

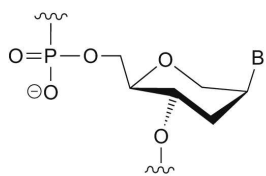
CHAPTER 1



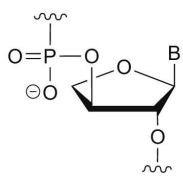
OLIGONUCLEOTIDES

Part 3 – noncanonical backbone – Xeno Nucleic Acids

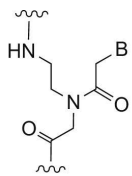
XNA – Xeno Nucleic Acids



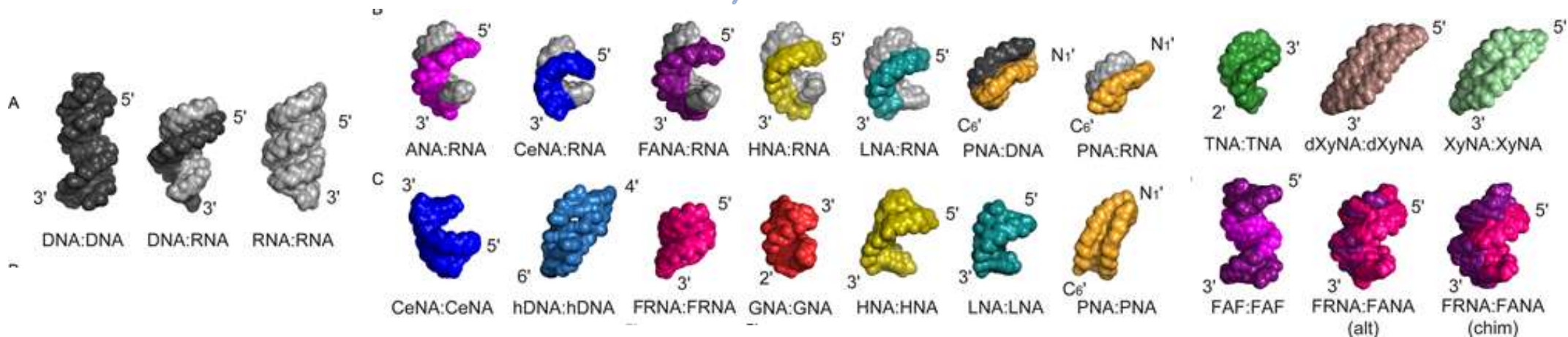
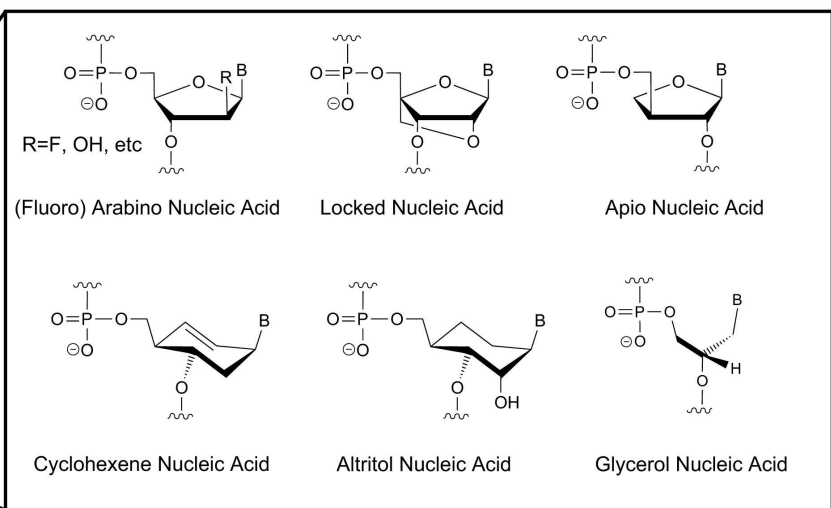
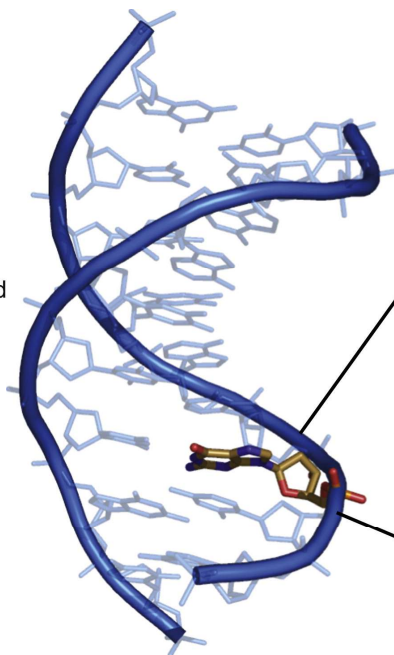
Hexitol Nucleic Acid (HNA)



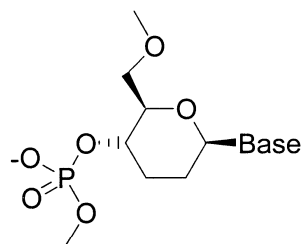
Threose Nucleic Acid (TNA)



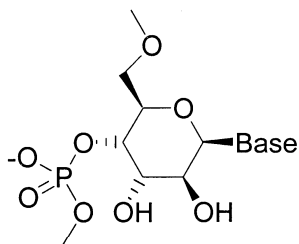
Peptide Nucleic Acid (PNA)



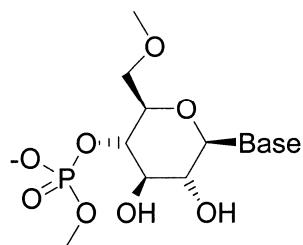
Overview of XNA



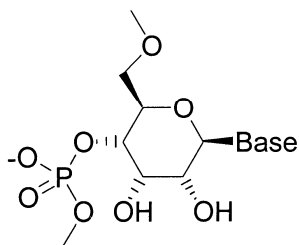
Homo-DNA
 β -D, 4' \rightarrow 6'



Altopyranosyl-NA
 β -D, 4' \rightarrow 6'

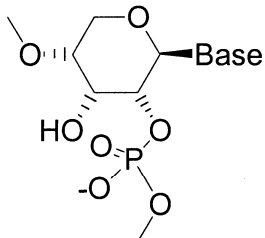


Glucopyranosyl-NA
 β -D, 4' \rightarrow 6'

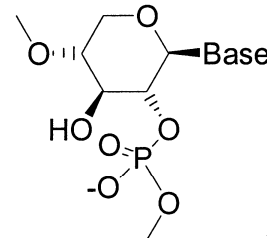


Allopyranosyl-NA
 β -D, 4' \rightarrow 6'

