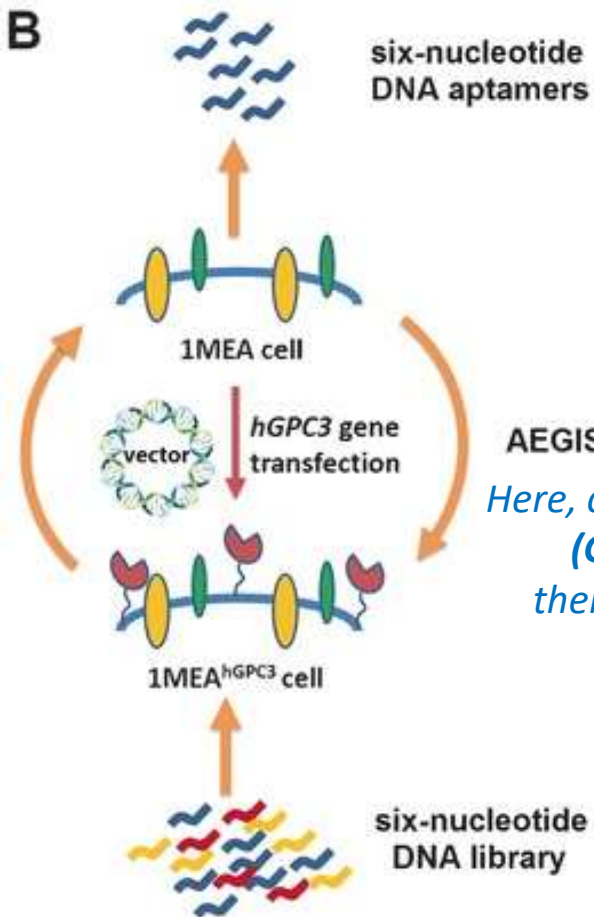
The previously selected 6-letter aptamer which binds liver cancer cells

This architecture, built with an expanded genetic alphabet, is reminiscent of antibodies conjugated to drugs, which presumably act by this mechanism as well, but with the antibody replaced by an aptamer.

L. Zhang *et al.*, *Angew. Chem., Int.Ed.*, 2020, 59, 663-668



ACGTZP-aptamers against a specific protein



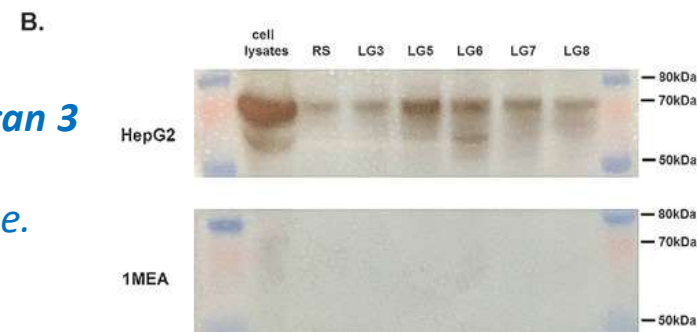
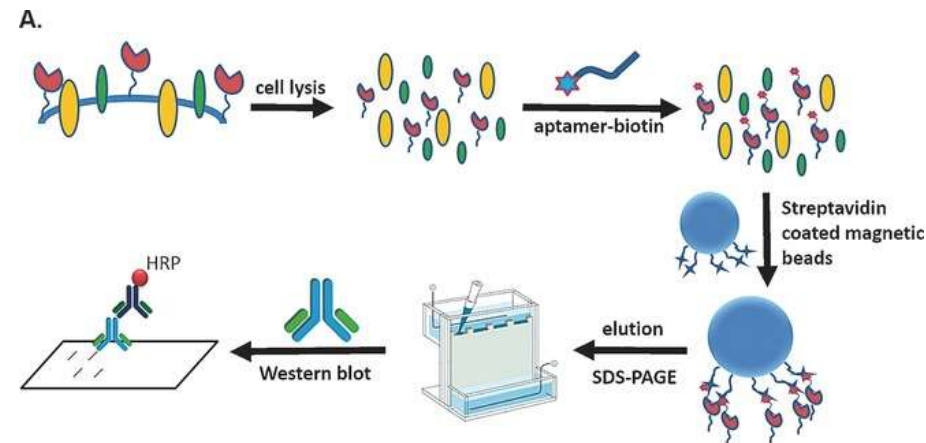
Laboratory in vitro evolution (LIVE) might deliver DNA aptamers that bind proteins expressed on the surface of cells.

AEGIS-LIVE

Here, cell engineering was used to place **glypican 3 (GPC3)**, a possible marker for liver cancer theranostics, on the surface of a liver cell line.

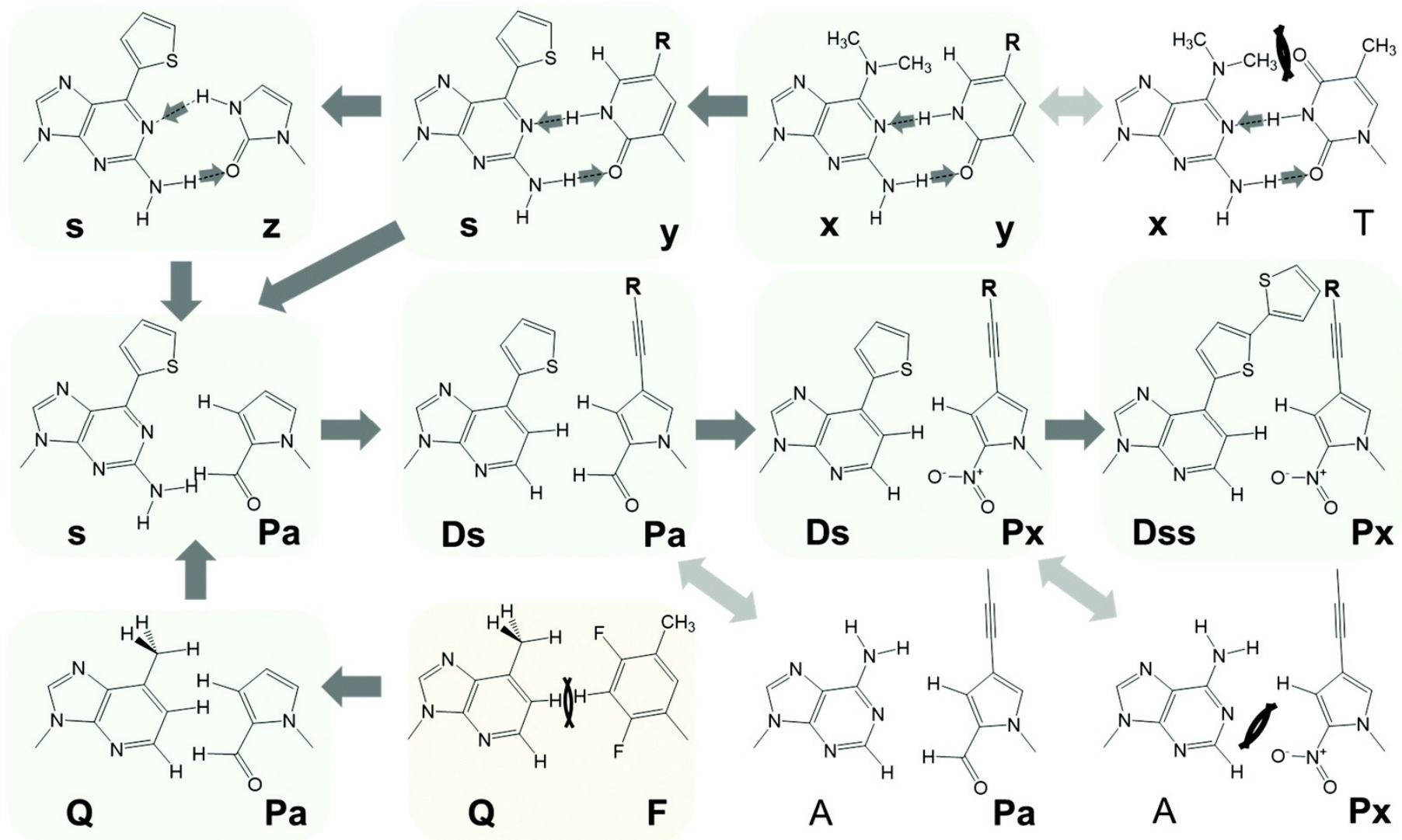
Libraries were then built from a six-letter genetic alphabet. With counterselection against non-engineered cells, eight AEGIS-containing aptamers were recovered. Five bound selectively to GPC3-overexpressing cells.

LG5 $K_d = 6$ nM (without Z – no binding)

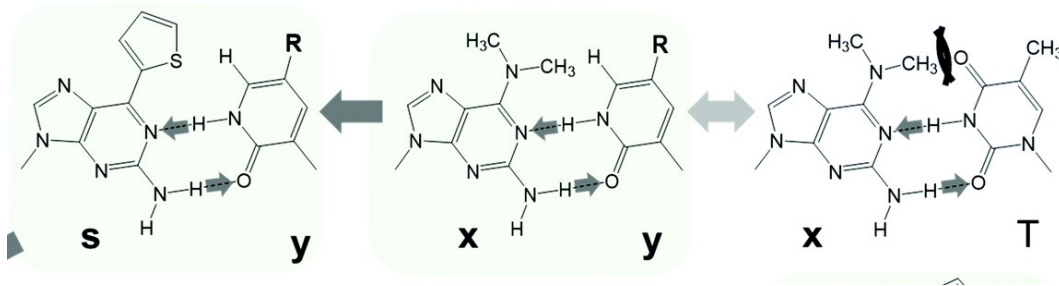


Name	Sequence	Percentage
LG1	~PGGTGGGCGGAGGTCTZGCTACAPGPTTTGGPGGC~	11.37%
LG2	~PGCCCGGGPTAPPGTGPTGGGTGTTTCGCTATCCAG~	7.98%
LG3	~GGTAACTAGTAGTTGACCCTGPAGTZTGTPTCTG~	6.01%
LG4	~GGCGGGGTZGPGTAAGGGGTCTAAGGCATTTGGGTC~	4.48%
LG5	~GGAGGAAGTGGTCCTTTGCTTTGCTZTCGTATCTGGG~	2.57%
LG6	~GGTZGATTATTPGGTTCAATAACACPTCCTGGTGG~	1.96%
LG7	~PGCACAGTGTGZZCCATAGGTTGTAATGACPTZTG~	1.04%
LG8	~GGCAGCZCCTGPAGTPGAGTGTTPATGGCTTATTCG~	0.91%

Steric exclusion and hydrophobic non-natural base pairs



Steric exclusion and hydrophobic non-natural base pairs



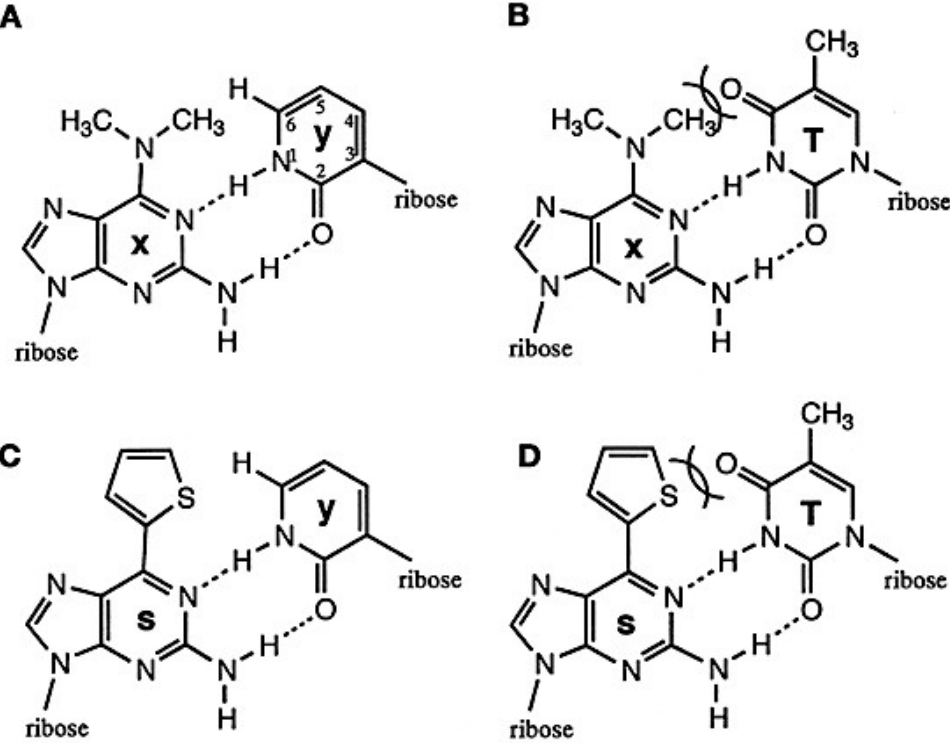
Hirao (2001): the steric hindrance concept to hydrogen-bonded UBPs to exclude the mispairing with natural bases
→ a series of hydrogen-bonded UBPs: **x-y** and **s-y** pairs

large residues at position 6 of **x** and **s** sterically and/or electrostatically clash with the 4-keto group of **T**, but not with hydrogen of the **y** base.

x-y and **s-y** pairs function in transcription with T7 RNA polymerase (T7 transcription), and the **y** substrate is incorporated (>96% selectivity **s-y**) site-specifically into RNA transcripts opposite **x** or **s** in DNA templates.

Problem: the **y** base cannot exclude the mispairing with A. Therefore, these UBPs cannot be used in replication

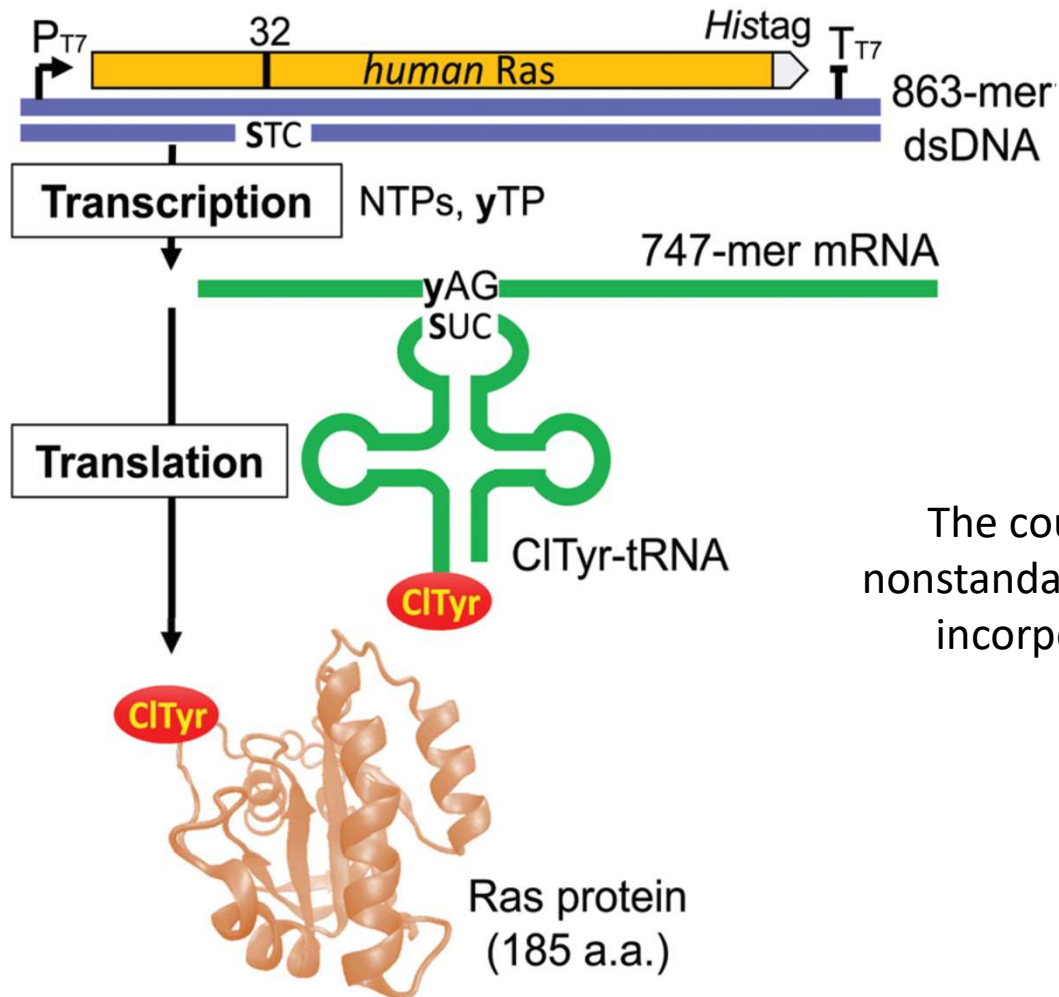
Unnatural aminoacid incorporation using a noncanonical base pair



Non-template strand 5'-d(ATAATACGACTCACTATAGGG)
 Template strand 3'-d(TATTATGCTGAGTGATATCCCTTGCCTCNTCACGCC)
 N = s, x, A, or G
 +1 +12 +19
 T7 RNA polymerase
 1 mM NTPs, [α - 32 P]ATP, GMP
 Full-length product (19-mer)
 pGpGpGp*Ap*ApCpGpCpGp*ApGpN'p*ApGpTpGpCpGpG
 RNase T₂ digestion
 2D-TLC
 32 P-labeled nucleotides
 Gp* x 2, Ap* x 1, N'p* x 1

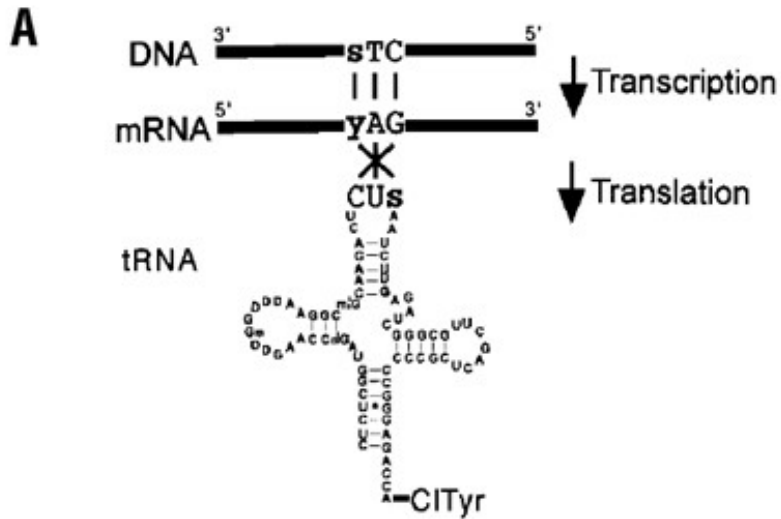
I. Hirao et al. Nature Biotechnology 20, 177–182 (2002)

Unnatural aminoacid incorporation using a noncanonical base pair



The coupled transcription–translation system using the nonstandard codon–anticodon interaction for the site-specific incorporation of 3-chlorotyrosine into the Ras protein.

I. Hirao *et al.* *Nature Biotechnology* **20**, 177–182 (2002)



B

```

AUGACCGAAUACAAACUGGUUUGUAGUUGGCCGCUUGGUGUAGGCCAAAAGCGCGUGACC 60
M T E Y K L V V V G A G G V G K S A L T 20

AUUCAGUUGAUCCAGAACCACUUCGUAGAUAGAGYAGGACCCGACUAUUGAAGACUCUUAC 120
I Q L I Q N H F V D E cy D P T I E D S Y 40

CGUAAGCAGGUUGUUAUCGACGGUGAGACCUGUUGCUGGACAUCCUUGAUACCGCAGGC 180
R K Q V V I D G E T C L L D I L D T A G 60

CAAGAAGAUAUCUCUGCUAUGCGUGAUCAGUAUAUGCGUACCGGCGAAGGCCUCCUGUC 240
Q E E Y S A M R D Q Y M R T G E G F L C 80

GUUUUCGUUAUCAACAACACCAAUUCUUUGAAGACAUCAUAUACCGUGAACAGAUUC 300
V F A I N N T K S F E D I H O Y R E O I 100

AAACGUGUUAAGACUCUGAUGACGUUCGUAUGGUUCUGGUUGGUUAACAAUUGCGACUUG 360
K R V K D S D D V P M V L V G N K C D L 120

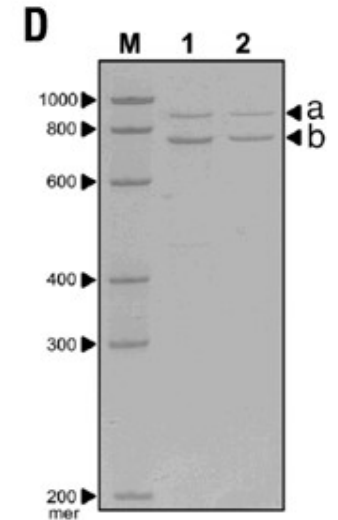
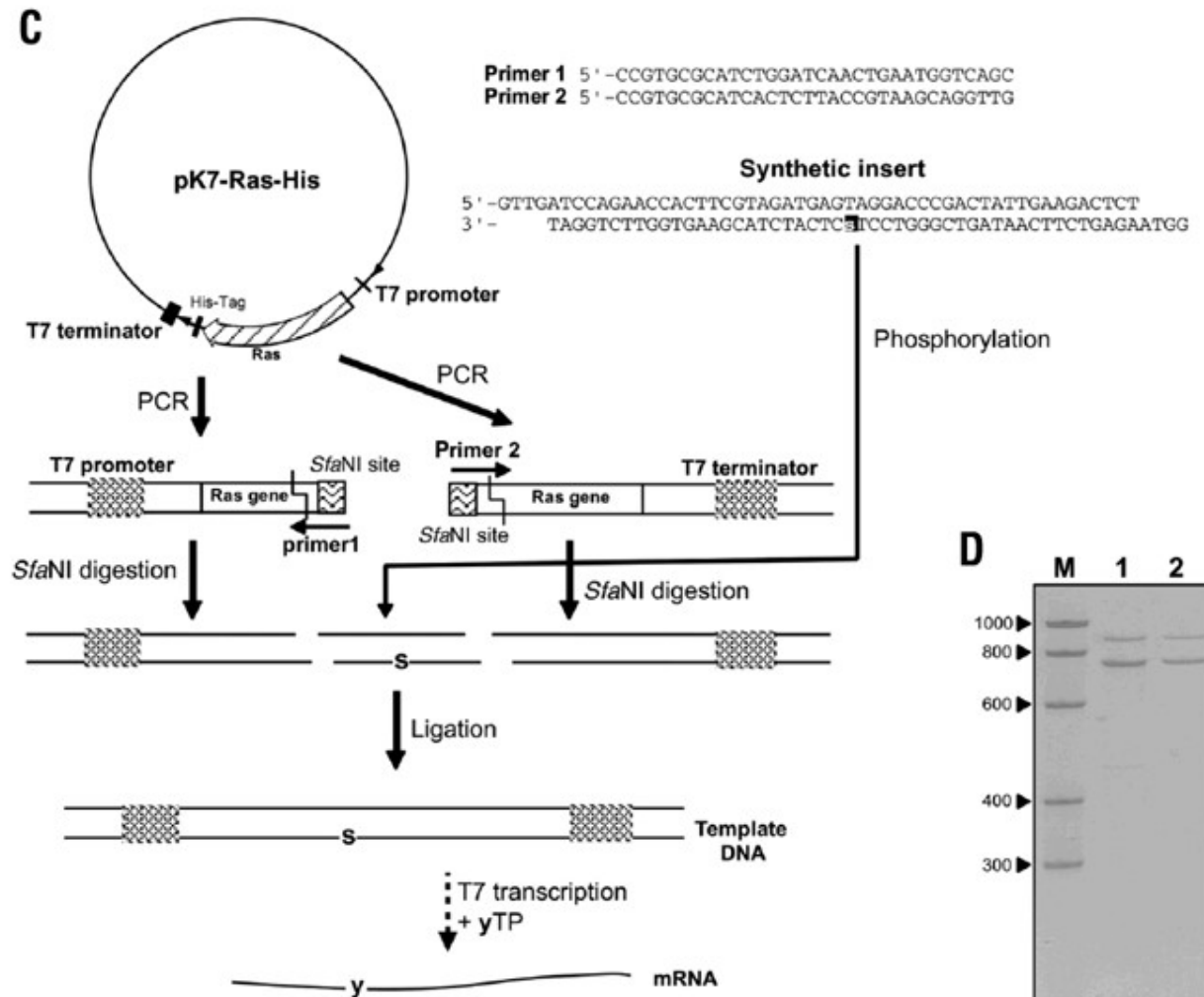
GCAGCCGUAUCUGUUGAAUUCUGUCAGGCUCAGGAUCUGGCUUGUUCUUAACGGAAUUCG 420
A A R T V E S R Q A Q D L A R S Y G I P 140

UACAUCGAAACCCUCUGUAAAACUCGUCAGGCUGAAGACCGUUCUUAACACCUUGGUU 480
Y I E T S A K T R Q G V E D A F Y T L V 160

CGUGAAAUCGUGACGACAAGCUGCGUAAGCUUGGAUCCUUGGUGCCACGCGGUAGUCAC 540
R E I R Q H K L R K L G S L V P R G S H 180

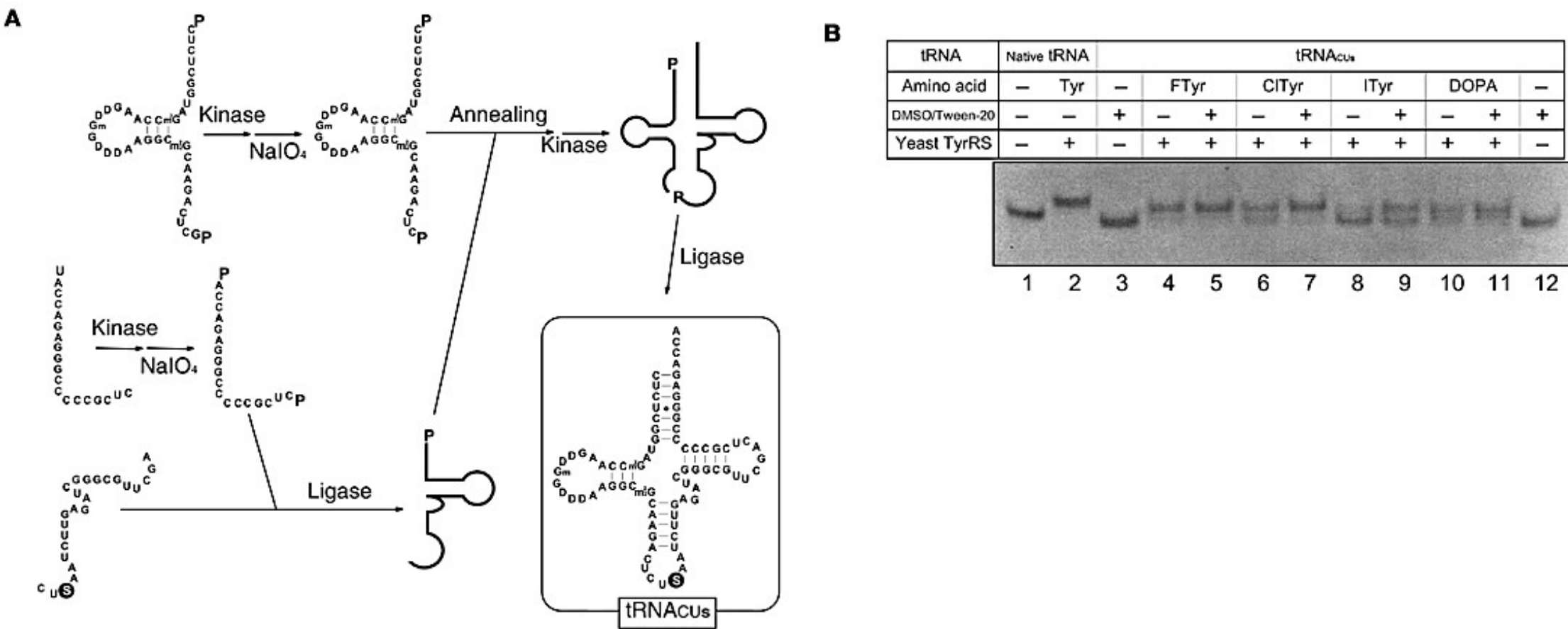
CACCACCACCACCACUAAUAA 561
H H H H H * * 185

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I. Hirao *et al.* *Nature Biotechnology* 20, 177–182 (2002)

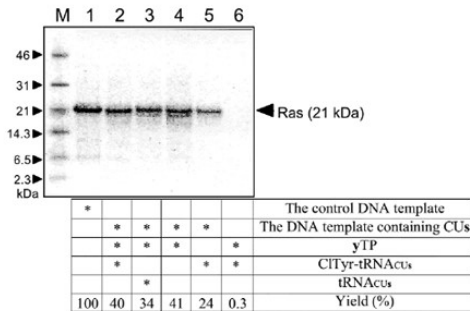
Unnatural aminoacid incorporation using a noncanonical base pair



(A) Construction of tRNA_{CU^S}. (B) Acidic-gel electrophoresis of the products after aminoacylation of *S. cerevisiae* tRNA and tRNA_{CU^S} with tyrosine and the 3'-substituted analogs, in the absence or presence of 20% DMSO and 0.25% Tween-20. The upper bands are the aminoacylated tRNAs, and the lower bands are the noncharged tRNAs.

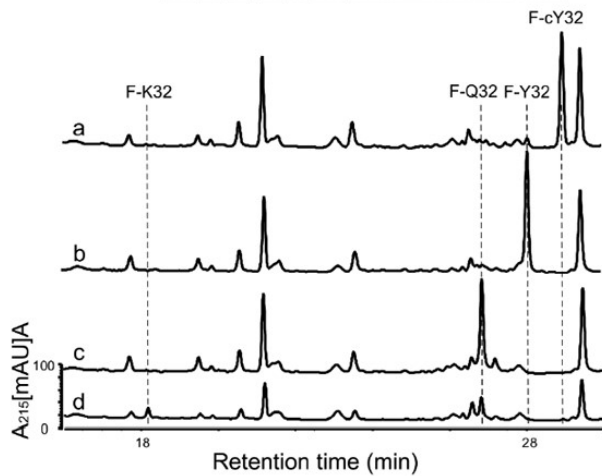
I. Hirao *et al.* *Nature Biotechnology* **20**, 177–182 (2002)

A



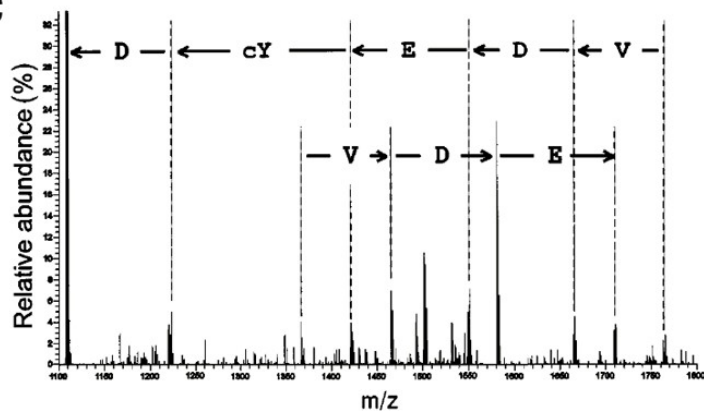
A) Autoradiogram of *in vitro* transcription–translation products labeled with l-[¹⁴C]leucine. The conditions are noted at the bottom of each lane.

B



B) LC patterns of the products digested by Lys-C. Chart a shows the products obtained from the reaction in the presence of the DNA template containing the CTs sequence, yTP, and C¹⁴Tyr-tRNA_{CUS}; chart b shows those obtained in the presence of the standard DNA template and Tyr; chart c shows those obtained in the presence of the DNA template containing CTs but in the absence of yTP and tRNA_{CUS}; and chart d shows those obtained in the presence of the DNA template containing CTs and yTP but in the absence of tRNA_{CUS}.

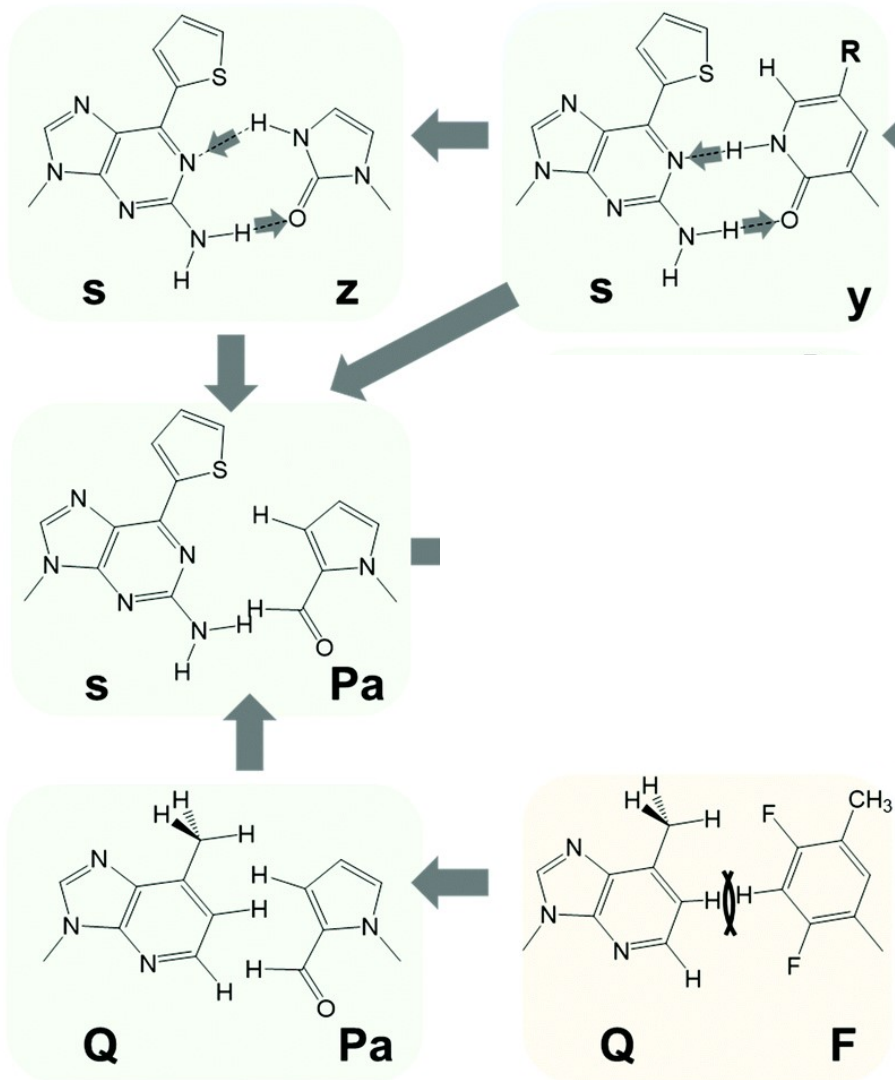
C



C) Tandem mass spectrum of the F-cY32 fragment. The partial sequence, VDEcYD, of F-cY32 was confirmed from the ion series

I. Hirao *et al. Nature Biotechnology* **20**, 177–182 (2002)

Steric exclusion and hydrophobic non-natural base pairs