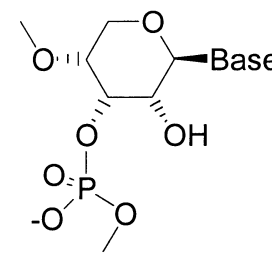
The 2' \rightarrow 4' linked pentopyranosyl family



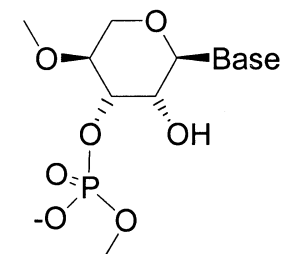
β -D-Ribopyranosyl-NA
(pRNA)



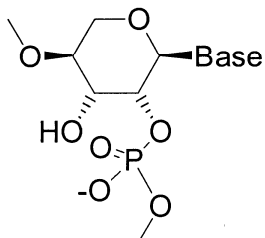
β -D-Xylopyranosyl-NA



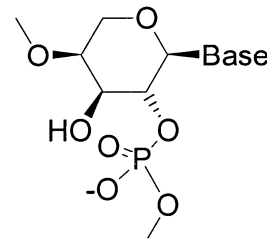
β -D-Ribopyranosyl-NA
3' \rightarrow 4'



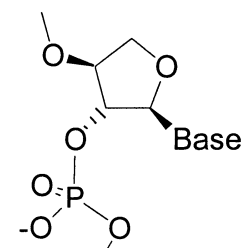
α -L-Lyxopyranosyl-NA
3' \rightarrow 4'



α -L-Lyxopyranosyl-NA



α -L-Arabinopyranosyl-NA

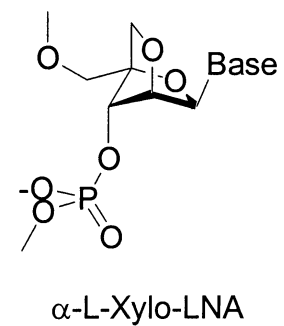
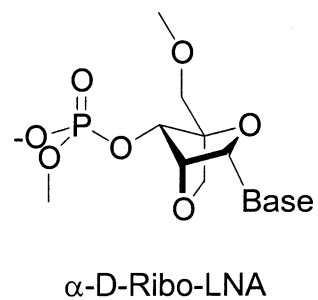
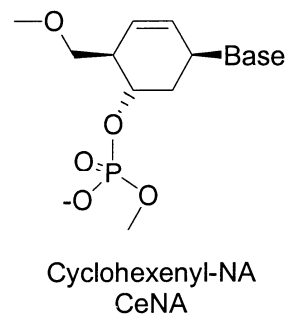
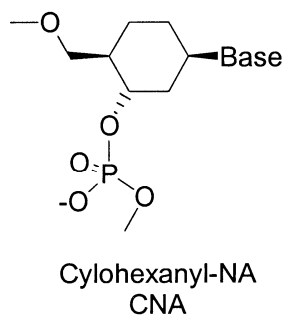
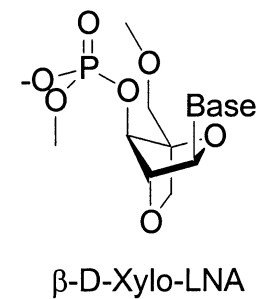
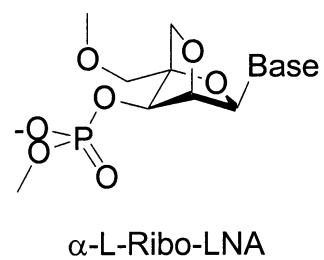
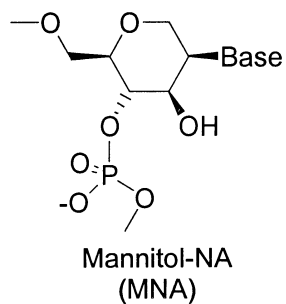
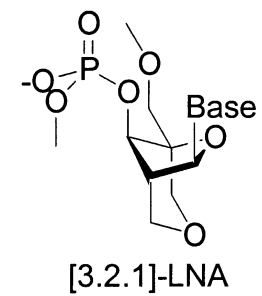
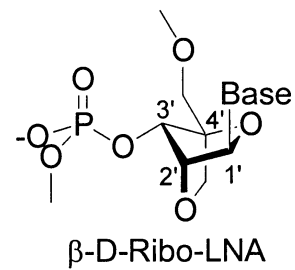
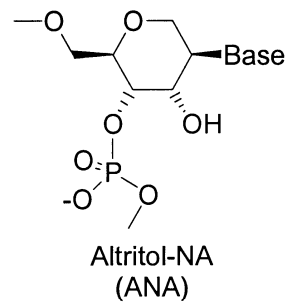
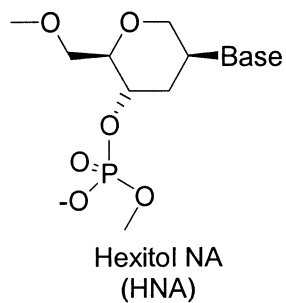


α -L-Threofuranosyl-NA
TNA

J. Hunziker, H. J. Roth, M. Bohringer, A. Giger, U. Diederichsen, M. Gobel, R. Krishnan, B. Jaun, C. Leumann and A. Eschenmoser, *Helv. Chim. Acta*, **1993**, *76*, 259–352

Review on the oligonucleotide modifications:
A. Eschenmoser *Angew. Chem., Int. Ed.* **2011**, *50*, 12412–12472
C. J. Leumann, *Bioorg. Med. Chem.*, **2002**, *10*, 841–854

Overview of XNA



XNA – Xeno Nucleic Acids

XNA - synthetic alternative to DNA and RNA as information-storing biopolymers that differs in the sugar backbone.

- at least 6 XNAs can store and retrieve genetic information
- Ongoing research to create synthetic polymerases to transform XNA →

Xenobiology

- (XNA) as information carriers, expanded genetic code and, incorporation of non-proteinogenic amino acids into proteins
- the **origin of life**: *Primordial soup* → (XNA →) RNA → RNA(+DNA)+Proteins
- development of industrial production systems with novel capabilities (pathogen resistance, biopolymer engineering)
- „genetic firewall” – excludes the risk of contaminating currently existing organisms (horizontal gene transfer)

The **long-term goal** - a cell that stores its genetic information on XNA, with different base pairs, using non-canonical amino acids and an altered genetic code.

So far cells have been constructed that incorporate only one or two of these features

XNA – Xeno Nucleic Acids

XNA are not recognized by natural polymerases.

One of the major challenges is to find or create novel types of polymerases that will be able to replicate these new-to-nature constructs. The method of polymerase evolution and design successfully led to the storage and recovery of genetic information (of less than 100bp length) from six alternative genetic polymers based on simple nucleic acid architectures not found in nature.

XNA aptamers, which bind their targets with high affinity and specificity, were also selected, demonstrating that beyond *heredity*, specific XNAs have the capacity for *Darwinian evolution* and *folding into defined structures*.

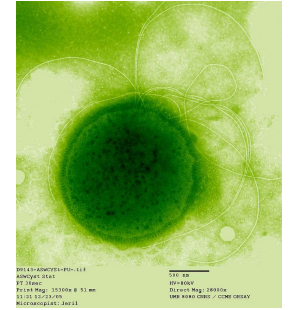
Thus, heredity and evolution, two hallmarks of life, are not limited to DNA and RNA but are likely to be emergent properties of polymers capable of information storage.

Engineering XNA polymerases

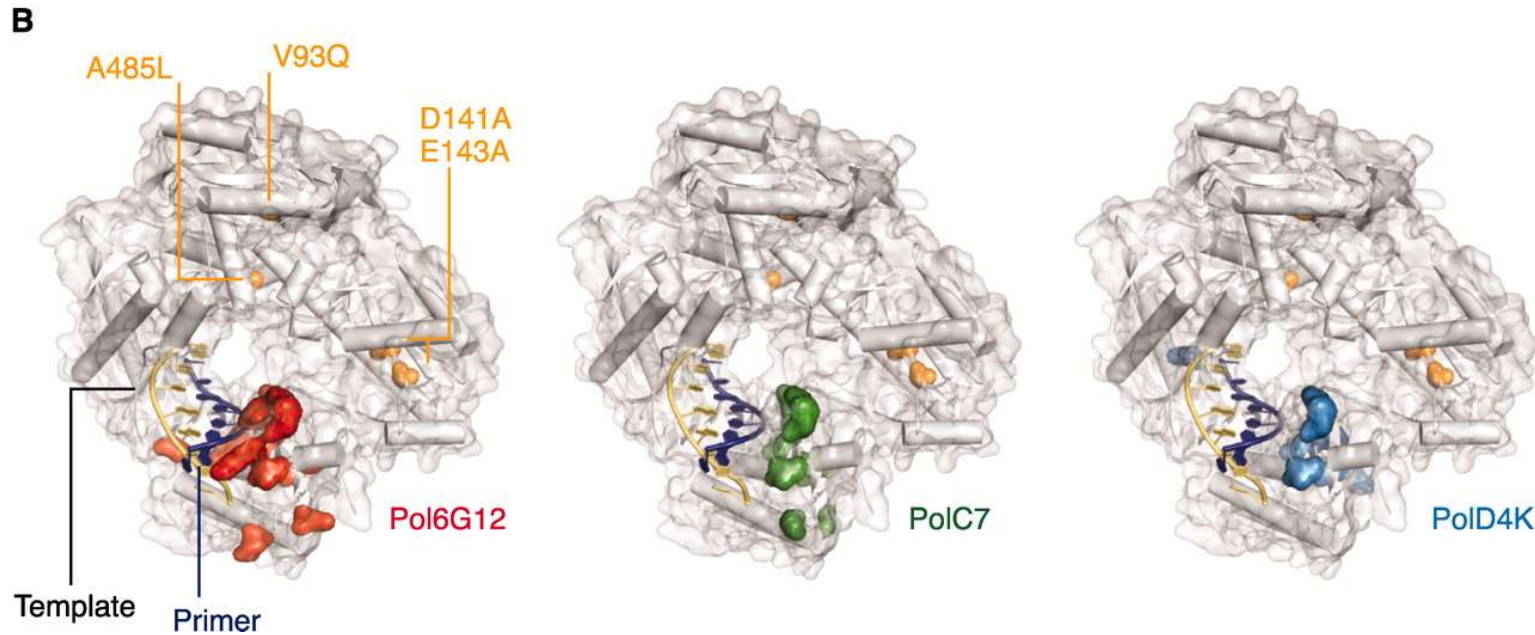
TgoT, a variant of the replicative polymerase of *Thermococcus gorgonarius*

A

	402	404	588	590	608	611	653	682	703	710	729	731
TgoT	YLD	..	FVT	..	LEIV	..	YEVPPPEKLVIIYEQITRDLKDYKATGPHVAV	..	VLKGS	GRI	..	AEY
Pol6G12	YLD	..	F AT	..	L KMV	..	YEVPPPEQLVIY QPITKQL HDY RARGPHVSV	..	V PKGS	GRI	..	AGY
PolC7	YLD	..	FVT	..	LEIV	..	YQVPP QQLAIYQPITRALQ DYK AKGPHVAV	..	VLKGS	GKI	..	AEY
PolD4K	Y PD	..	FVT	..	LEIV	..	YEVPT QHLVIHKQITRALN DYK AI GPHVAV	..	VLKGS	GRI	..	AEY



Thermococcus gorgonarius
(Angels Tapias)



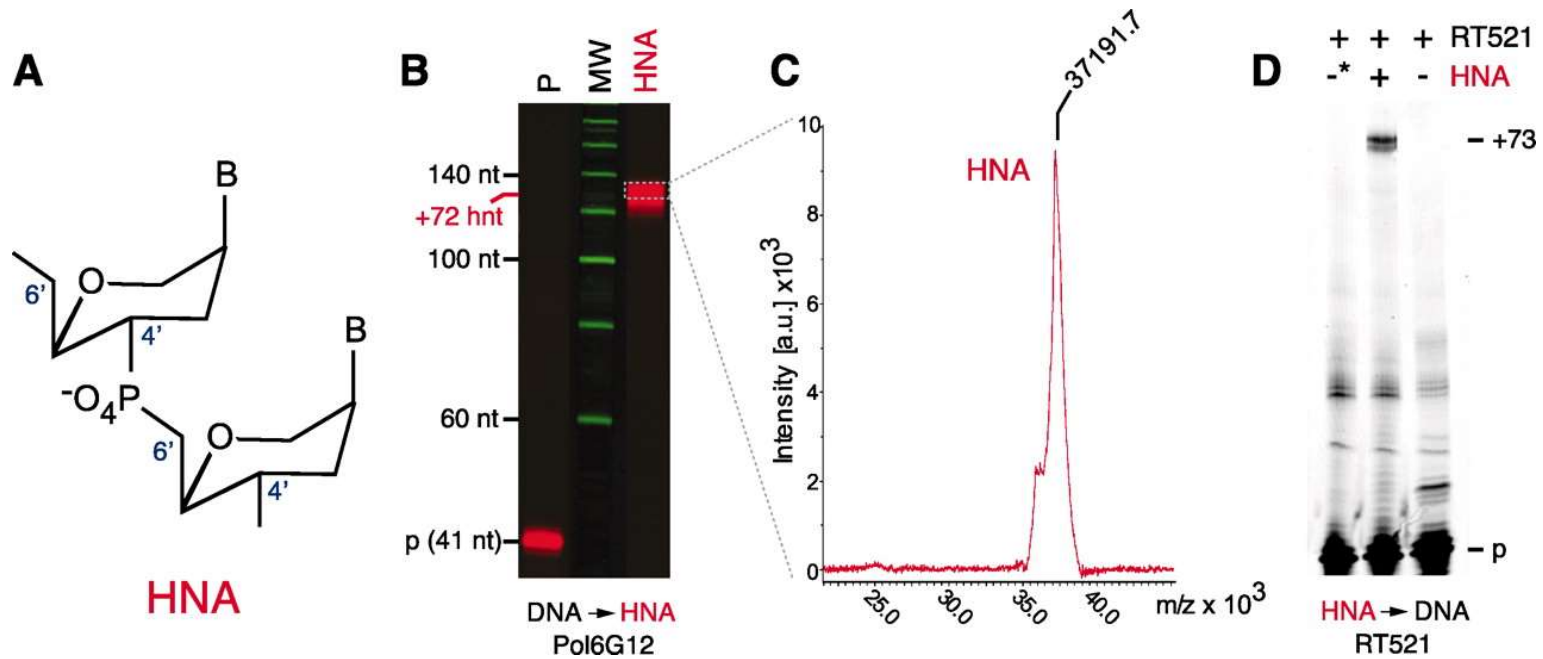
(A) Sequence alignments showing mutations from wtTgo in polymerases Pol6G12 (red), PolC7 (green), and PolD4K (blue).