Kool (1998): non-hydrogen-bonded **Z-F** pair (an isostere of A-T) (Z is 4-methylindole, F base is 2,4-difluorotoluene.), but lack of Z and F interactions with polymerases.

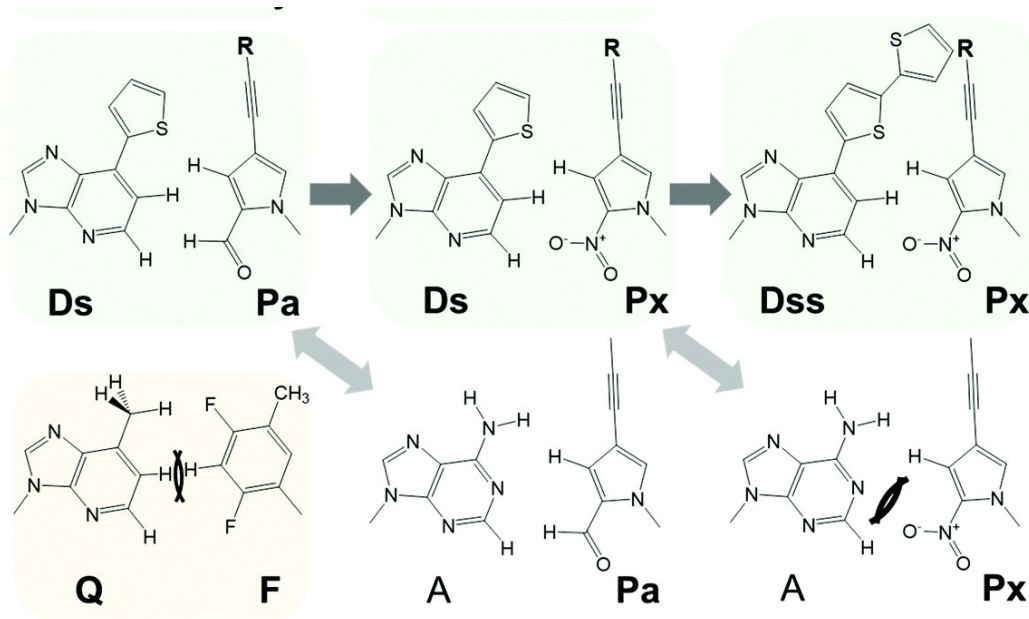
Kool (1999): Q-F pair - shape-complementarity rather than the hydrogen-bond interactions, → a new strategy of UBP development using hydrophobic UBs without any hydrogen-bond interactions between the pairing bases.

Hirao (2003): the Q-Pa pair to avoid steric clashes.

Hirao (2007): Pa could be used as a pairing partner of the s base, and the s substrate was incorporated specifically into RNA opposite Pa in templates by T7 transcription.

Hirao (2004): The s-z pair increased the s incorporation selectivity opposite z in T7 transcription, as compared to that opposite y in the s-y pair

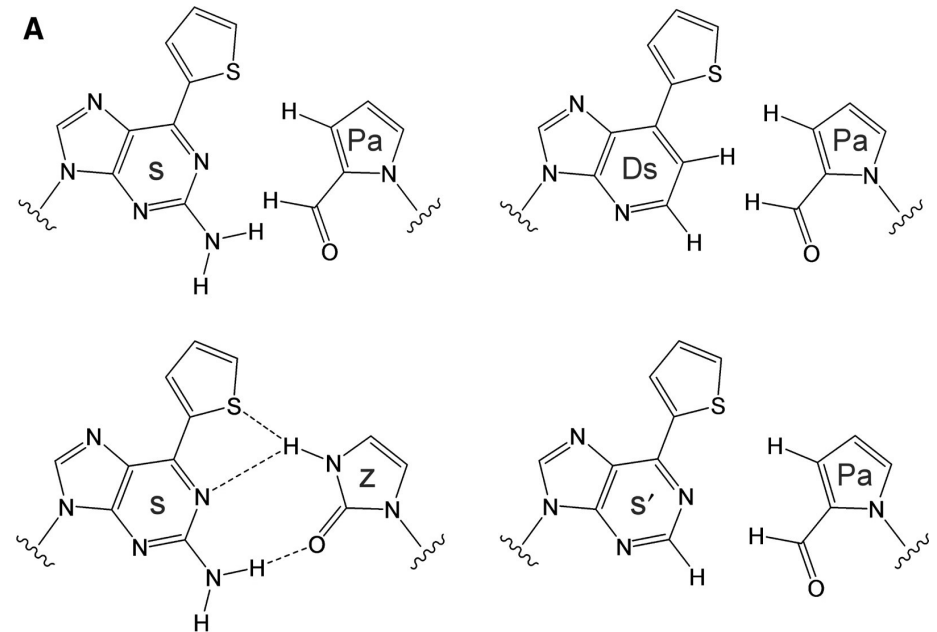
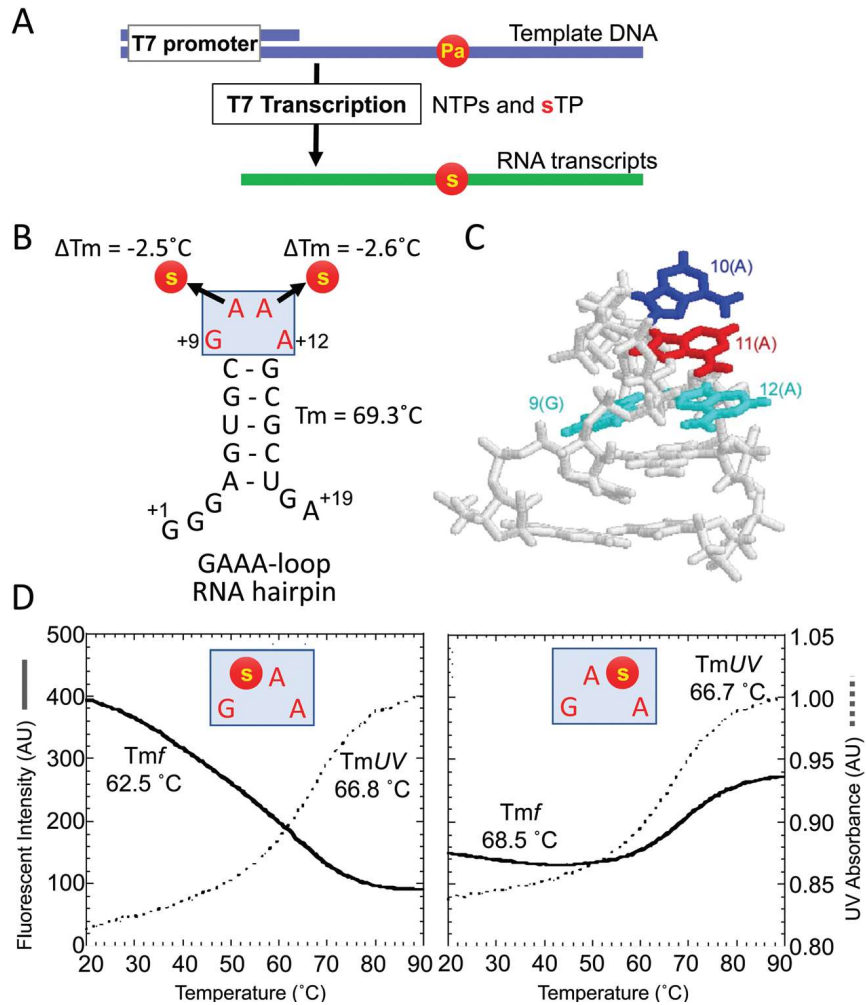
Steric exclusion and hydrophobic non-natural base pairs



Hirao (2006) the hydrophobic **Ds** base (improved **s**). The **Ds–Pa** pair exhibited high incorporation efficiency in replication. **Problems:** the non-cognate **Ds–Ds** and **A–Pa** pairings (solved by using γ -amido-triphosphates of **Ds** and **A**, which significantly reduced their mispairing with **Ds** and **Pa** - ~99.9% selectivity per cycle in PCR).

Hirao (2007): the **Ds–Px** pair - electrostatic clash with the 1-nitrogen of **A** (no **A–Px** pairing), The additional propynyl group reduces the **Ds–Ds** self-pairing. The **Ds–Px** pair exhibits high fidelity and high efficiency in PCR (>99.9% per cycle).

Fluorescent probing for RNA molecules by an unnatural base-pair system

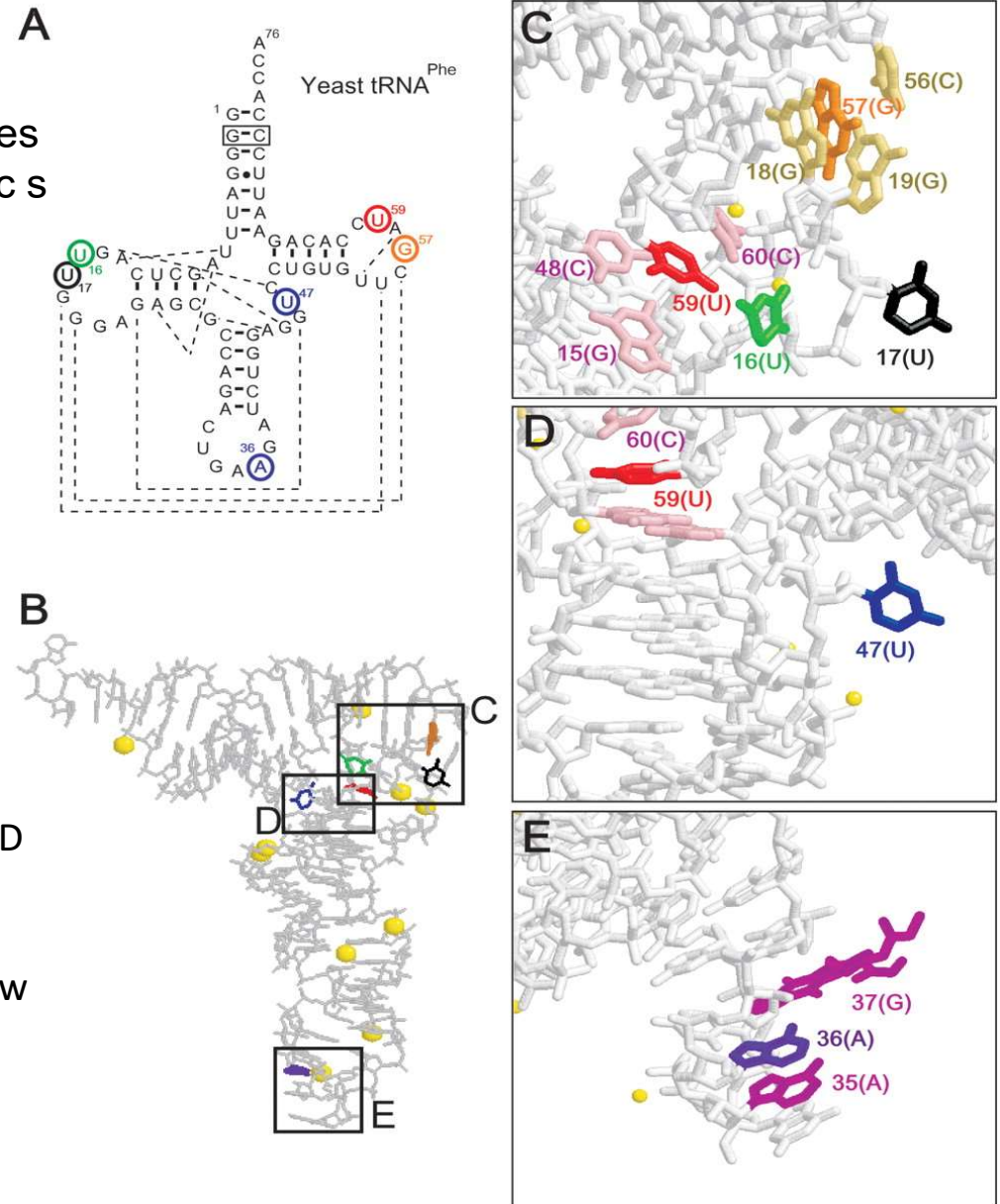


(B) Incorporation of the fluorescent **s** base into GNRA hairpins. *(left)* The secondary structure of the RNA hairpin with a GAAA loop. The second A and third A in the loop are shown in blue and red, respectively. *(right)* The 3D structure of the GAAA-loop hairpin

M. Kimoto, T. Mitsui, Y. Harada, A. Sato, S. Yokoyama and I. Hirao, *Nucleic Acids Res.*, **2007**, *35*, 5360–5369

The „s” incorporation sites in yeast tRNA^{Phe}

The fluorescent intensity of „s” in RNA molecules changes according to the structural environment. The site-specific s labeling of RNA hairpins and tRNA molecules provided characteristic fluorescent profiles, depending on the labeling sites, temperature and Mg²⁺ concentration.

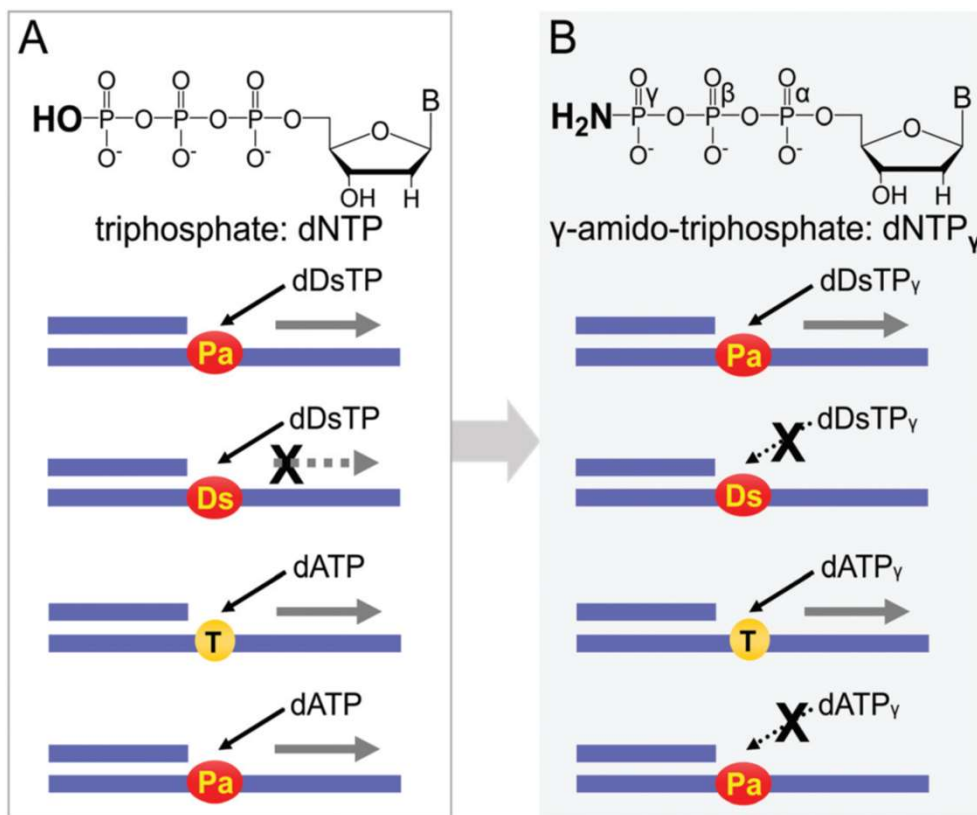


(A) The secondary structure of the original tRNA transcript. The positions substituted with s are circled. The broken lines show base–base interactions for the 3D structure.

(B–E) The deep-colored bases were substituted with s, which stacks with the light-colored bases, and the yellow spheres represent Mg²⁺.

M. Kimoto, T. Mitsui, Y. Harada, A. Sato, S. Yokoyama and I. Hirao, *Nucleic Acids Res.*, **2007**, *35*, 5360–5369