(B) Mutations are mapped on the structure of Pfu (PDB: 4AIL).

Yellow - template; dark blue - primer; orange - mutations present in the parent polymerase TgoT

P. Herdewijn, P. Holliger, *et al. Science* **2012**, *336*, 341-344

HNA synthesis

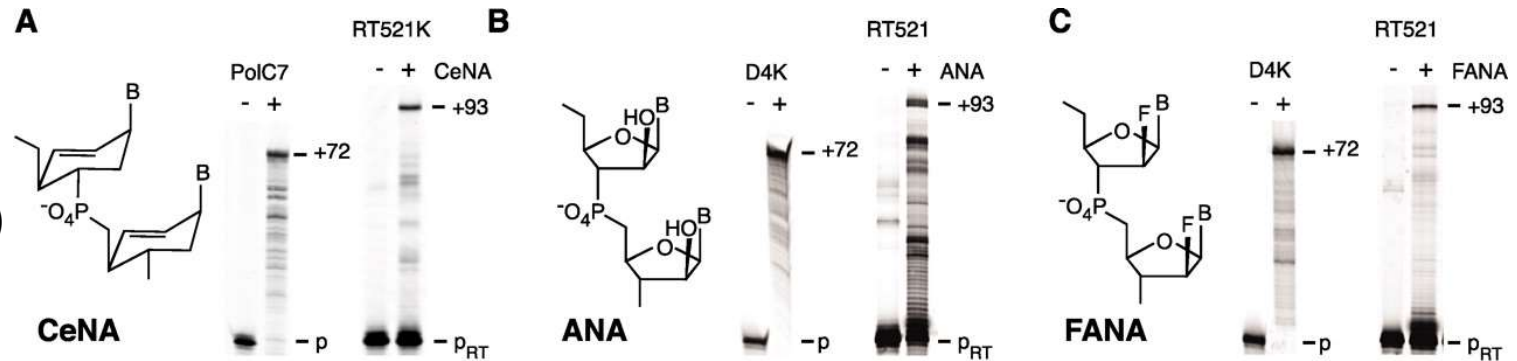


Pol6G12 extends the primer (p) incorporating 72 hNTPs against template T1 to generate a full-length hybrid molecule with a 37,215-dalton expected molecular mass.

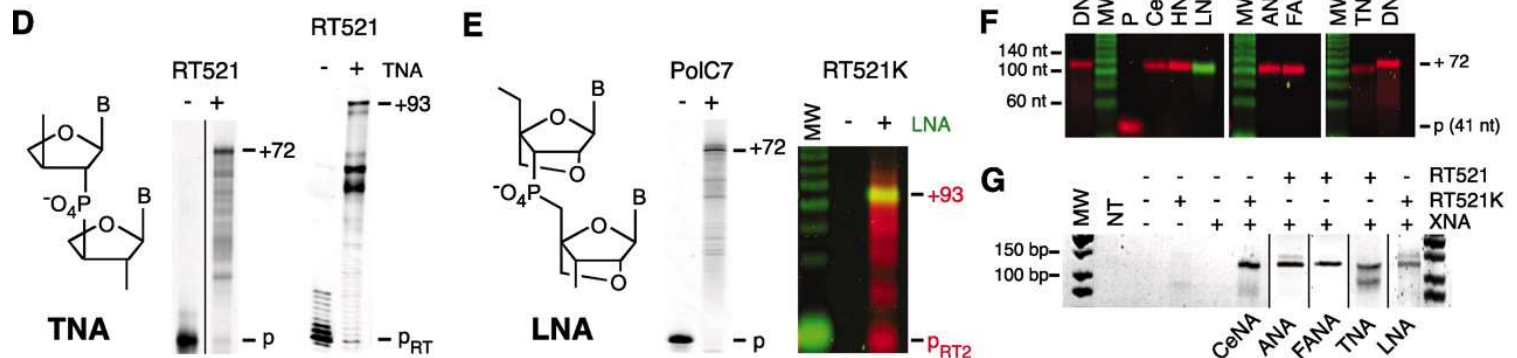
HNA reverse transcription (DNA synthesis from an HNA template). Polymerase-synthesized HNA (from template YtHNA4) is used as template by RT521 for HNA-RT

XNA genetic polymers.