Steric exclusion and hydrophobic non-natural base pairs

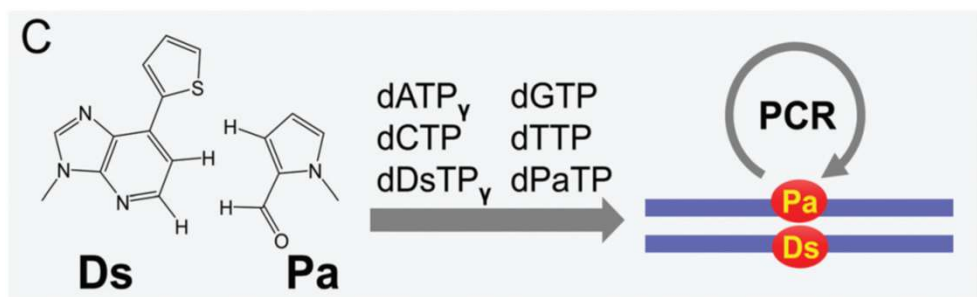


The Ds–Pa pair for faithful replication in combination with γ -amidotriphosphates.

(A) The substrates, dDsTP and dATP, are incorporated opposite Pa and T in the templates, respectively. However, dDsTP and dATP are also misincorporated opposite Ds and Pa, respectively. The Ds incorporation opposite Ds inhibits further primer extension.

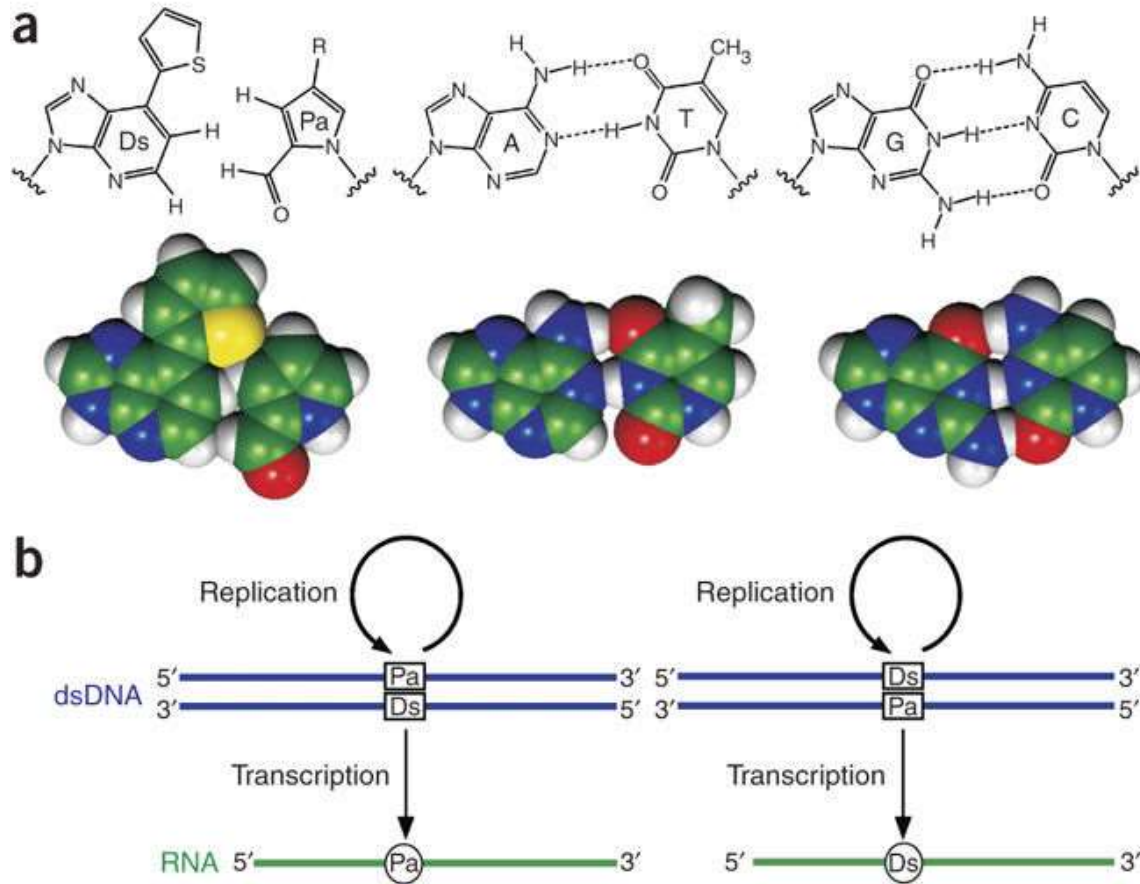
(B) The γ -amido-triphosphates, dDsTP _{γ} and dATP _{γ} , reduce the Ds–Ds and A–Pa mispairings in replication.

(C) The combination of the usual triphosphates (dG/C/T/PaTP) and the γ -amido-triphosphates (dDs/ATP _{γ}) enables the faithful PCR amplification of 6-letter DNA

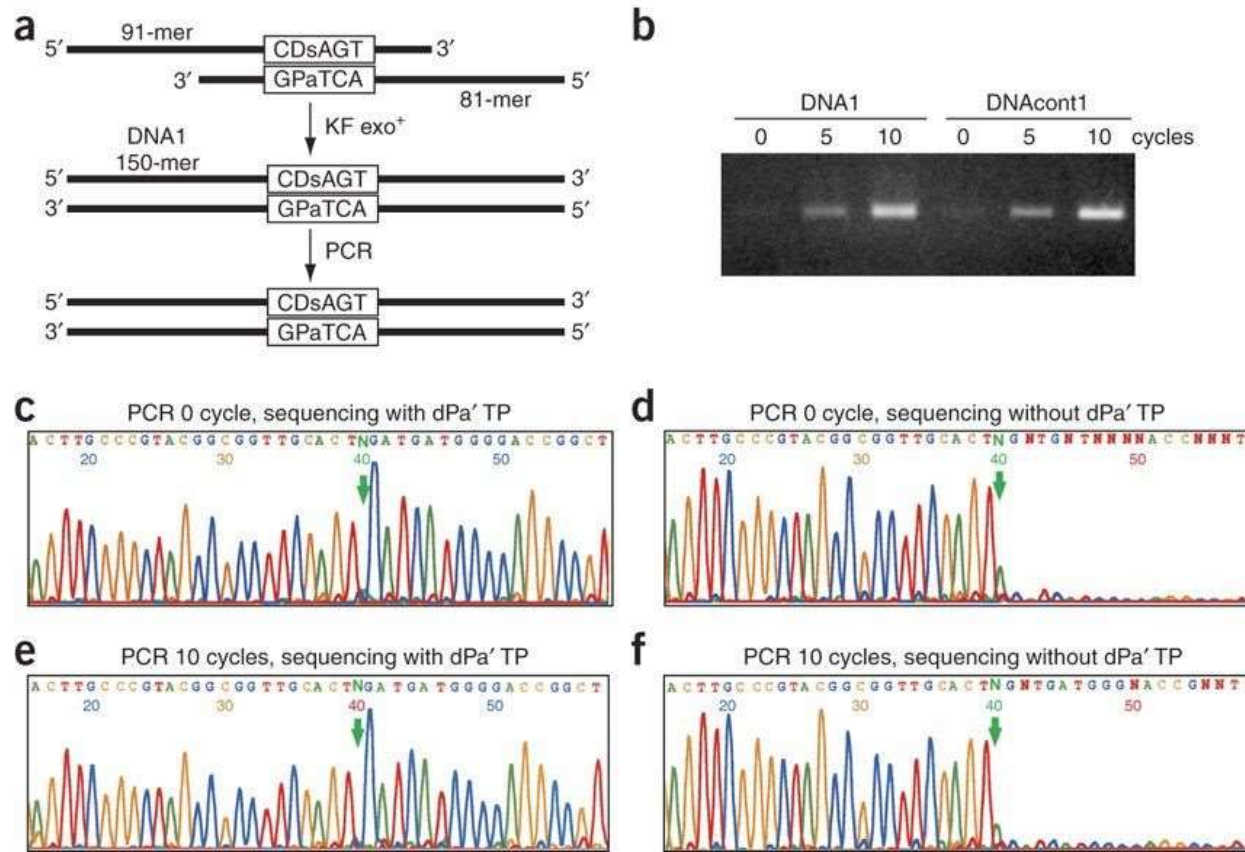


M. Kimoto, I. Hirao *Chem. Soc. Rev.* **2020**, *49*, 7602-7626

Replication and transcription of the hydrophobic UBP

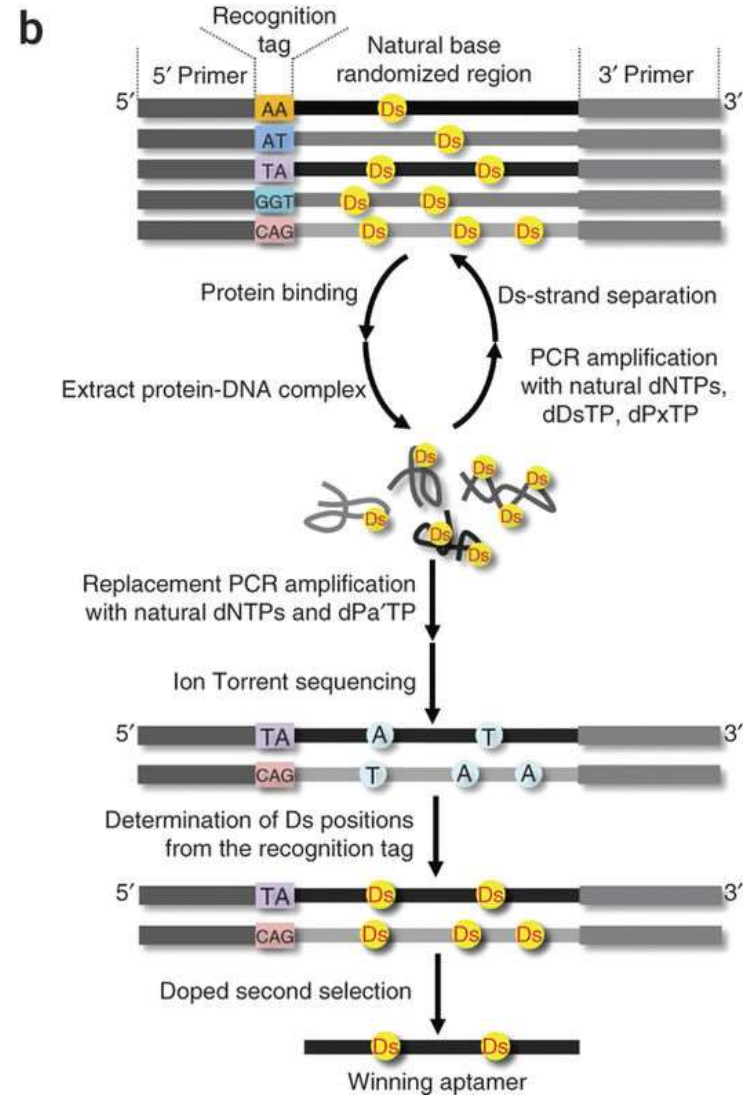
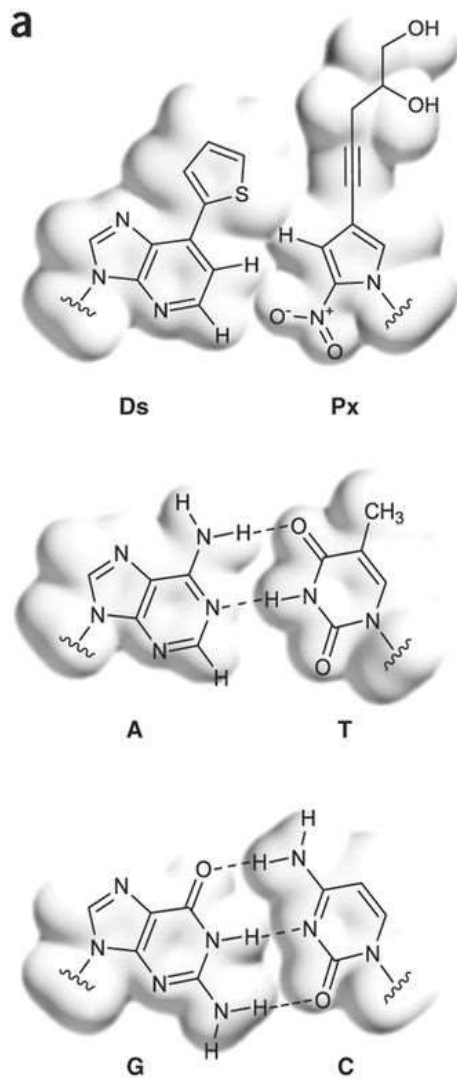


(a) The unnatural Ds-Pa and natural base pairs (Pa: R = H, Pa': R = C≡C-CH₃). **(b)** The unnatural base pair system that functions in PCR amplification, primer extension, DNA sequencing and T7 transcription. Original DNA templates were prepared by chemical synthesis and ligation, and were amplified by PCR with unmodified dNTPs (dPaTP, dGTP, dCTP and dTTP) and modified dNTP_Ns (γ-amidotriphosphates, dDsTP_N and dATP_N). RNA molecules containing Pa or modified Pa bases at specific positions were transcribed from DNA templates containing Ds in the template strands, by T7 RNA polymerase with PaTP (or modified PaTP) and the natural NTPs (left). RNA molecules containing Ds were transcribed from DNA templates containing Pa in the template strands, with DsTP and the natural NTPs (right).



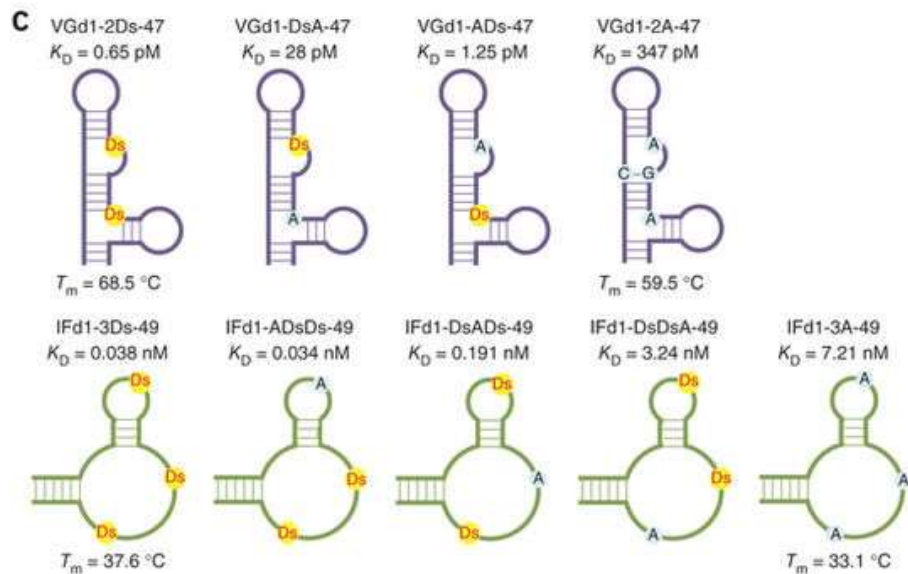
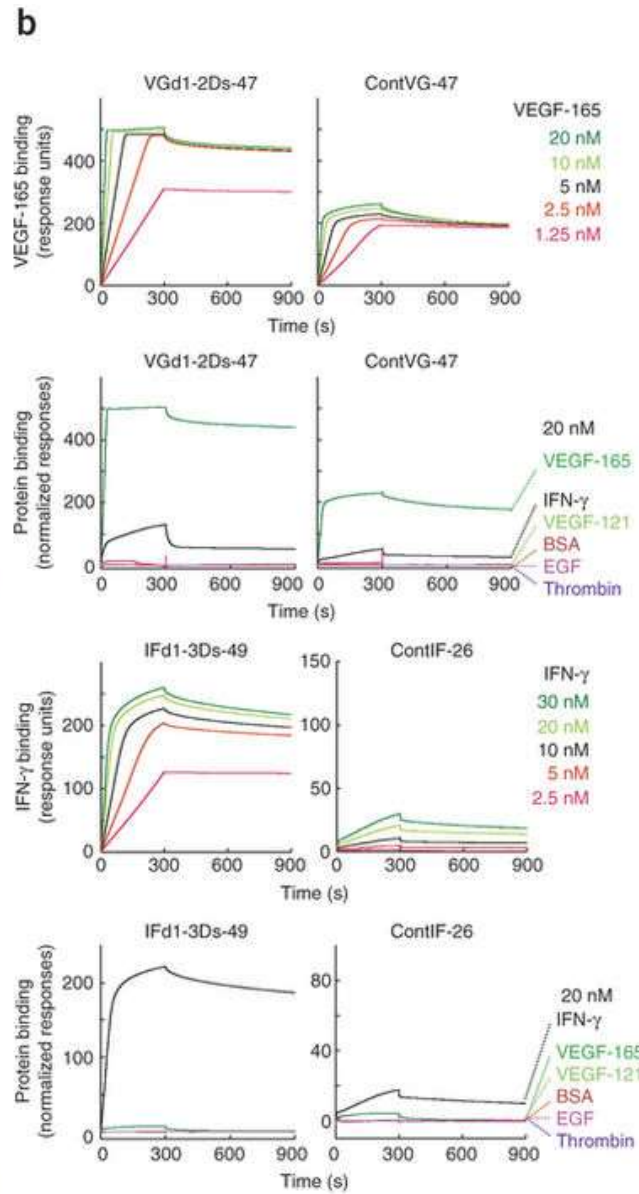
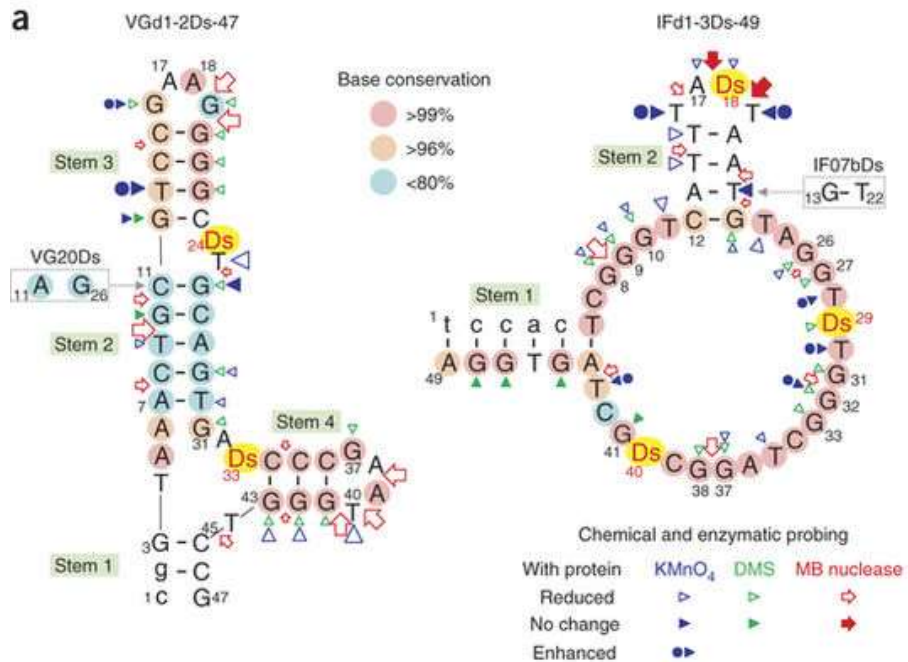
(a) The double stranded DNA fragment (150-mer, DNA1) was prepared by primer extension using chemically synthesized DNA fragments (91-mer and 81-mer) containing Ds and Pa. (b) Agarose-gel analysis of original DNA fragments (0 cycle) and PCR products after 5 and 10 cycles of amplification. For DNA1, PCR was performed with 0.04 unit/ μ l Vent DNA polymerase and the following cycle conditions: 0.5 min at 94 °C, 0.5 min at 45 °C and 4 min at 65 °C. For DNAcont1 consisting only of the natural bases, PCR was performed with 0.01 unit/ μ l Vent DNA polymerase with the following cycle conditions: 0.5 min at 94 °C, 0.5 min at 45 °C and 1 min at 72 °C. (c–f) DNA sequencing, in the presence (c,e) or absence (d,f) of dPa' TP, of the original DNA1 (c,d) and PCR-amplified DNA1 after 10 cycles using the unnatural base pair system (e,f).

Ds-Px noncanonical base pair – High-affinity DNA aptamers



Targets:
VEGF-165
and IFN- γ

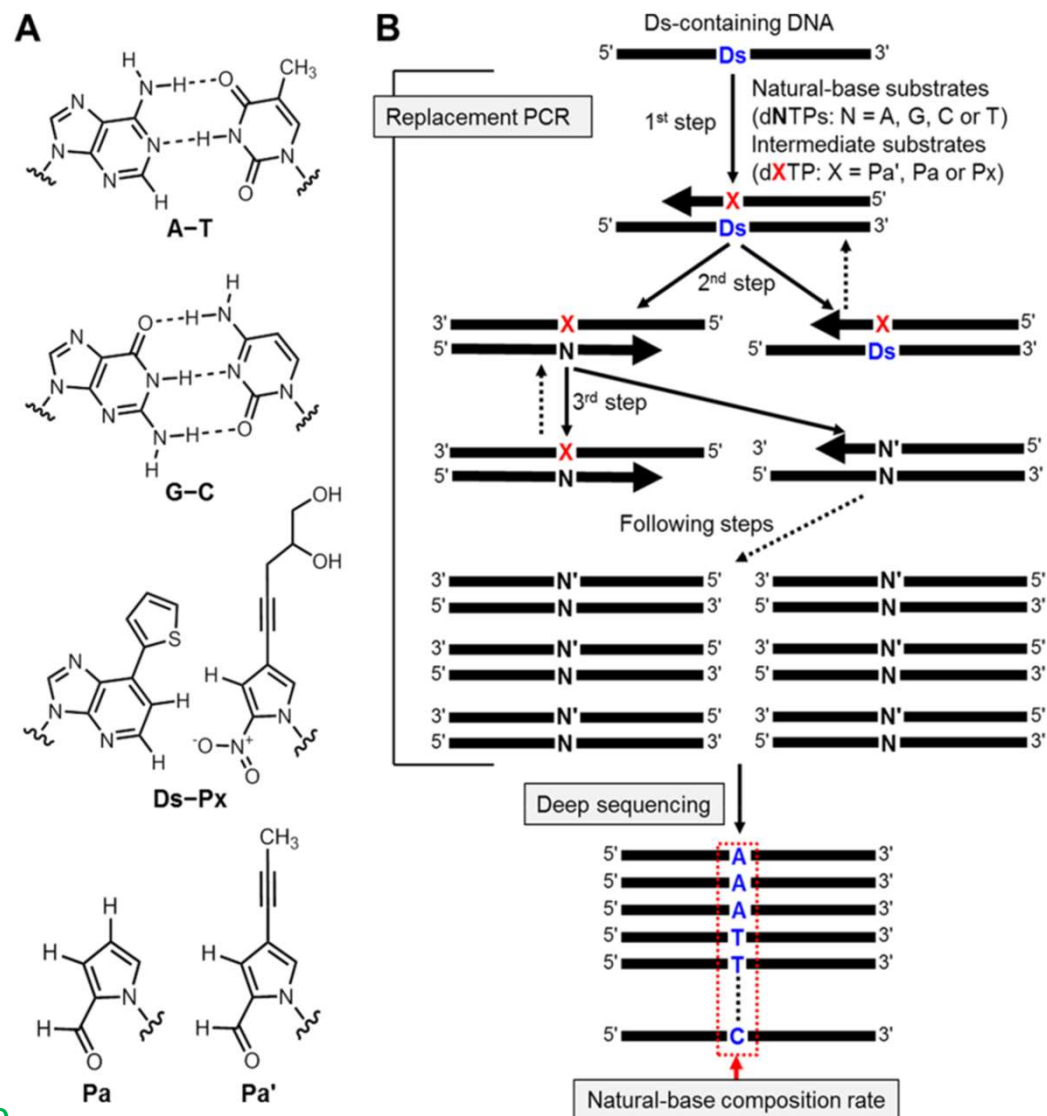
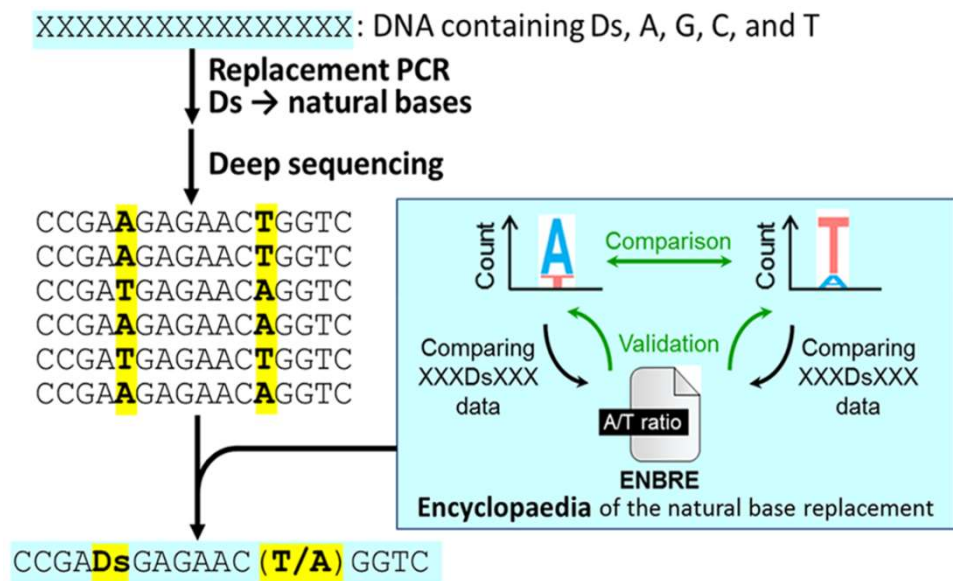
I. Hirao *et al.* *Nature Biotechnology* 2013, 31, 453-458



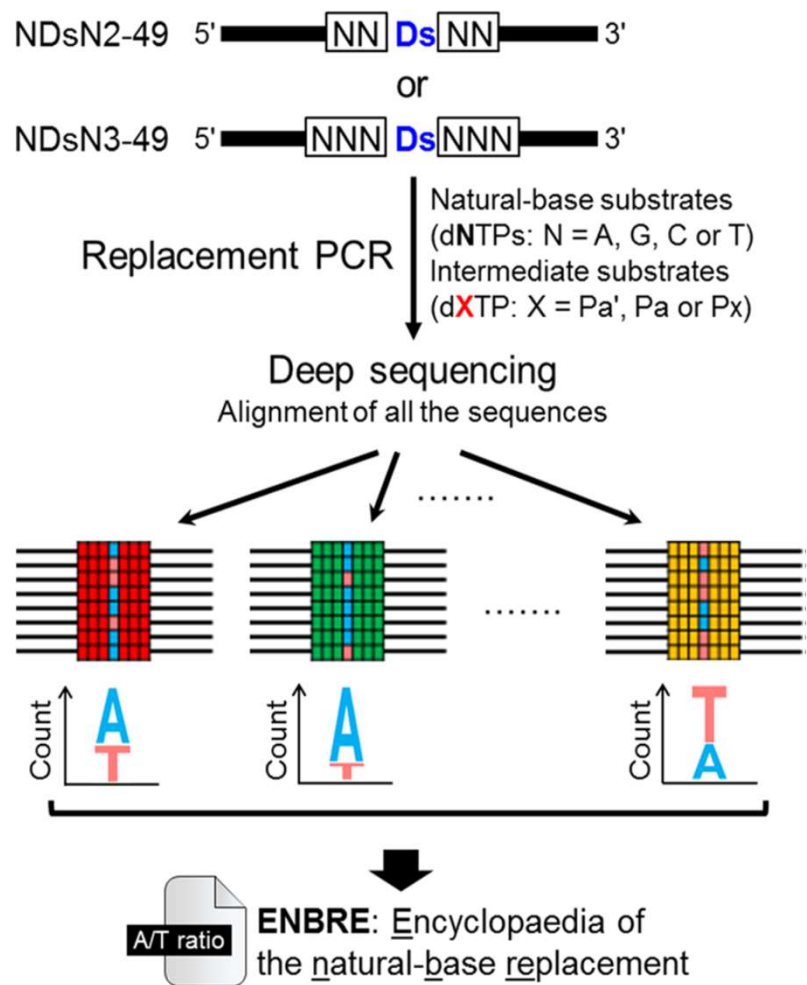
Characterizations and binding affinities of anti-VEGF-165 aptamer (VGd1-2Ds-47) and anti-IFN-γ aptamer (IFd1-3Ds-49)

I. Hirao et al. Nature Biotechnology 2013, 31, 453-458

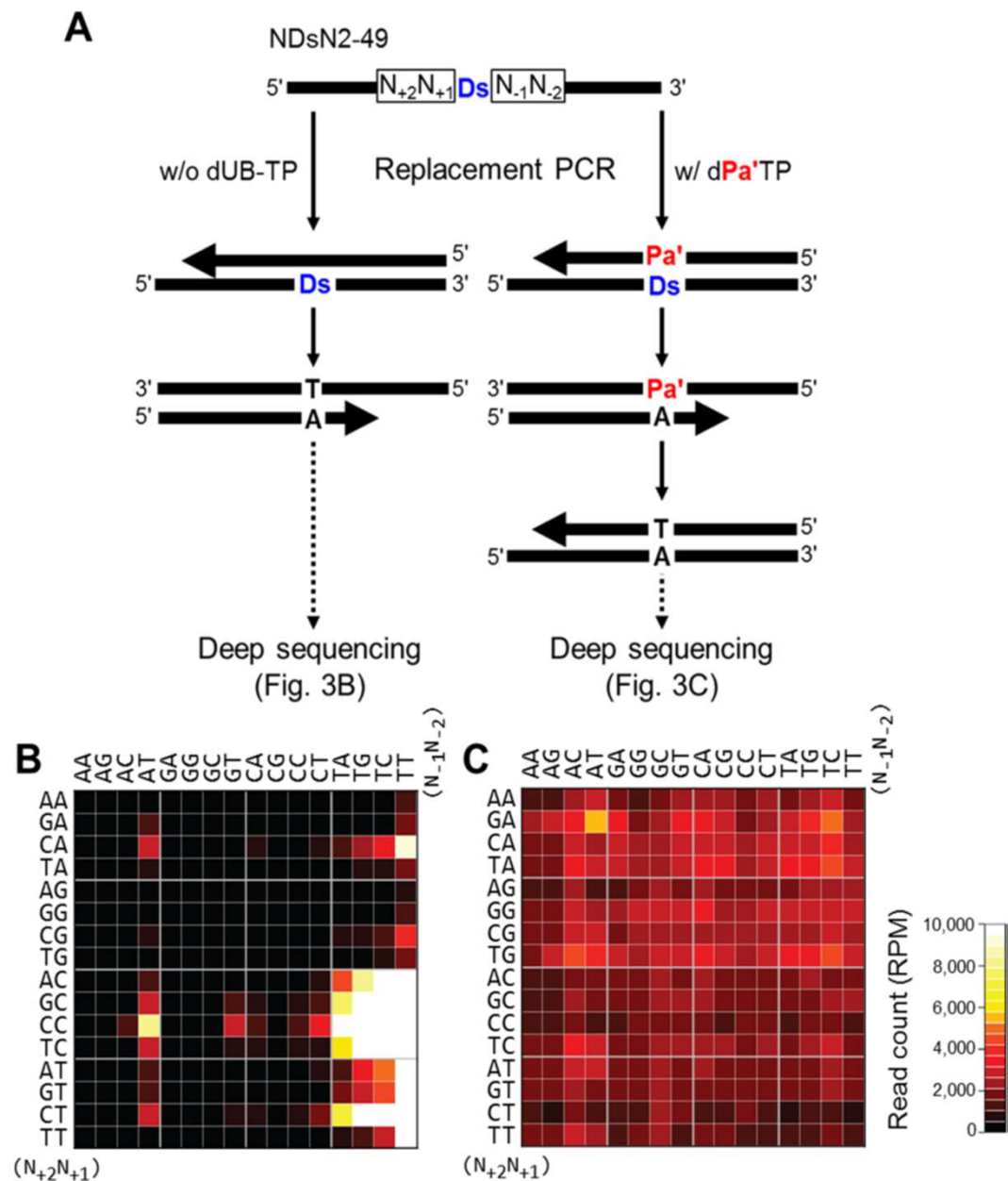
Ds-Pa – need for deep sequencing in the amplification process



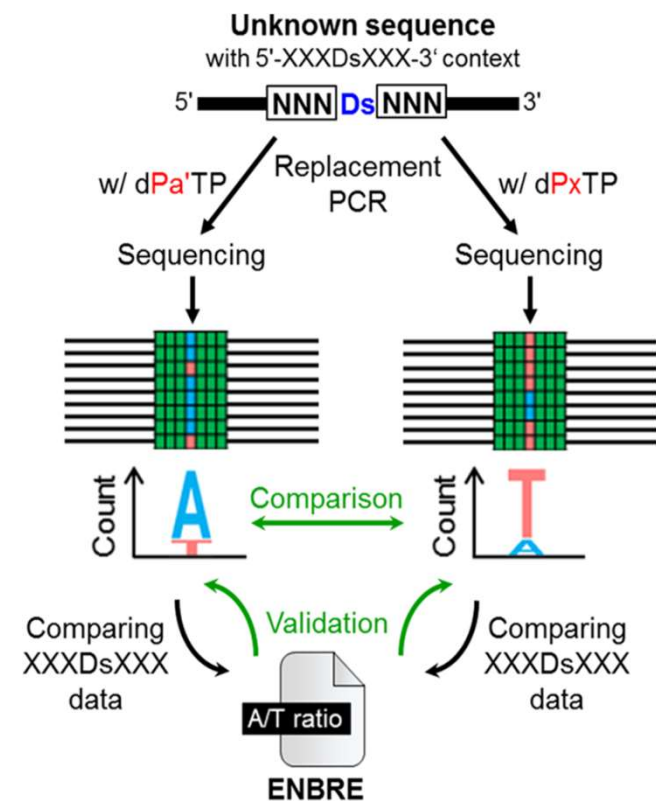
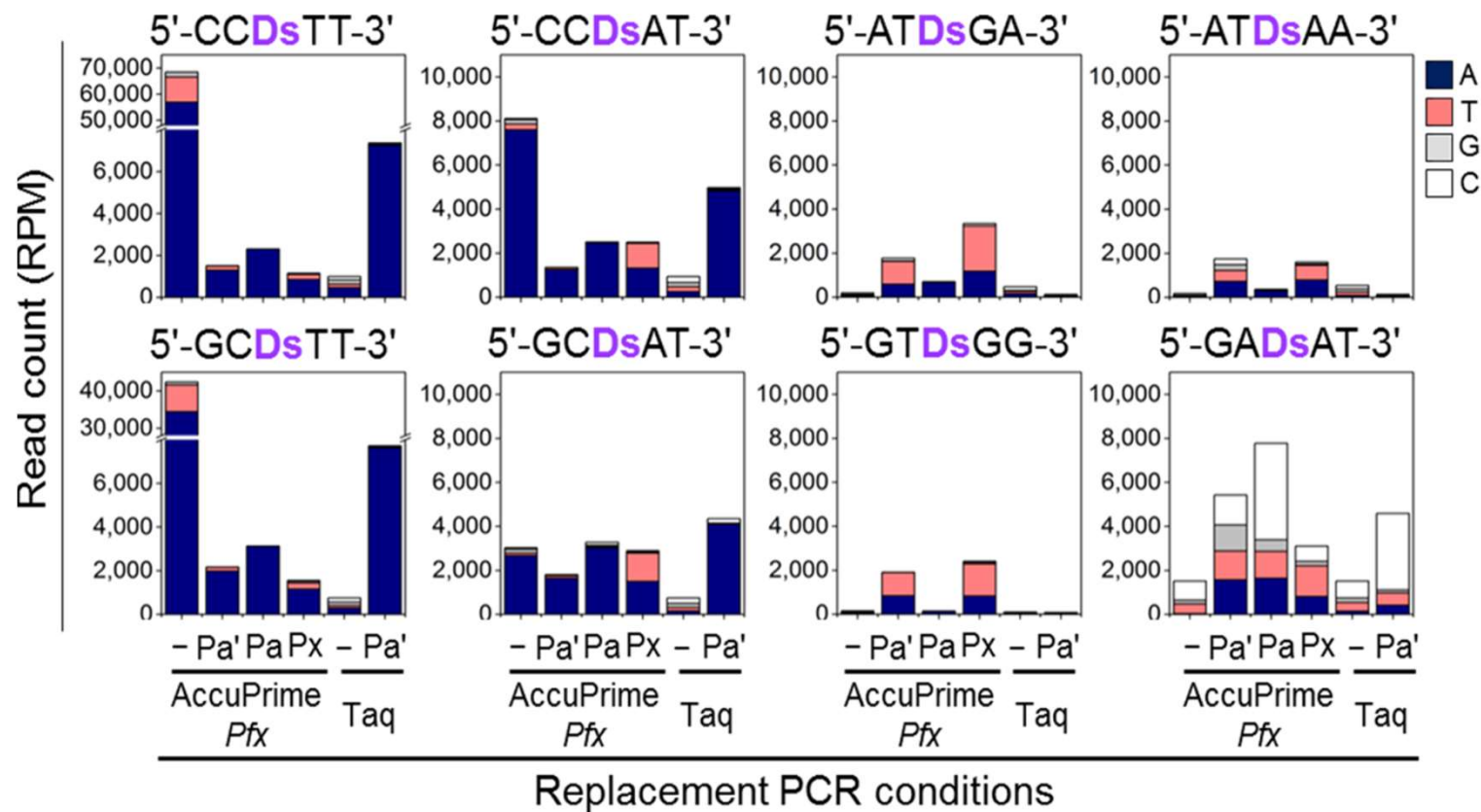
Ds-Pa – deep sequencing



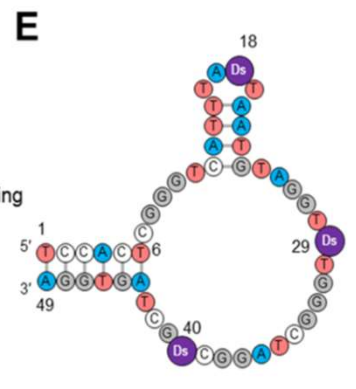
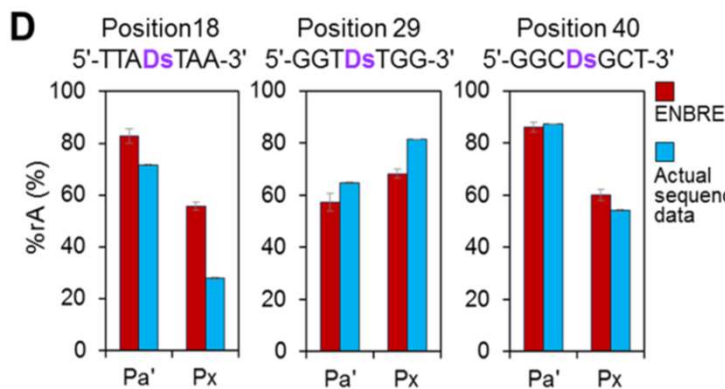
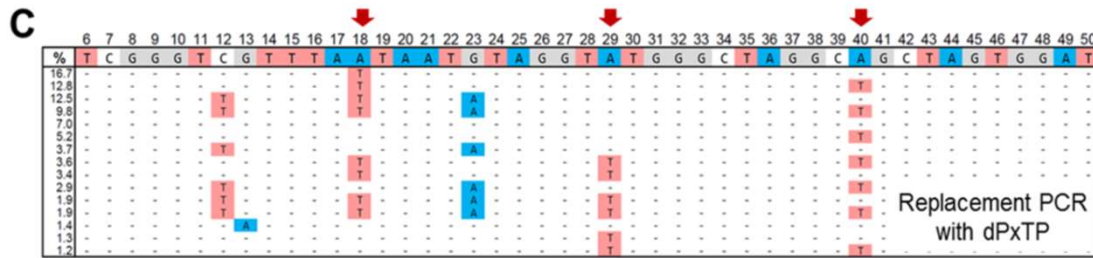
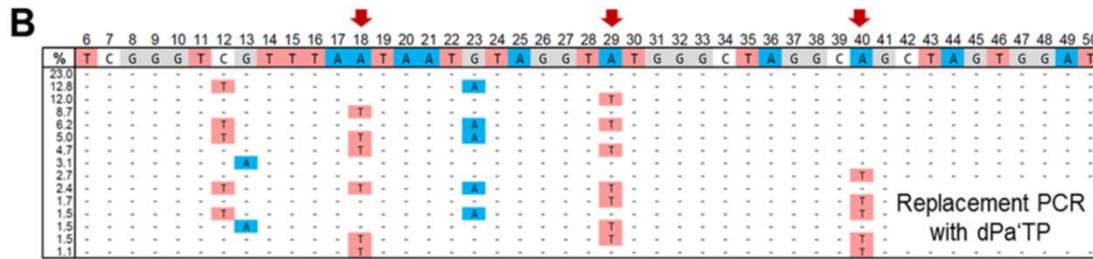
K. Hamashima, I. Hirao *et al.* *ACS Synth. Biol.* **2019**, *8*, 1401-1410



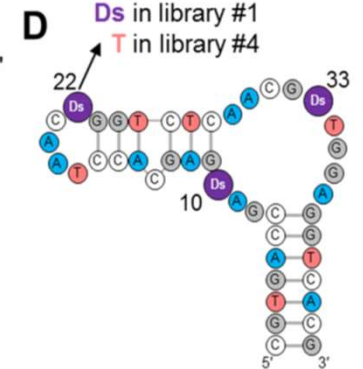
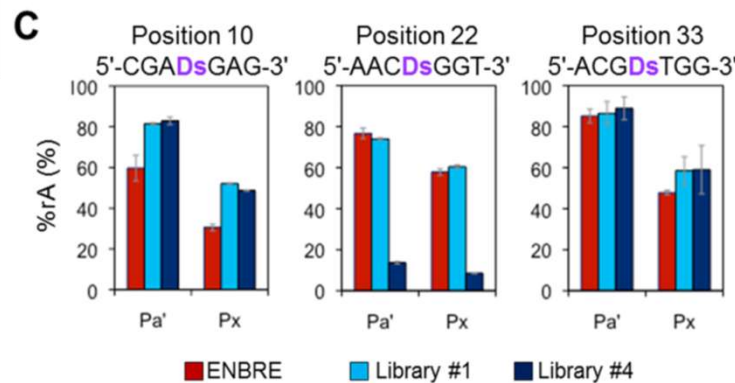
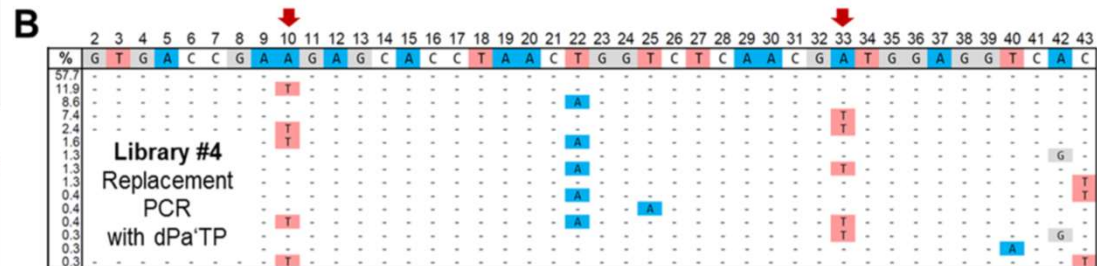
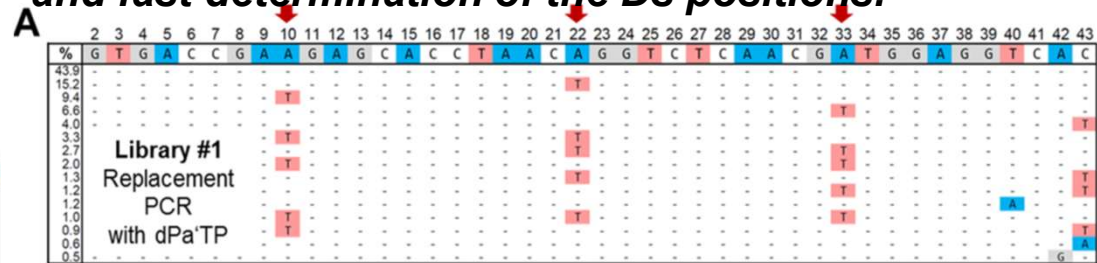
Ds-Pa – deep sequencing



Ds-Pa – deep sequencing

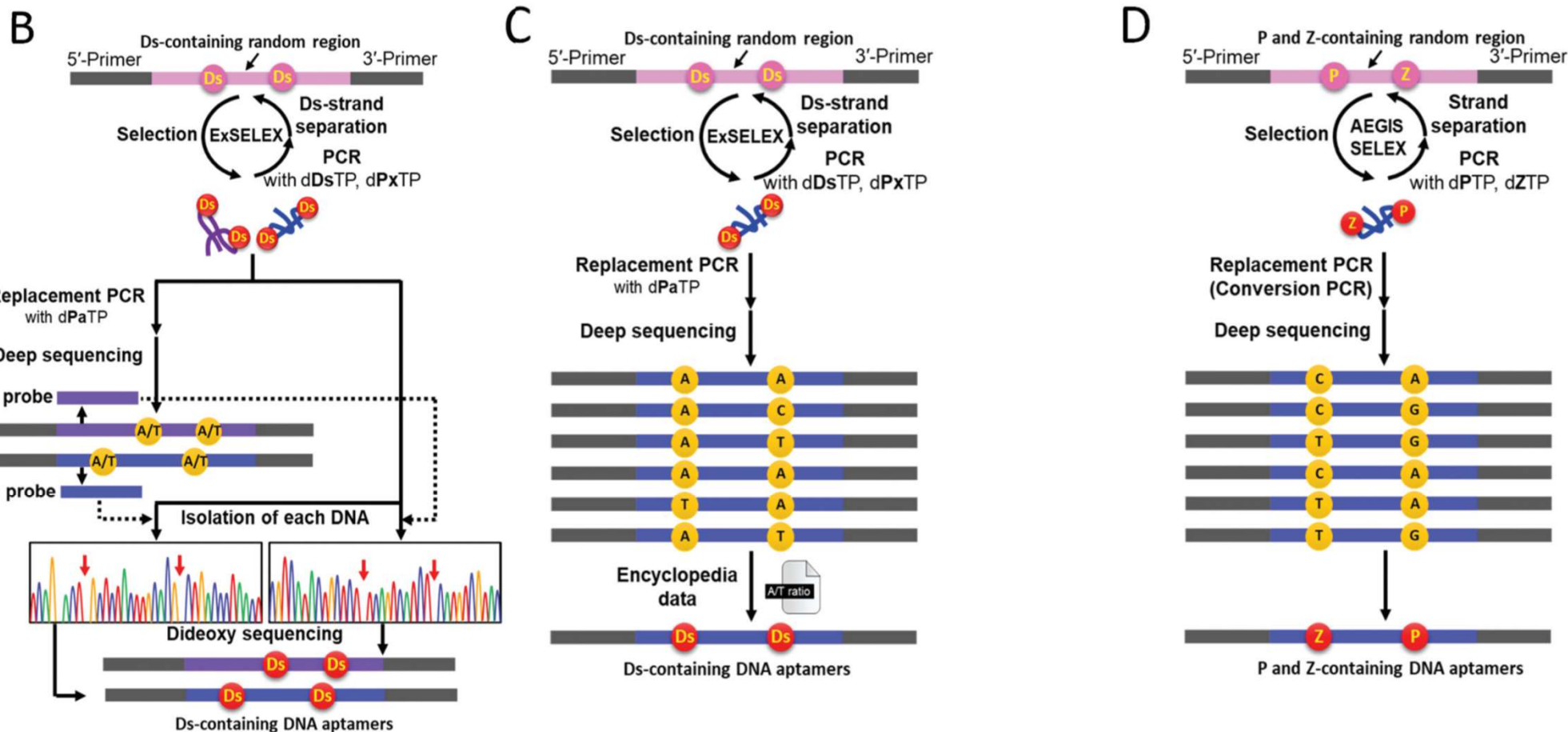


Referring to the encyclopedia data allows for simple and fast determination of the Ds positions.



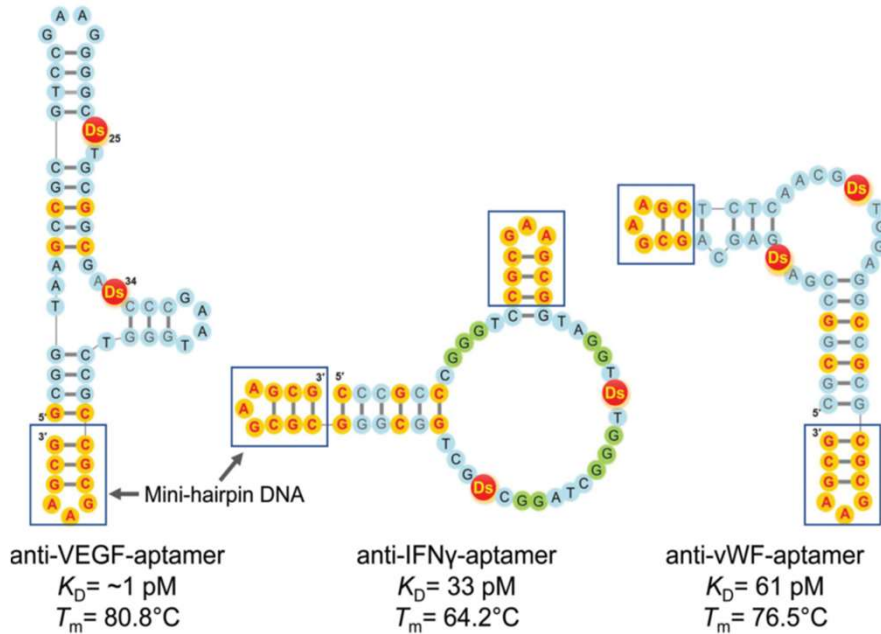
Comparison of the replacement patterns between two conditions enables the Ds positions to be distinguished from other natural-base positions.

Ds-Pa aptamer selection using deep sequencing

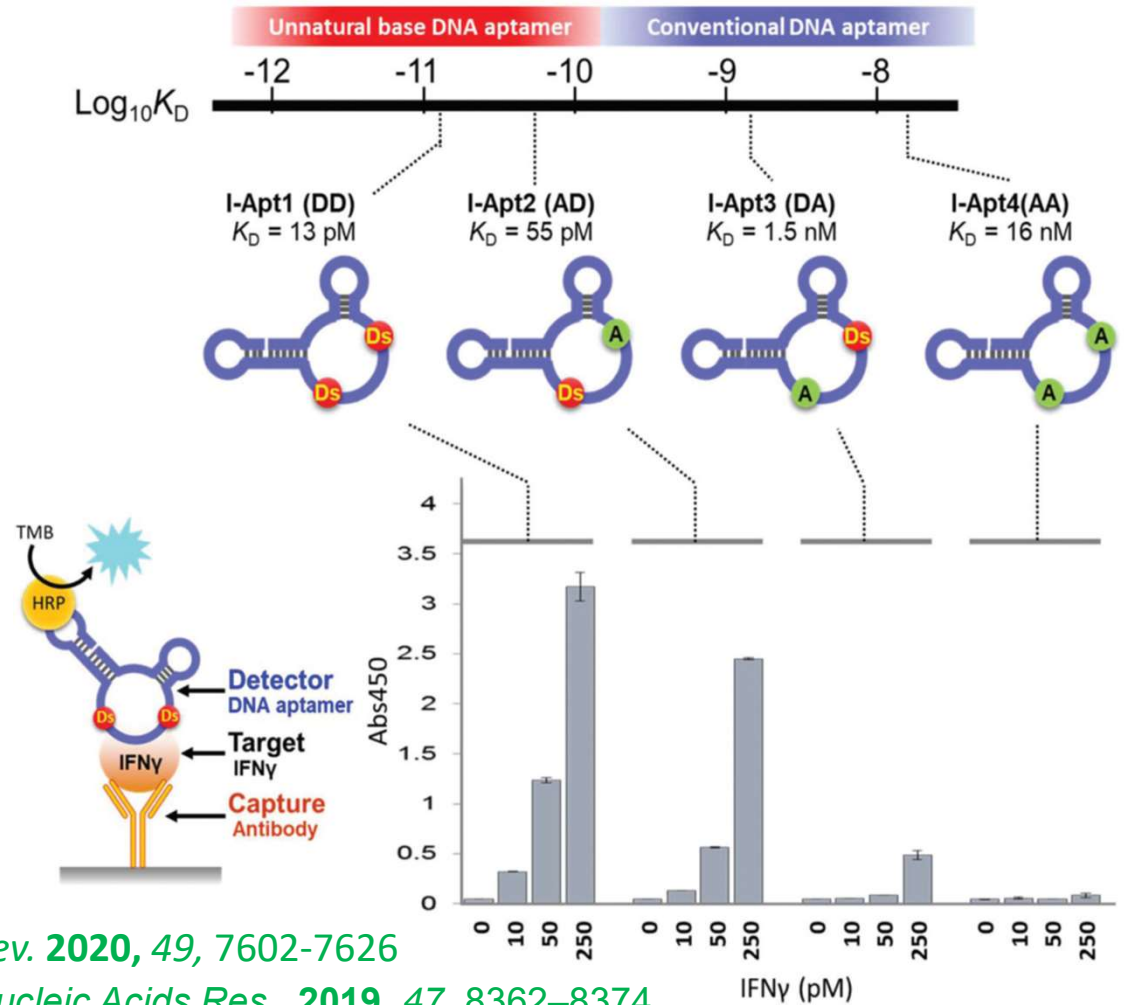


Ds-Pa aptamer selection using deep sequencing

Secondary structures of the optimized Ds-DNA aptamers targeting VEGF165, IFN γ , and vWF.



Generation of a molecular affinity ruler using anti-IFN γ Ds-DNA aptamer variants, replacing the Ds base with the natural A base.

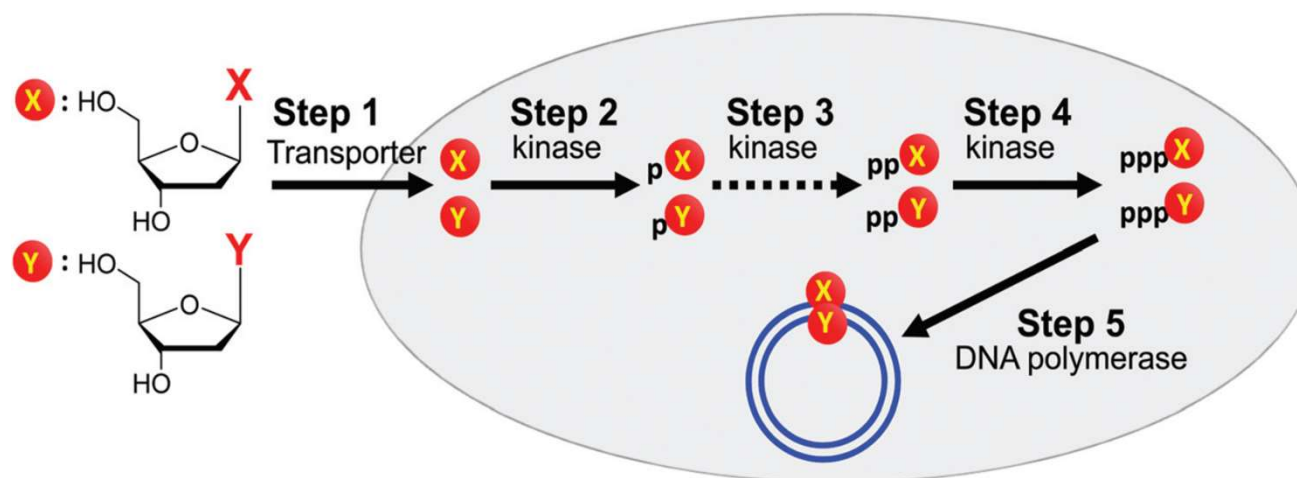


M. Kimoto, I. Hirao *Chem. Soc. Rev.* **2020**, *49*, 7602–7626

M. Kimoto, Y. W. S. Lim and I. Hirao, *Nucleic Acids Res.*, **2019**, *47*, 8362–8374

A semi-synthetic organism with an expanded genetic alphabet

Nucleoside phosphorylation: a biosynthetic pathway to provide unnatural substrates (dX/dYTP) in a cell, using their unnatural nucleosides (dX/dY) as a source.



*In Step 2, the nucleoside kinase from *D. melanogaster* (DmdNK) was explored for its ability to phosphorylate the unnatural nucleosides by three teams in vitro. Benner's team confirmed that the kinase in Step 4 was available for their Z and P bases in vitro. All UB triphosphates are, at least, accepted by the Klenow fragment of *E. coli* Pol I in vitro*

A semi-synthetic organism with an expanded genetic alphabet

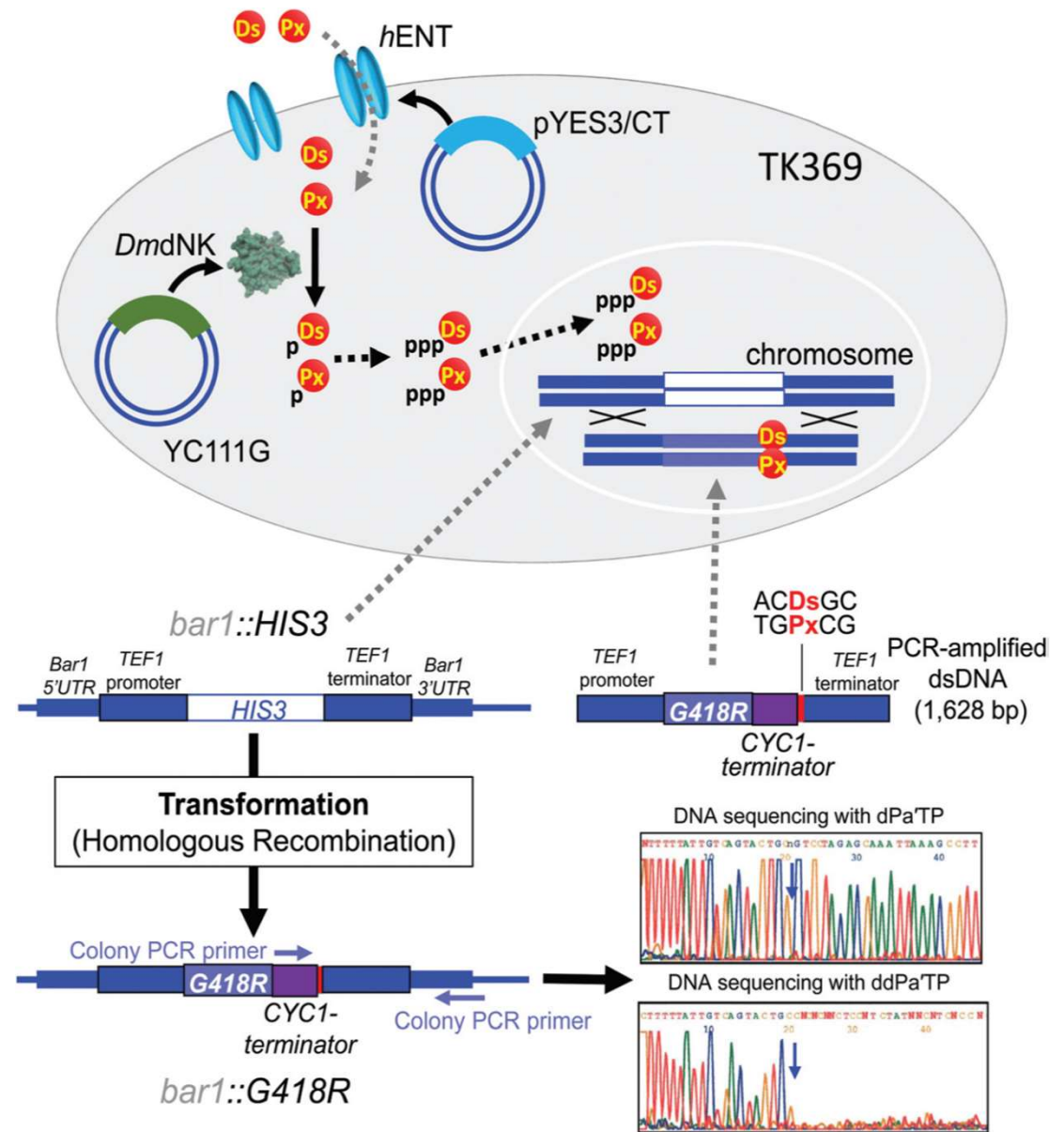
Homologous recombination strategy using the yeast strain TK369, to integrate dsDNA with the Ds–Px pair.

DmdNK – nucleoside kinase

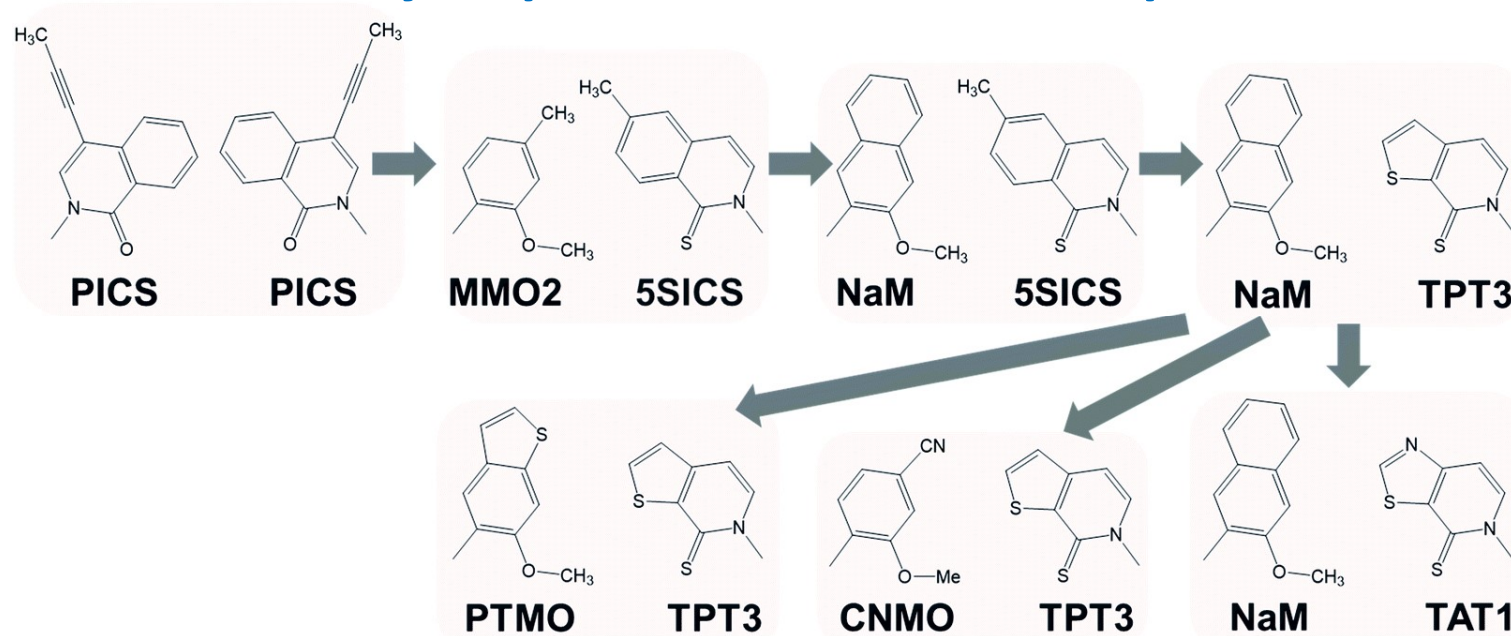
hENT - human equilibrium nucleoside transporter

The Ds and Px nucleosides supplied in the media.
The long dsDNA with the Ds–Px pair was prepared by fusion/overlapping PCR,