Structures and PAGE of synthesis (+72 xnt), and reverse transcription (+93 nt)



AAGE of XNA and DNA polymers of identical sequence

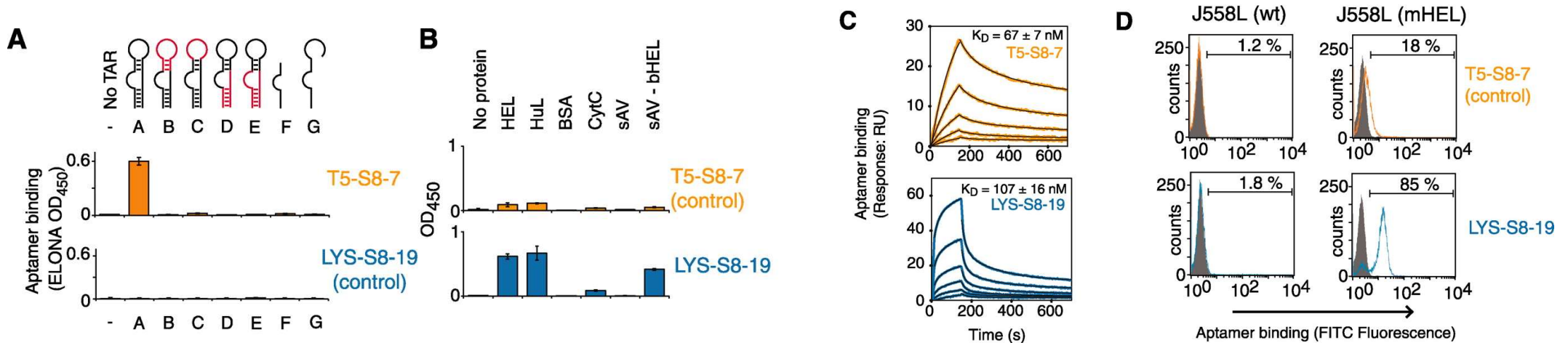


(E) PAGE of LNA synthesis [primer (41 nt) + 72 Int] and LNA-RT (red). LNA synthesis (green) migrates at its expected size (113 nt) and comigrates with reverse transcribed DNA (red) synthesized from primer PRT2 (20 nt).

XNART-polymerase chain reaction. Amplification products of expected size (133 base pairs) are obtained only with both XNA forward synthesis and RT (RT521 or RT521K)

P. Herdewijn, P. Holliger, *et al. Science* **2012**, *336*, 341-344

HNA aptamers



Characterization of HNA aptamers. Anti-TAR aptamer T5-S8-7 and anti-HEL aptamer LYS-S8-19.

(A and B) Aptamer binding specificity against TAR variants (red, sequence randomized but with base-pairing patterns maintained) and different protein antigens (human lysozyme, HuL; cytochrome C, CytC; streptavidin, sAV; biotinylated-HEL bound to streptavidin, sAV-bHEL). OD, optical density.

(C) Affinity measurements of aptamer binding by SPR. RU, response units.

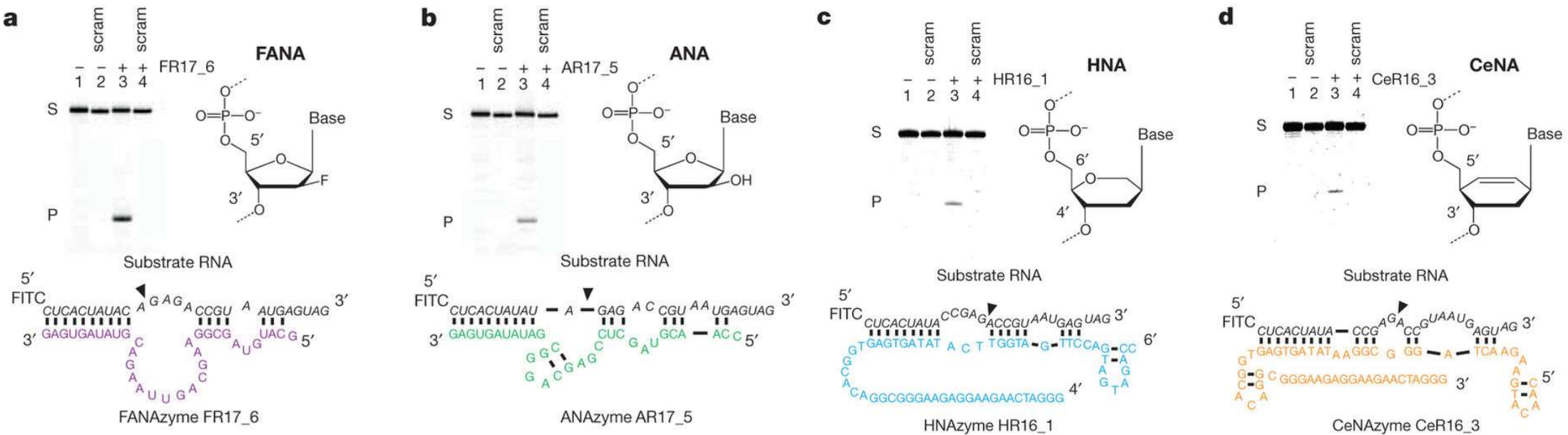
(D) FACS analysis of fluorescein isothiocyanate (FITC)-labeled aptamers binding to plasmacytoma line J558L with and without expression of membrane-bound HEL (mHEL). wt, wild type.

XNA – Xeno Nucleic Acids

XNA – complementarity to DNA, also used as genetic catalysts.

FANA, HNA, CeNA and ANA - cleave RNA (**XNAzymes**).

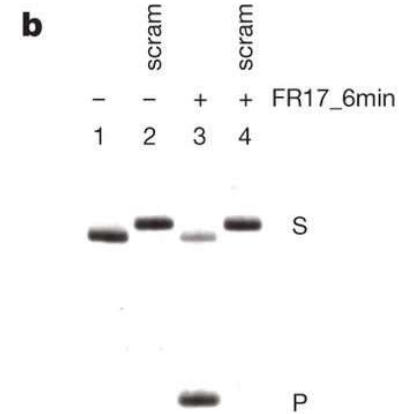
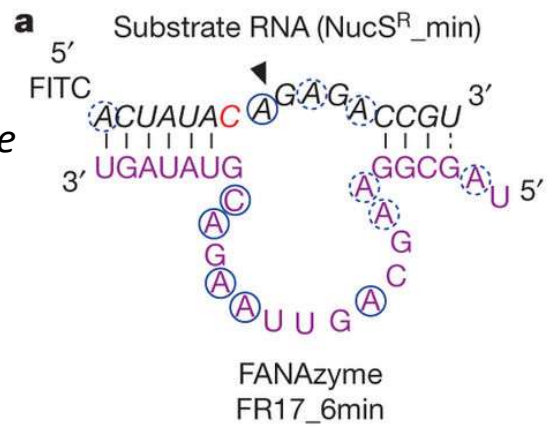
FANA XNAzymes can also ligate DNA, RNA and XNA substrates.



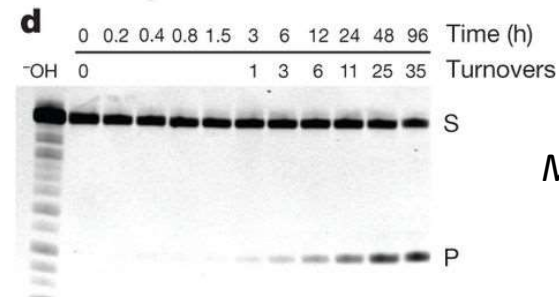
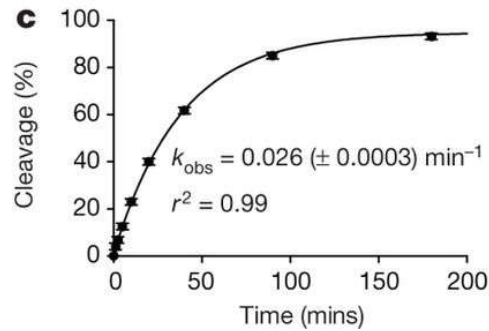
P. Herdewijn, P. Holliger, *et al.* *Nature* **2015**, *518*, 427-430

Chemical synthesis yields an active RNA endonuclease XNAzyme

Secondary FANAzyme structure



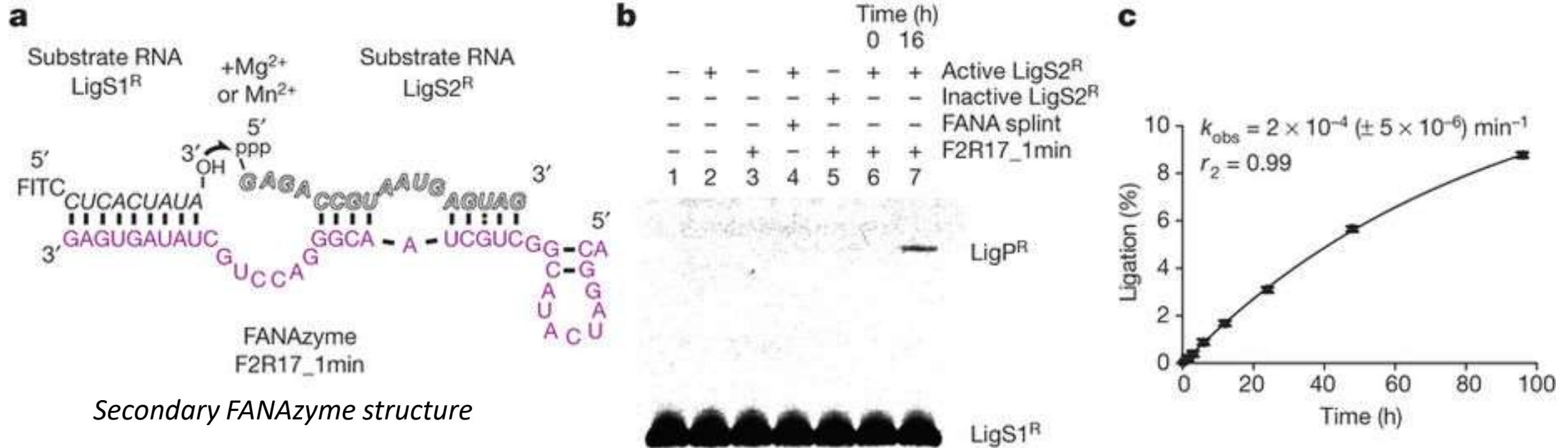
l. 1 and 3 - matching RNA
l. 2 and 4- scrambled RNA



Multiple turnovers

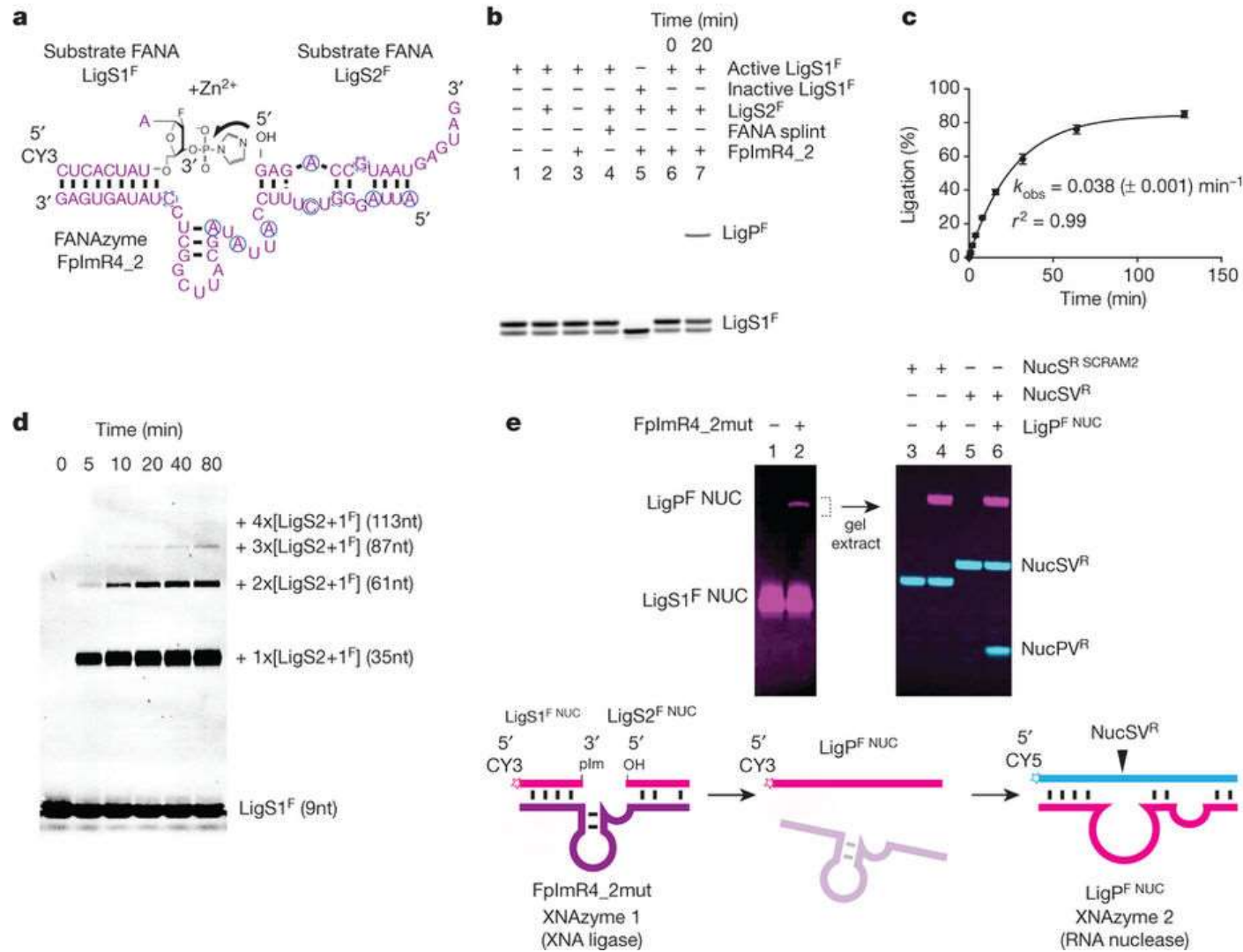
An RNA ligase XNAzyme (FANA)

FANA XNAzymes can also ligate DNA, RNA and XNA substrates.