Analysis: colony PCR with dDsTP and dPxTP, then modified Sanger sequencing.



Hydrophobic unnatural base pairs



Romesberg (1999): **PICS–PICS**, but the polymerase reaction is paused at the PICS–PICS pairing position due to self-stacking.

Romesberg (2008): the **MMO2–5SICS** pair - the methyl group of 5SICS prevented the disfavored 5SICS–5SICS self-pairing.

Further optimized into the **NaM–5SICS** pair (>99% fidelity in PCR and transcription).

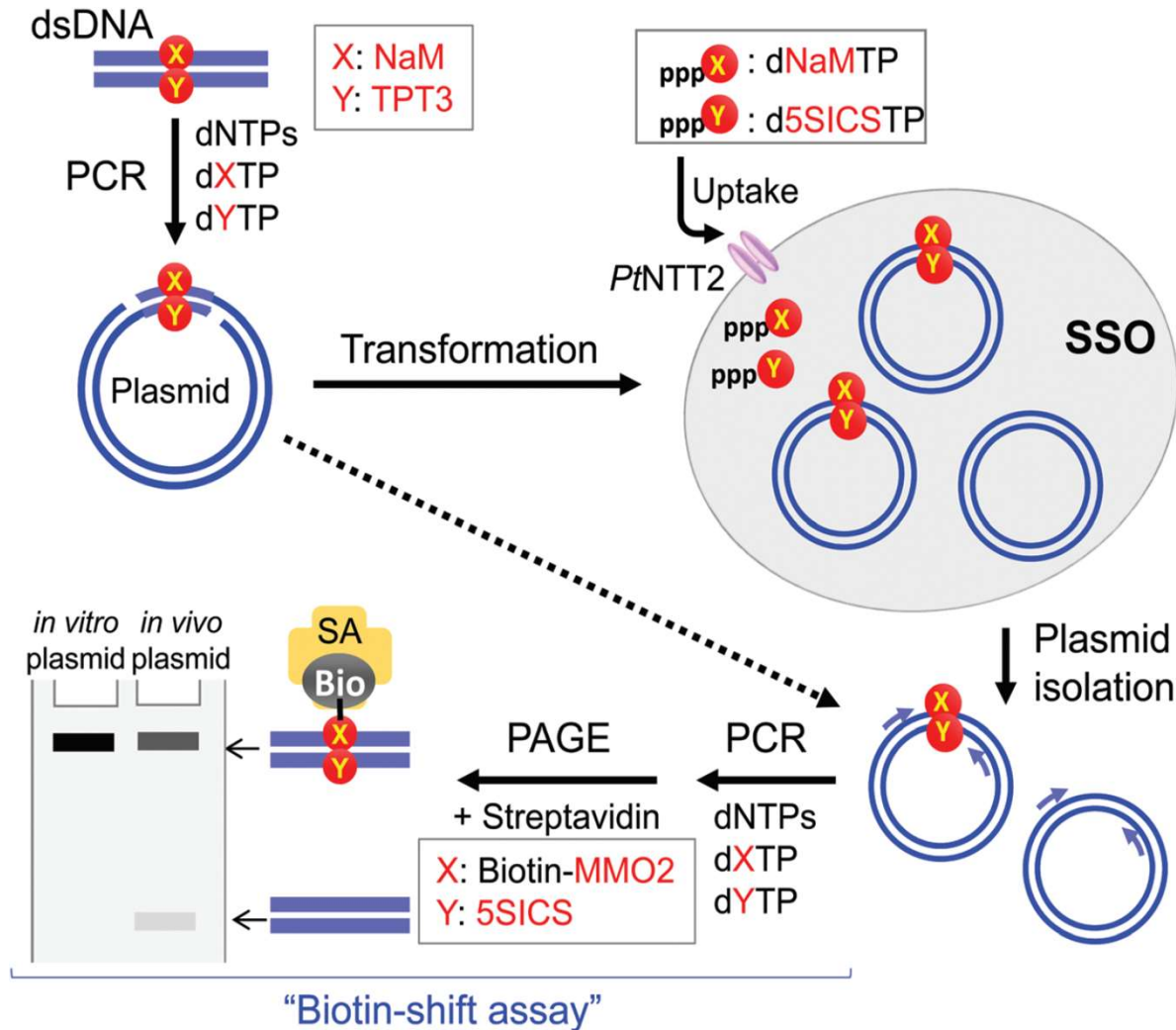
Romesberg (2014) the **NaM–TPT3** pair (systematic *in vitro* replication screening) → semi-synthetic organism (SSO) of *E. coli* with six-letter DNA.

Optimizations: the **CNMO–TPT3** pair to increase the UBP retention on a plasmid within the SSO,

the **NaM–TAT1** pair for efficient transcription and translation in the SSO.

Using these UBP systems, they reported protein synthesis with the site-specific incorporation of unnatural amino acids into proteins in the SSO.

A semi-synthetic organism with an expanded genetic alphabet

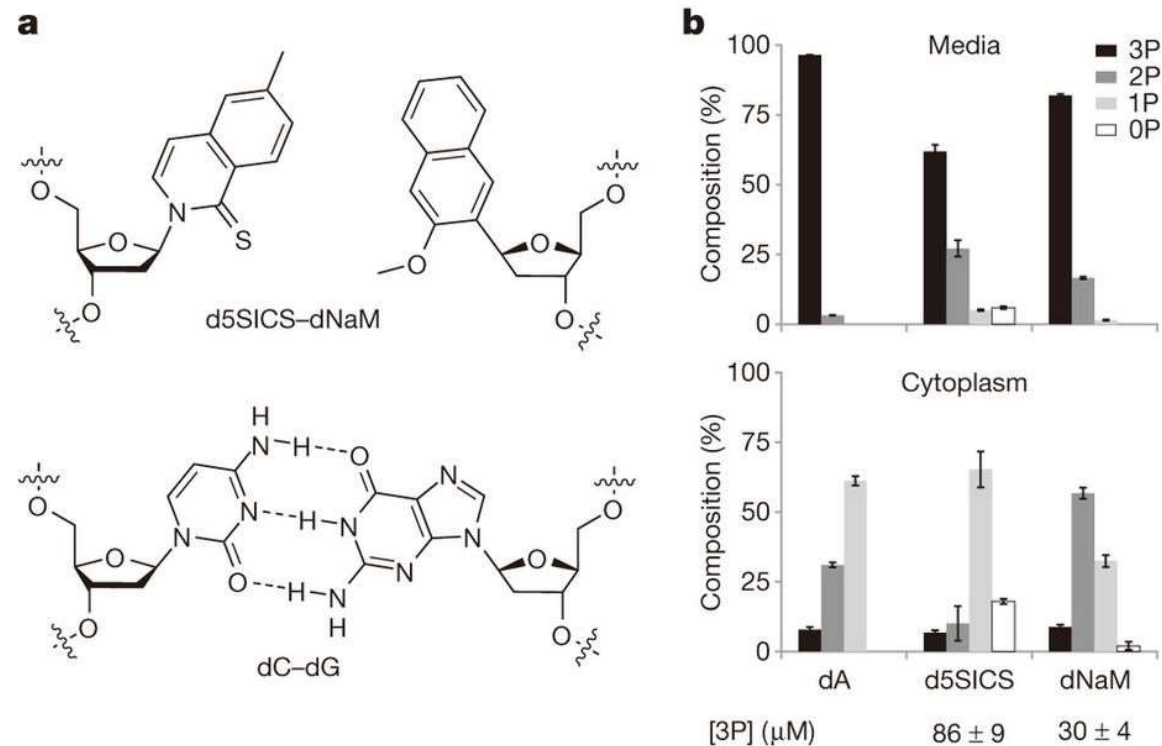


The first creation of an SSO, using the NaM–TPT3 and NaM–5SICIS pairs and *E. coli* C41(DE3) as the host strain.

*The plasmid containing the NaM–TPT3 pair was prepared by PCR and transformed into *E. coli* C41(DE3) with a PtNTT2 overexpression system. The transformants were cultured in inorganic phosphate-rich growth media in the presence of the NaM and 5SICIS triphosphates.*

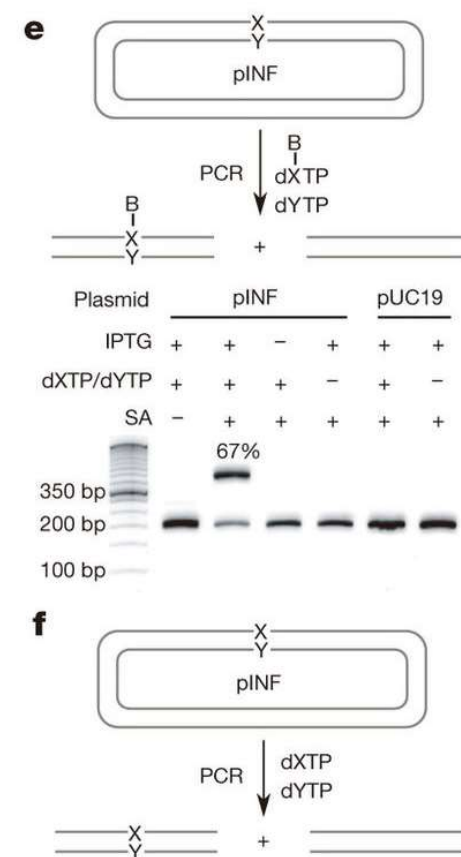
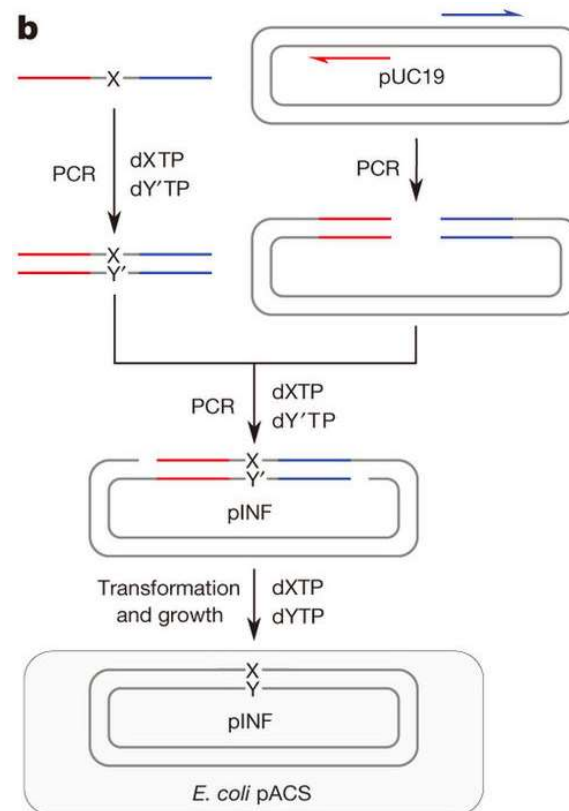
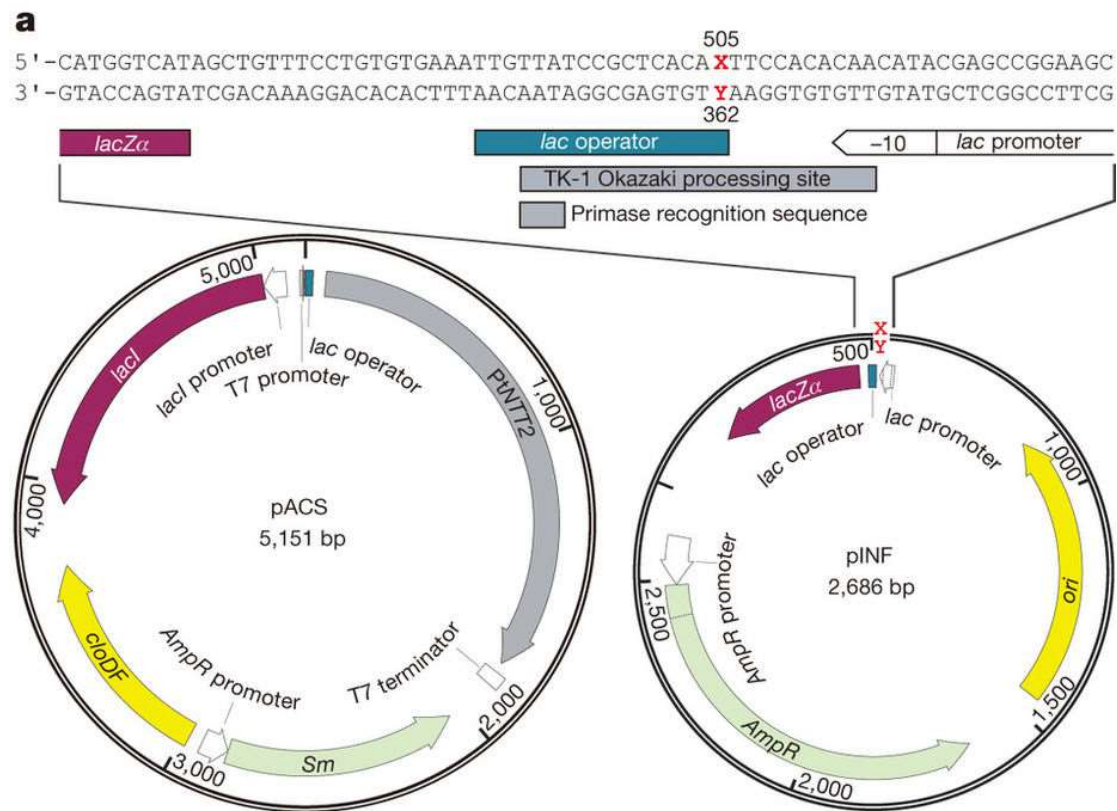
The propagated plasmids were isolated and subjected to the analysis of the NaM–5SICIS pair retention by a biotin-shift assay

A semi-synthetic organism with an expanded genetic alphabet



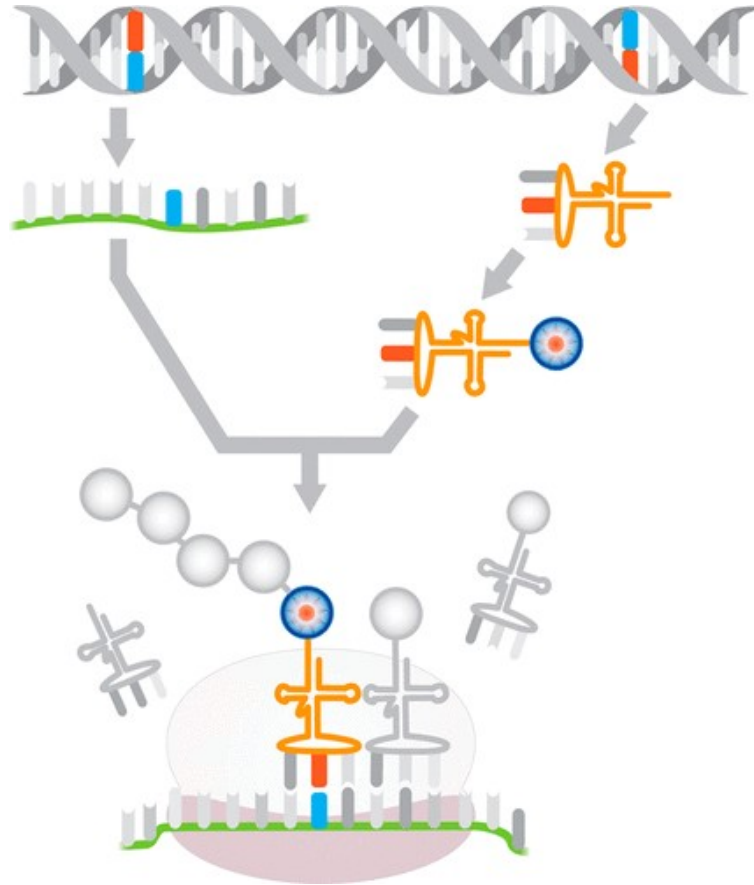
a, Chemical structure of the d5SICS–dNaM UBP compared to the natural dG–dC base pair. **b**, Composition analysis of d5SICS and dNaM in the media (top) and cytoplasmic (bottom) fractions of cells expressing *PtNTT2* after 30 min incubation; dA shown for comparison. 3P, 2P, 1P and 0P correspond to triphosphate, diphosphate, monophosphate and nucleoside, respectively; [3P] is the intracellular concentration of triphosphate.

Malyshv, Denis A.; Romesberg, Floyd E. *et al.* *Nature* **2014**, *509*, 385–388



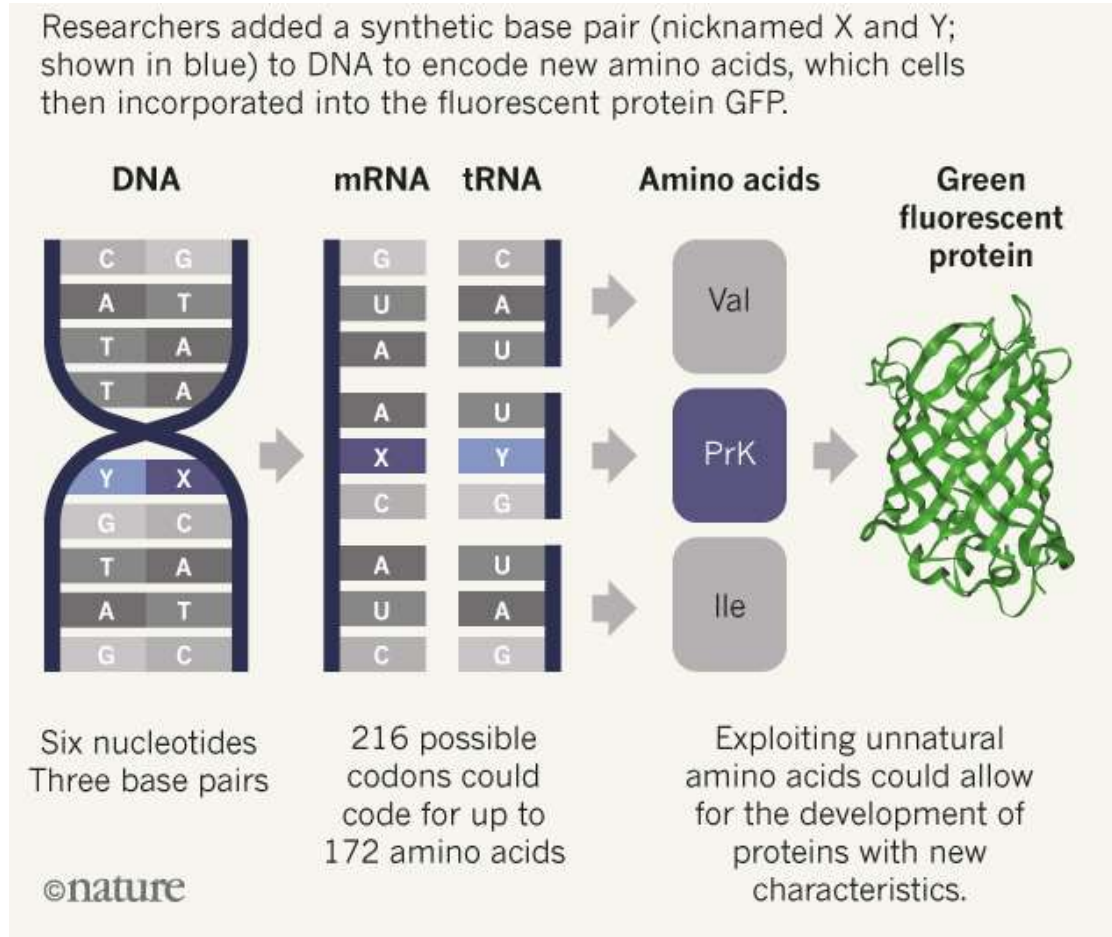
Malyshev, Denis A.; Romesberg, Floyd E. *et al. Nature* 2014, 509, 385–388

A semi-synthetic organism with an expanded genetic alphabet



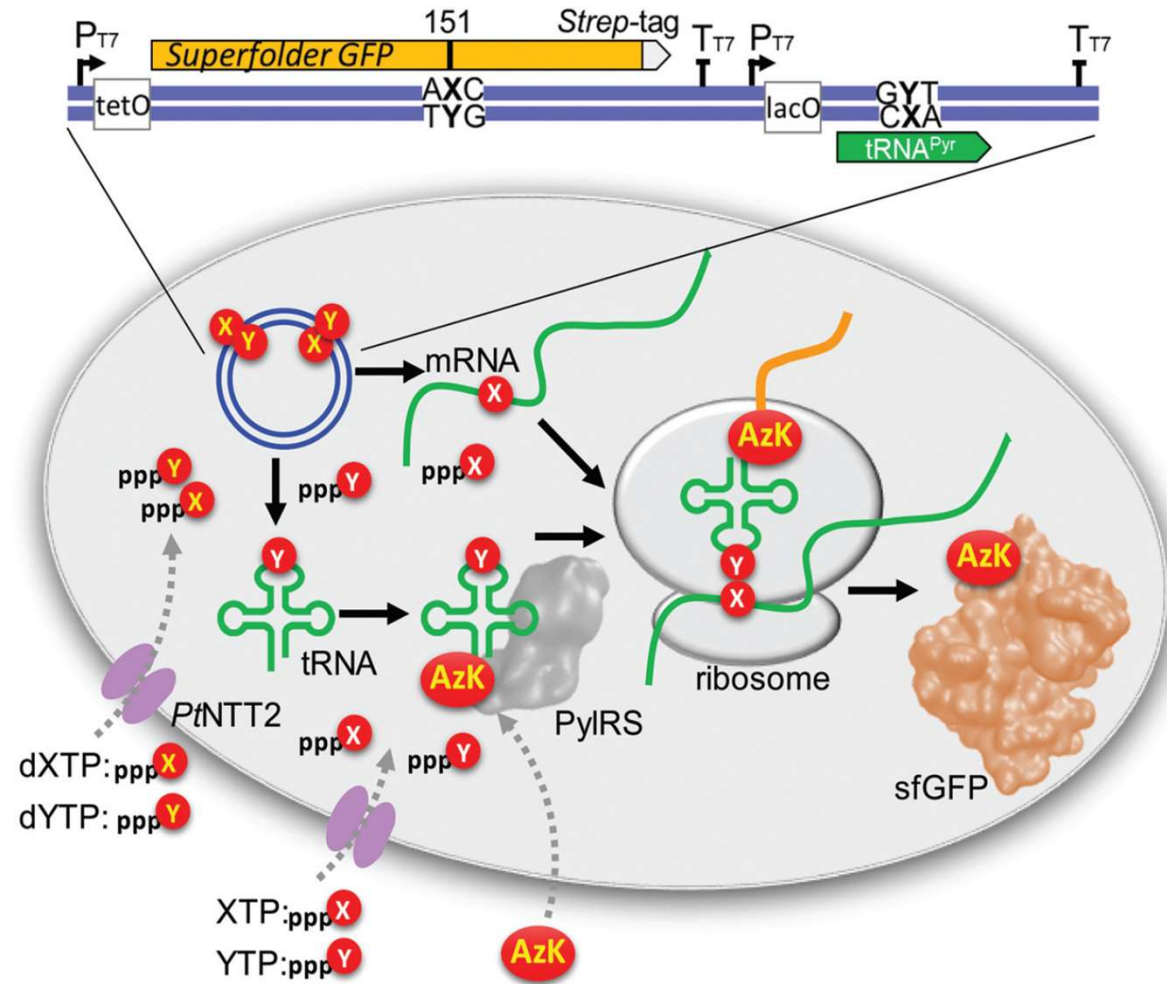
The SSO replicates DNA containing the dNaM-dTPT3 UBP (blue and red, respectively), transcribes mRNA and tRNA with complementary codons and anticodons containing **NaM** or **TPT3**, uses an orthogonal synthetase to charge the tRNA with an nCAA, and uses the charged tRNA to translate the mRNA into proteins containing nCAAs