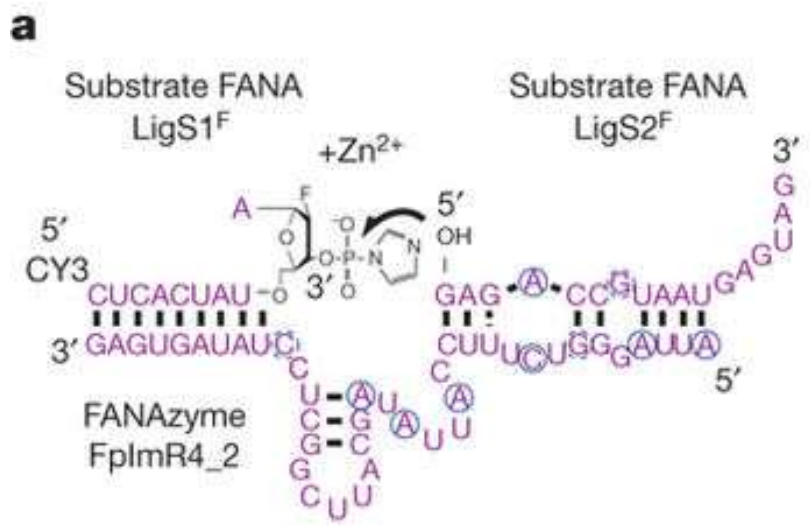
Pre-steady state trimolecular reaction rate (k_{obs}) at 25 °C ($n = 3$; error bars, s.d.).

XNA-XNA ligase XNAzyme (FANA): catalysis without natural nucleic acids



P. Herdewijn, P. Holliger, *et al.* *Nature* **2015**, *518*, 427-430

XNA–XNA ligase XNAzyme (FANA): catalysis without natural nucleic acids

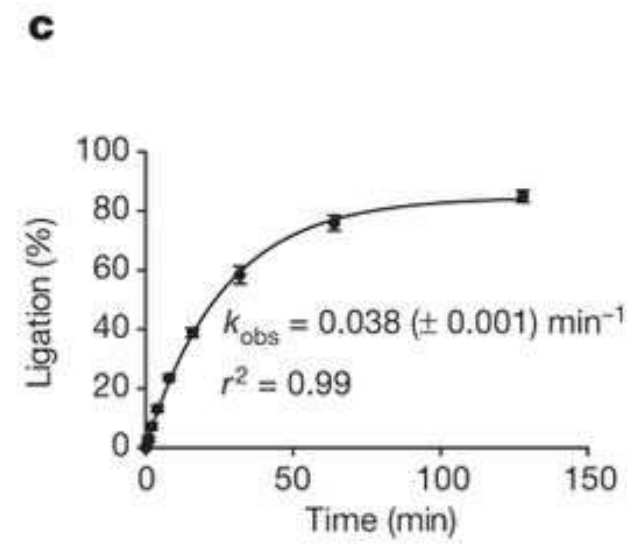


b

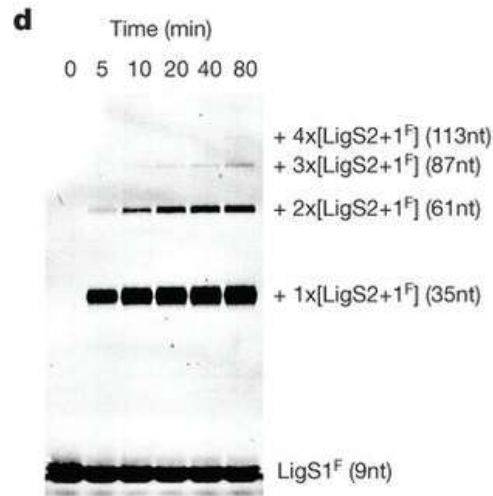
		Time (min)					
		0	20				
+	+	+	+	-	+	+	Active LigS1 ^F
-	-	-	-	+	-	-	Inactive LigS1 ^F
-	+	-	+	+	+	+	LigS2 ^F
-	-	-	+	-	-	-	FANA splint
-	-	+	-	+	+	+	FplmR4_2
1	2	3	4	5	6	7	

— LigP^F

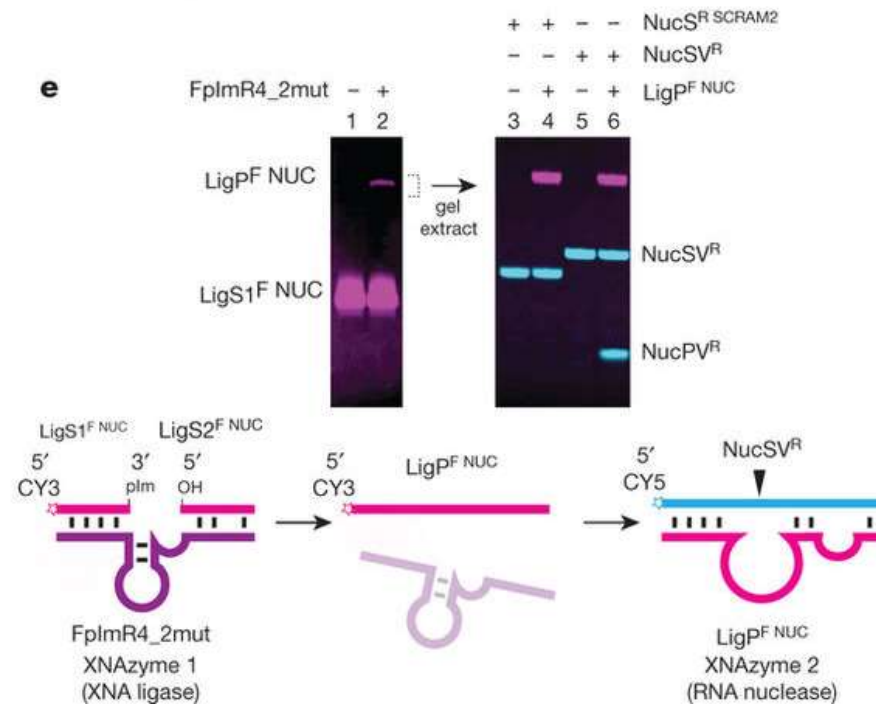
LigS1^F



XNA–XNA ligase XNAzyme (FANA): catalysis without natural nucleic acids



FplmR4_2-catalysed oligomerization of XNA (FANA) substrates



XNAzyme-catalysed assembly of an active XNAzyme. A variant XNA ligase (FplmR4_2mut) catalyzes ligation (lane 2) of FANA substrates LigS1^F NUC and LigS2^F NUC. The product (LigPF NUC) is a variant of XNAzyme FR17_6 min (Fig. 2), which cleaves RNA substrate NucSV^R (lanes 5 and 6), but not scrambled RNA (NucS^R SCRAM2)(lanes 3 and 4).