A semi-synthetic organism with an expanded genetic alphabet



Zhang, Y.; Romesberg, Floyd E. *et al.* *Nature* **2017**, *551*, 644-647

A semi-synthetic organism with an expanded genetic alphabet

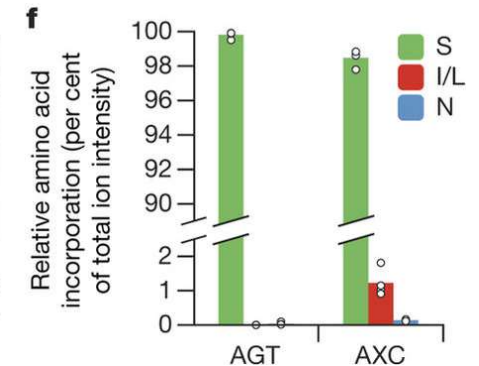
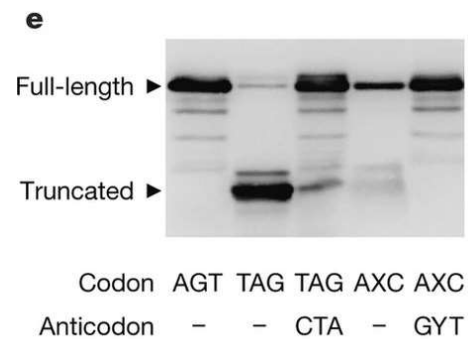
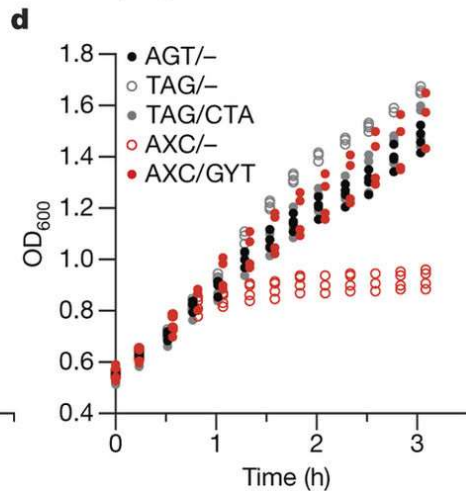
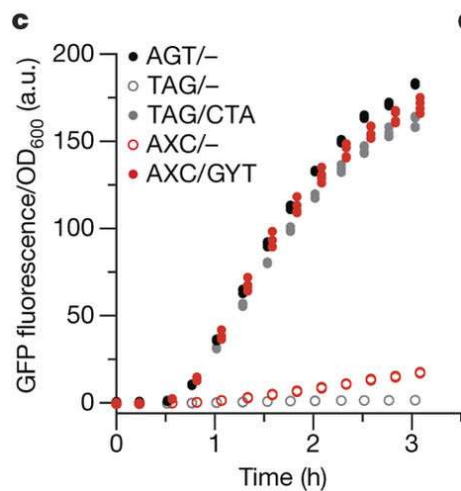
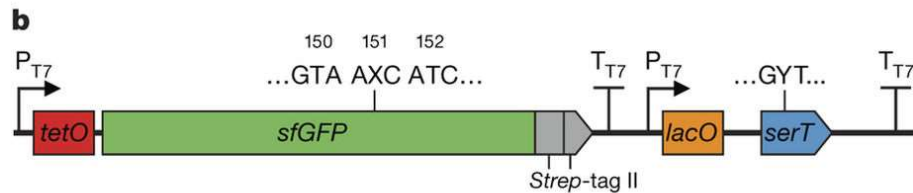
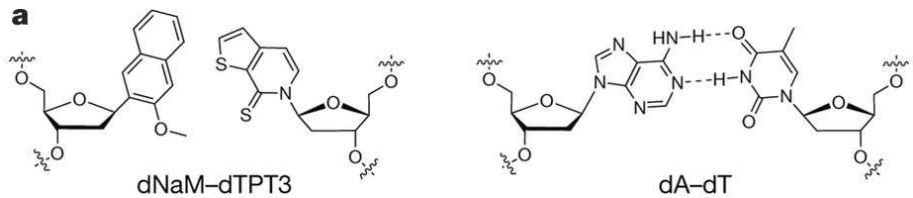


Zhang, Y.; Romesberg, Floyd E. *et al.* *Nature* **2017**, *551*, 644-647

M. Kimoto, I. Hirao *Chem. Soc. Rev.* **2020**, *49*, 7602-7626

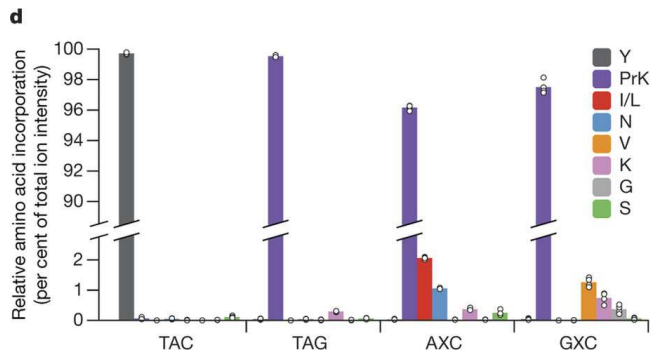
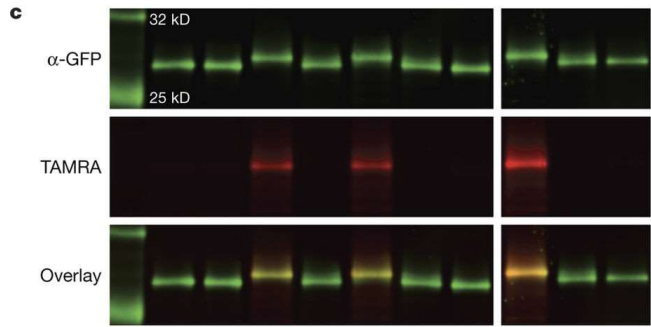
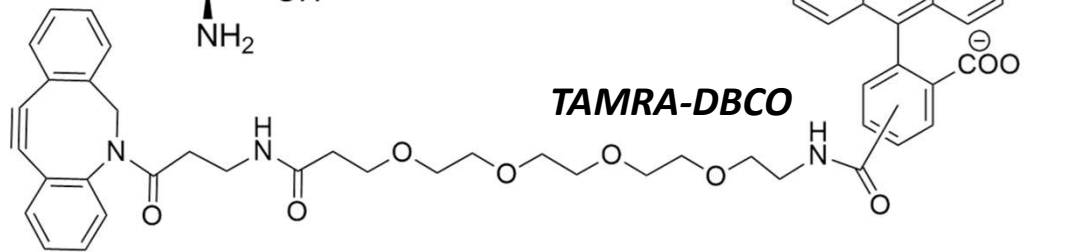
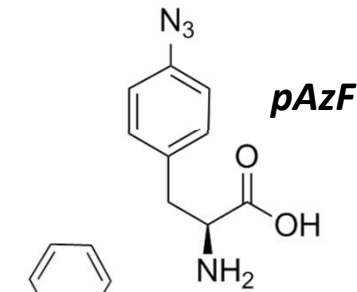
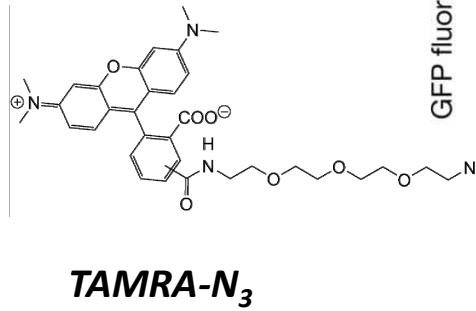
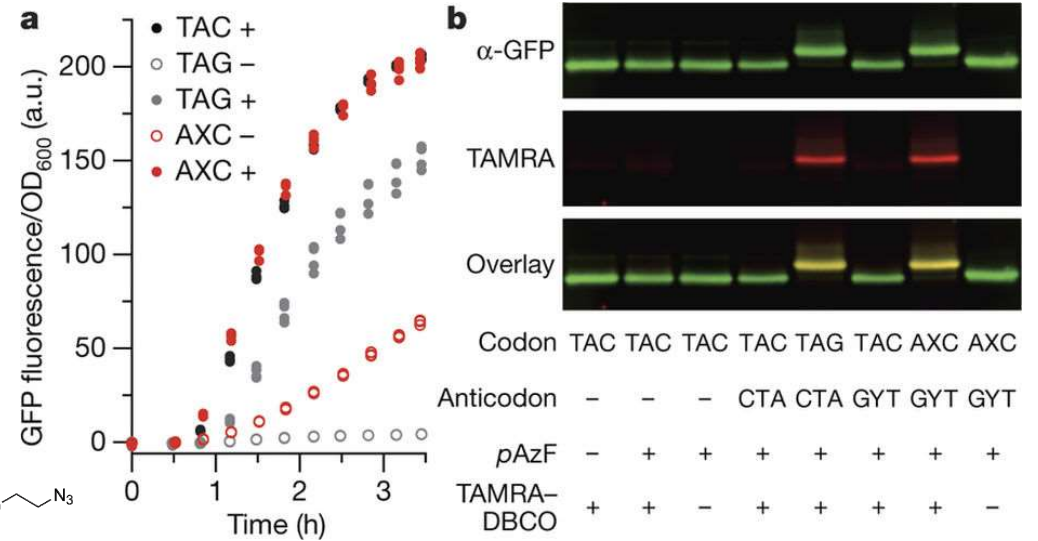
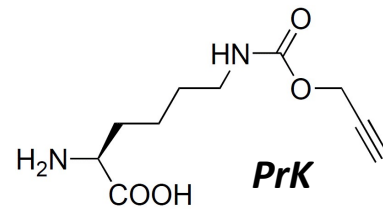
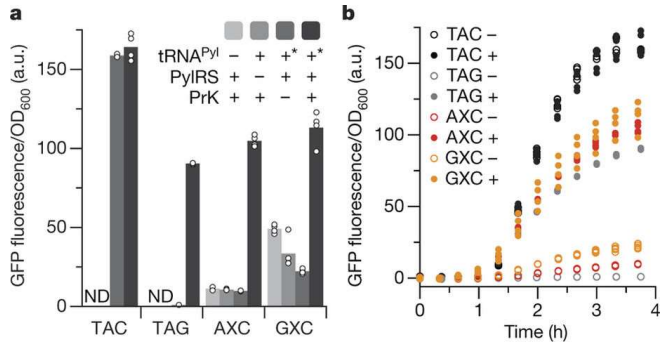
A semi-synthetic organism with an expanded genetic alphabet

The *in vivo* transcription of DNA containing dNaM and dTPT3 into mRNAs with two different unnatural codons and tRNAs with cognate unnatural anticodons, and their efficient decoding at the ribosome to direct the site-specific incorporation of natural or non-canonical amino acids into superfolder green fluorescent protein. The resulting semi-synthetic organism both encodes and retrieves increased information and should serve as a platform for the creation of new life forms and functions.



Zhang, Y.; Romesberg, Floyd E. *et al.* *Nature* **2017**, *551*, 644-647

A semi-synthetic organism with an expanded genetic alphabet



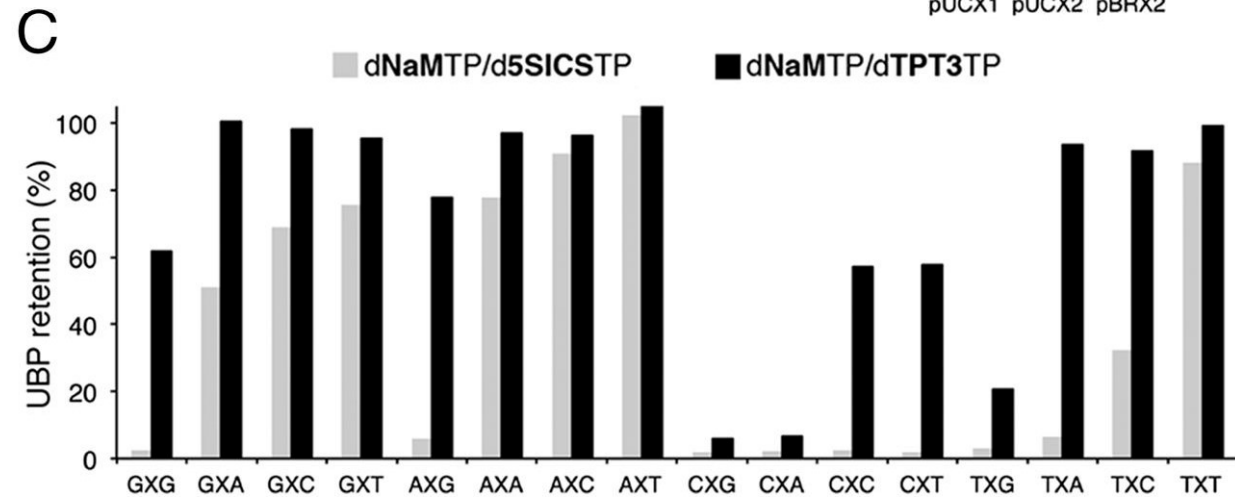
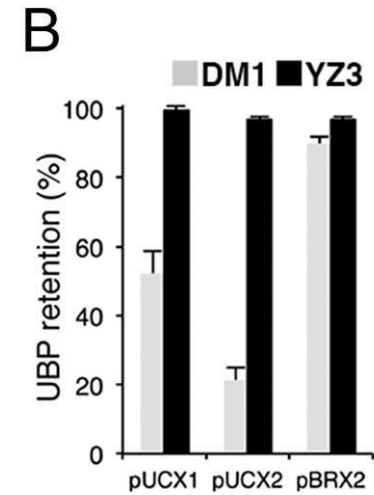
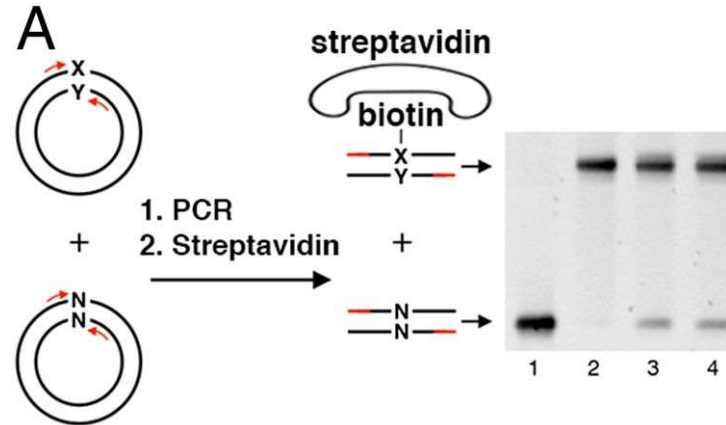
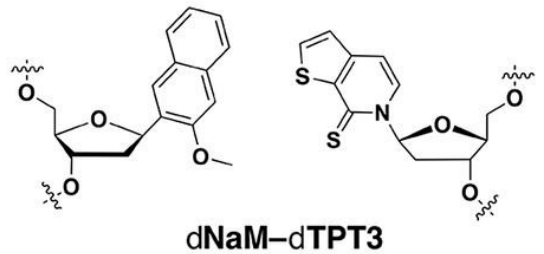
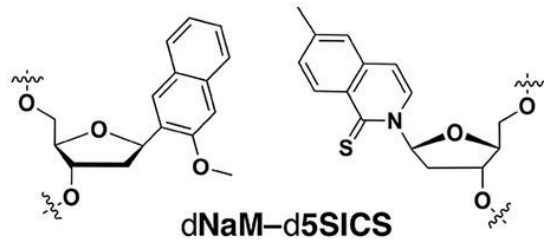
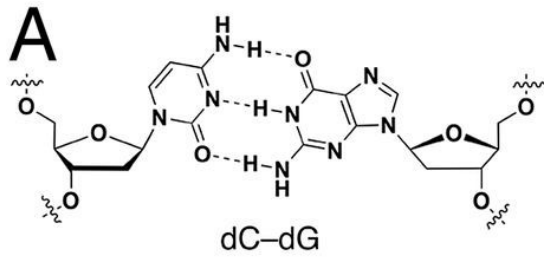
Zhang, Y.; Romesberg, Floyd E. *et al.* *Nature* 2017, 551, 644-647

A semi-synthetic organism with an expanded genetic alphabet

- An unnatural base pair (UBP) would increase the information storage potential of DNA
- and semisynthetic organisms (SSOs) that stably harbor this expanded alphabet would thereby have the potential to store and retrieve increased information,
- *Escherichia coli* grown in the presence of the unnatural nucleoside triphosphates dNaMTP and d5SICSTP, and provided with the means to import them via expression of a plasmid-borne nucleoside triphosphate transporter, replicates DNA containing a single dNaM-d5SICS UBP,
- to fortify and vivify the nascent SSO, a more chemically optimized UBP dTPT3 was used, and the power of the bacterial immune response was harnessed by using Cas9 to eliminate DNA that had lost the UBP.
- The optimized SSO grows robustly, constitutively imports the unnatural triphosphates, and is able to indefinitely retain multiple UBPs in virtually any sequence context. This SSO is thus a form of life that can stably store genetic information using a six-letter, three-base-pair alphabet

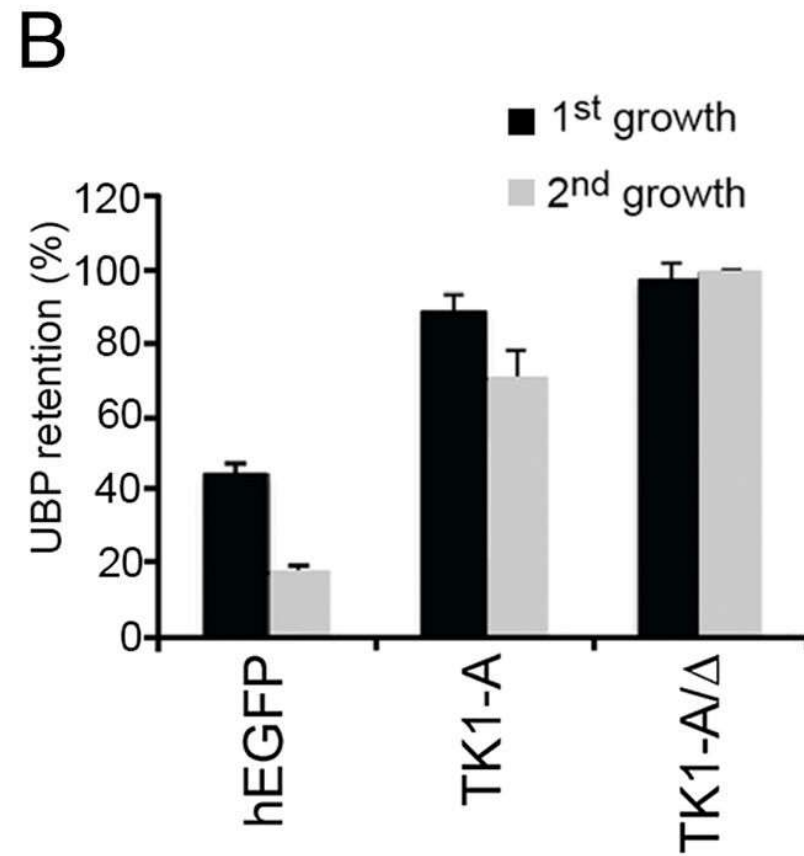
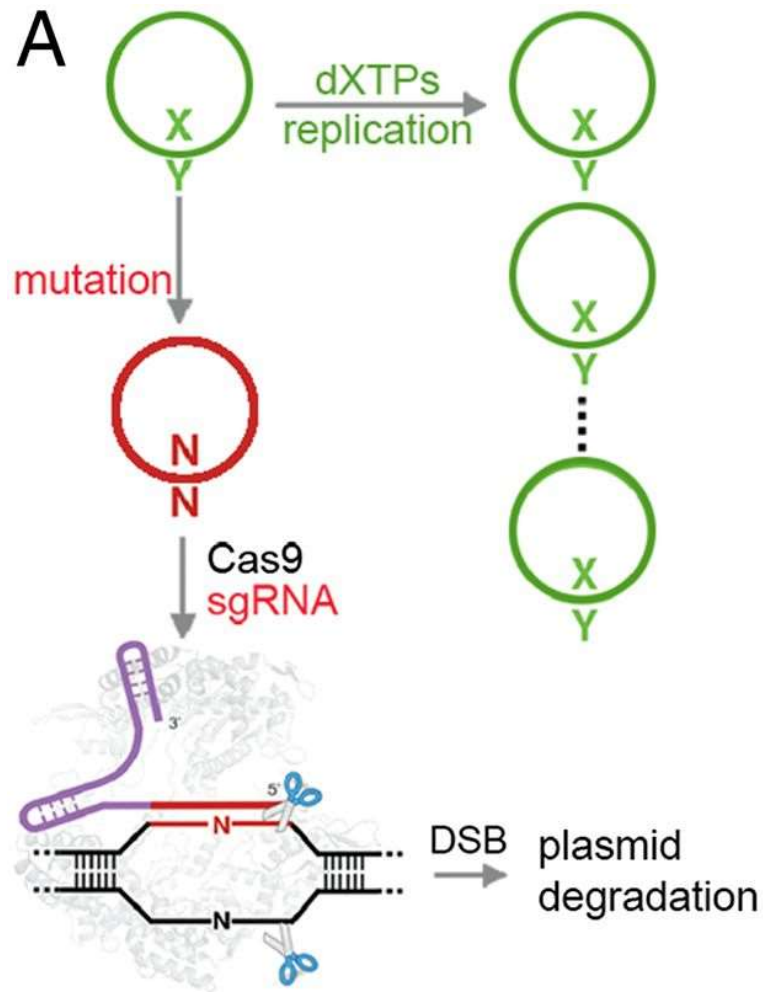
Romesberg, Floyd E. *et al.* *PNAS* **2017**, *114*, 1317-1322

A semi-synthetic organism with an expanded genetic alphabet



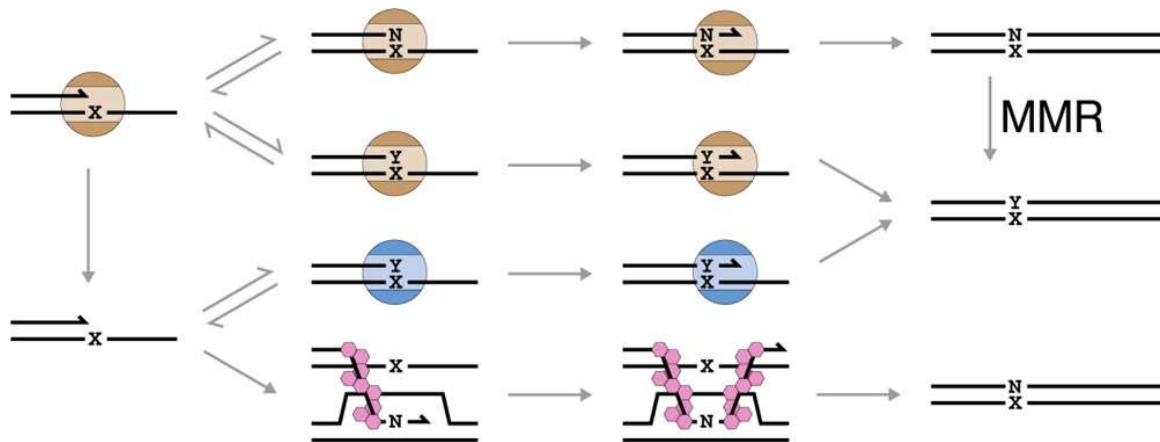
Romesberg, Floyd E. *et al.* *PNAS* 2017, 114, 1317-1322

A semi-synthetic organism with an expanded genetic alphabet



Romesberg, Floyd E. *et al.* *PNAS* **2017**, *114*, 1317-1322

Reprogramming the replisome of a semi-synthetic organism

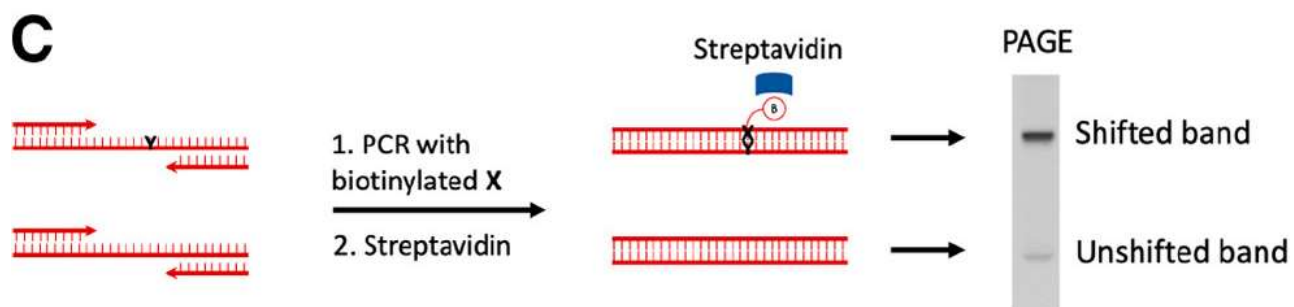
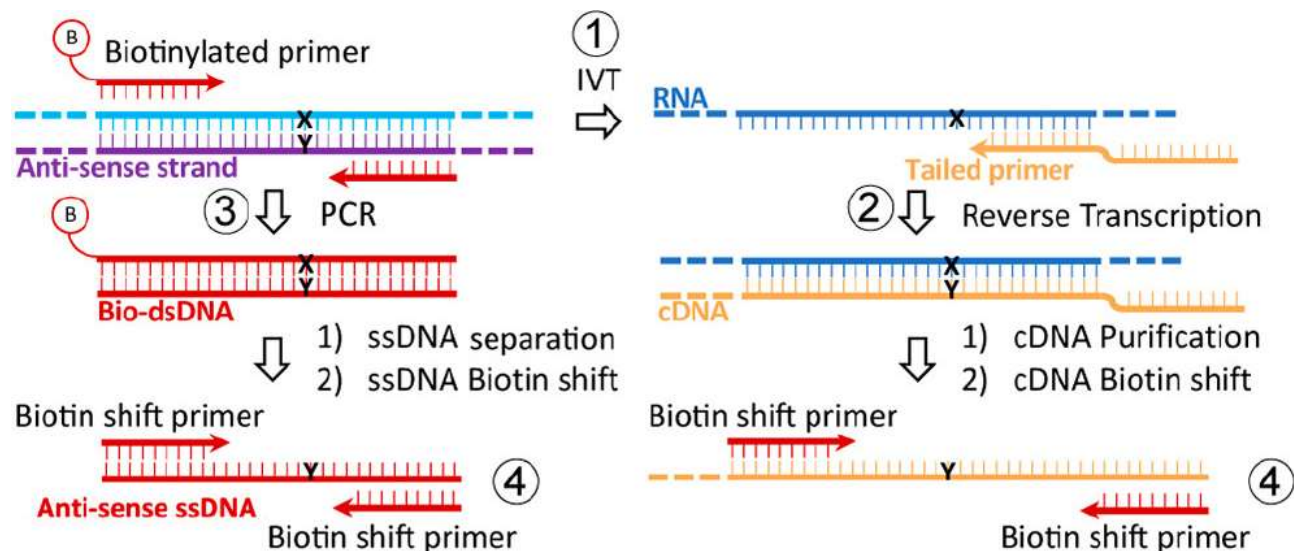
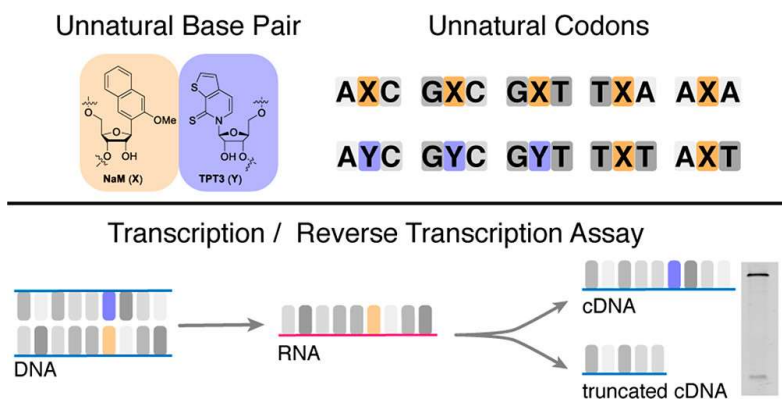


Proposed mechanism of UBP replication.
UBP retention is mediated by the activities of Pol III (tan), Pol II (blue), and MMR. UBP loss is mediated by polymerase replication errors or RecA (pink)-mediated RER.

UBPs are not well retained in all sequences, limiting the information that can be encoded, and are invariably lost upon extended growth. The contributions of the *E. coli* DNA replication and repair machinery to the propagation of DNA containing dNaM-dTPT3 have been explored and showed that replication by DNA polymerase III, supplemented with the activity of polymerase II and methyl-directed mismatch repair contribute to retention of the UBP and that recombinational repair of stalled forks is responsible for the majority of its loss.

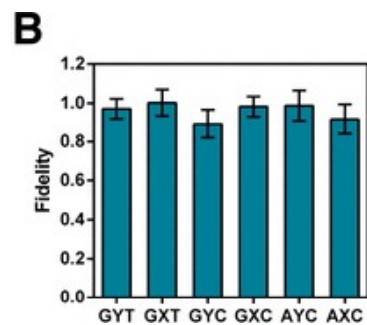
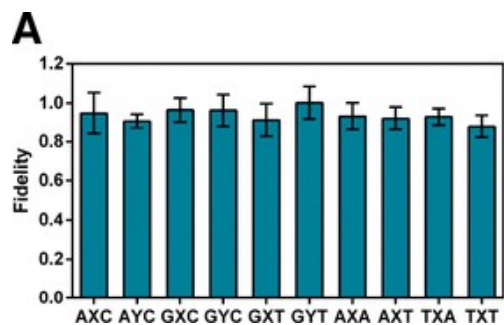
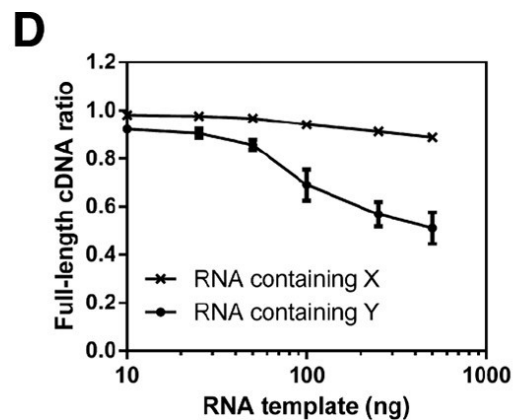
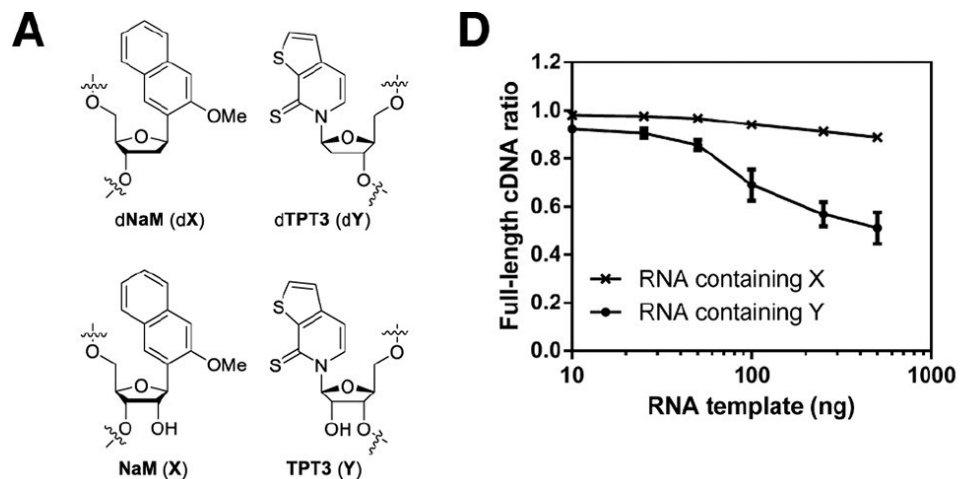
M. P. Ledbetter, R. J. Karadeema, and F. E. Romesberg *J. Am. Chem. Soc.* **2018**, *140*, 2, 758-765

Transcription and reverse transcription in vitro and in SSO

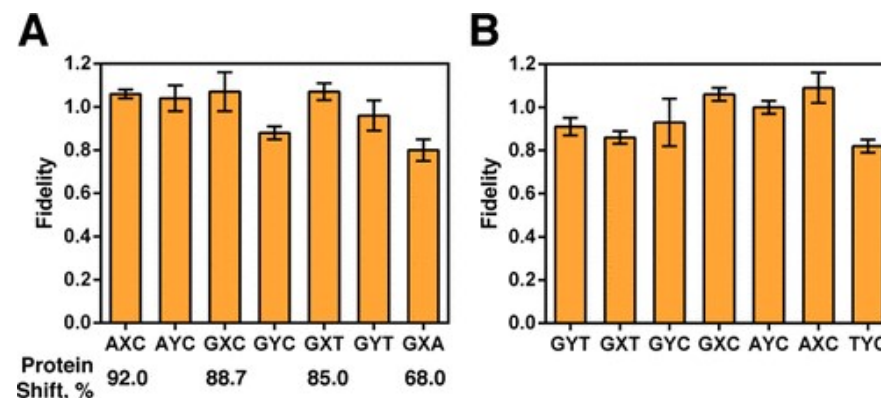


A. X.-Z. Zhou, X. Dong, F. Romesberg,
J. Am. Chem. Soc., **2020**, *142*, 19029-19032

Transcription and reverse transcription in vitro and in SSO



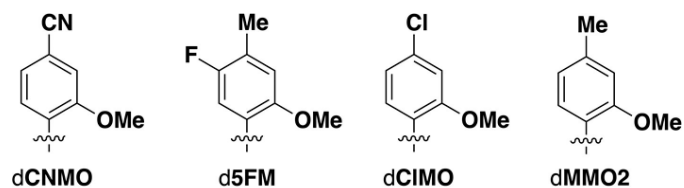
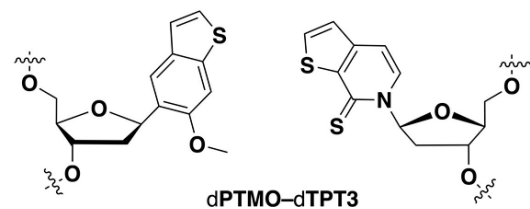
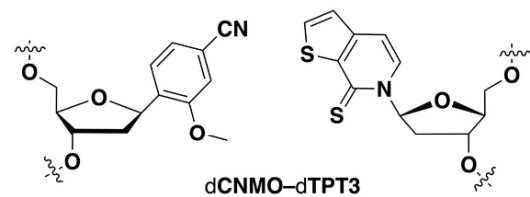
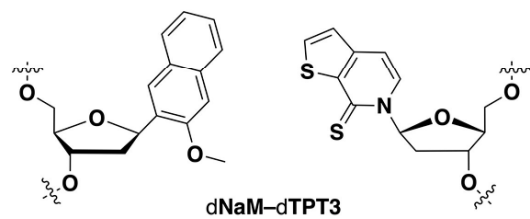
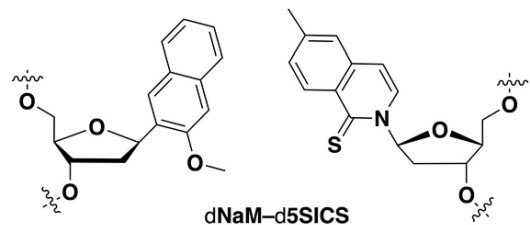
Transcription fidelity measured by T-RT assay of (A) mRNA and (B) tRNA made by *in vitro* transcription using T7 RNA polymerase.



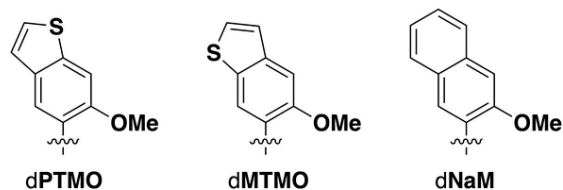
Transcription fidelity measured by T-RT assay of (A) mRNA and (B) tRNA extracted from SSO *in vivo* translation experiments

A. X.-Z. Zhou, X. Dong, F. Romesberg, *J. Am. Chem. Soc.*, **2020**, *142*, 19029-19032

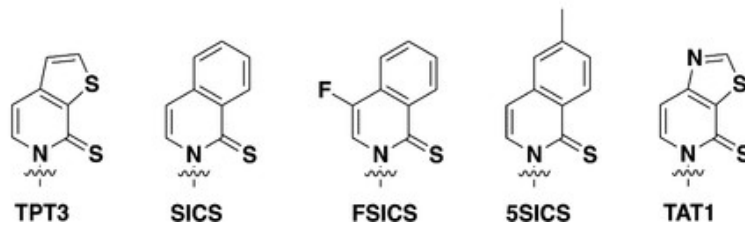
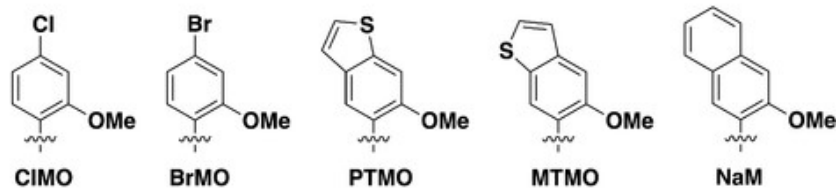
Expanded genetic alphabet - 2019



dXTP analogues



XTP analogues



YTP analogues

Romesberg, Floyd E. *et al.*

J. Am. Chem. Soc. **2019**, *141*, 27, 10644–10653

Unnatural nucleobases - overview