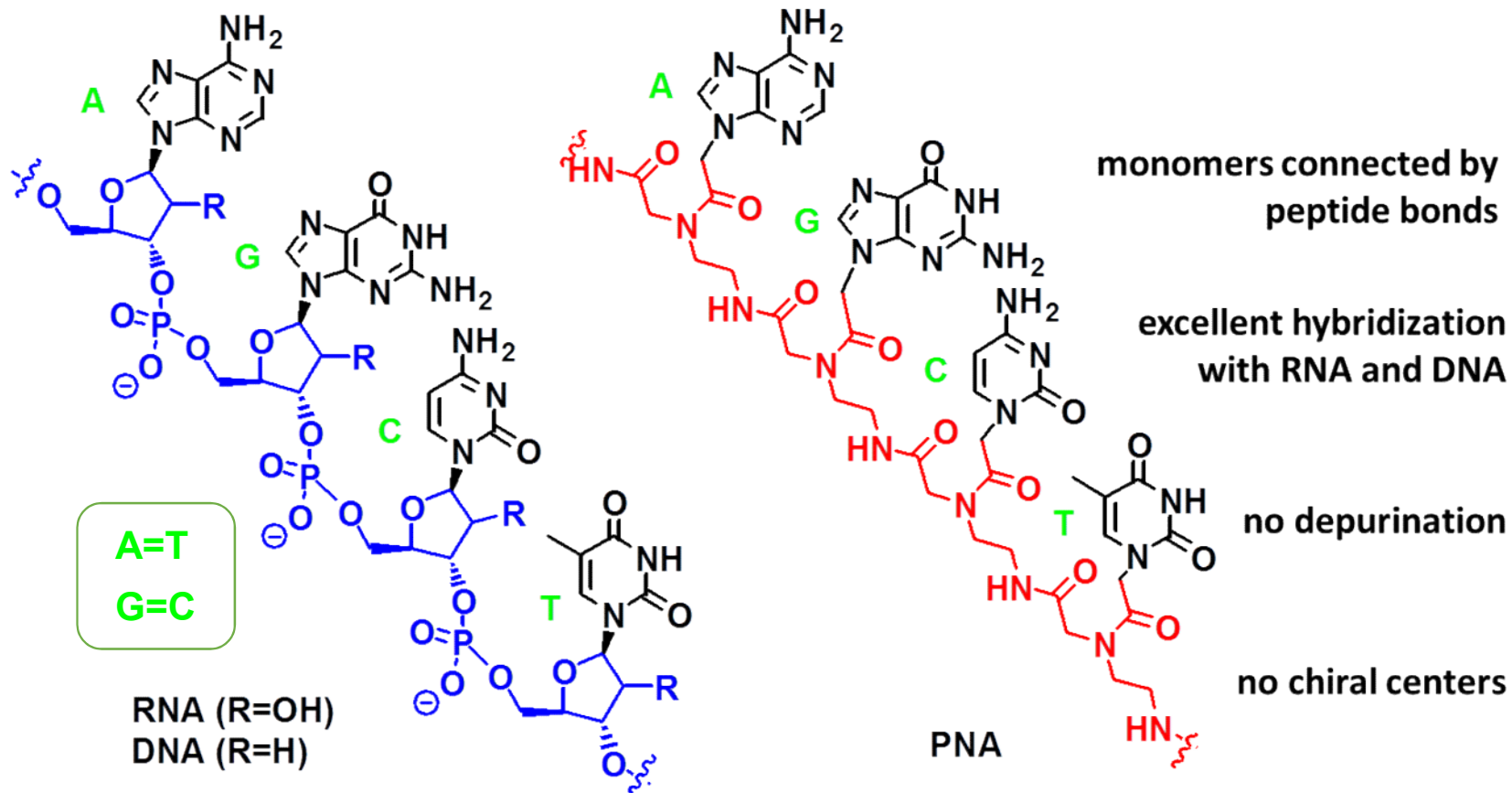
Table 1 Polymerase-mediated synthesis of XNAs

Pol Family	Polymerase	Novel Activity				
Pol A	Taq Tth Pol θ	2'F RNA 2'OMe RNA 2'-azido RNA	Pol X	(D-aa) ASFV pol	L-DNA L-RNA	
Pol B	Tgo KOD 9 ^o N Pfu phi29	CeNA LNA phNA HNA FANA CyDNA 2'F RNA ANA TNA 2'azido RNA tPhoNA	RNAP	T7 RNAP Syn5	2'F RNA 2'OMe RNA Ds-Pa UBP	
Pol Y	(D-aa) Dpo4	L-DNA	RT	HIV-RT	pyDAD-puADA UBP	

Table 2 FDA-approved nucleic acid therapeutics as of February 2020

Drug name (trade name)	Target	Modifications	Mechanism	Indication	Approval
Fomivirsen (Vitravene)	mRNA of the CMV immediate-early (IE)-2 protein	PS	ASO (translation blocking)	Cytomegalovirus retinitis (CMV)	FDA (1998) and EMA (1999) approved. FDA (2001) and EMA (2002) withdrawn
Pegaptanib (Macugen)	Vascular endothelial growth factor (VEGF165)	2'F, 2'OMe, PEG conjugate	Aptamer	Neovascular (wet) age-related macular degeneration	FDA approved (2004)
Mipomersen (Kynamro)	Apolipoprotein B-100 mRNA	2'MOE, PS, 5mC	ASO (RNase H)	Homozygous familial hypercholesterolemia	FDA approved (2013)
Eteplirsen (Exondys 51)	Exon 51 in dystrophin mRNA	PMO	ASO (splicing modulation)	Duchenne muscular dystrophy	FDA approved (2016)
Nusinersen (Spinraza)	Survival of motor neuron 2 (SMN2) pre-mRNA	2'MOE, PS, 5mC	ASO (splicing modulation)	Spinal muscular atrophy	FDA (2016) and EMA (2017) approved
Patisiran (Onpattro)	Transthyretin (TTR) mRNA	2'OMe	siRNA	Hereditary transthyretin-mediated amyloidosis	FDA and EMA approved (2018)
Inotersen (Tegsedi)	Transthyretin (TTR) mRNA	2'MOE, PS, 5mC	ASO (RNase H)	Hereditary transthyretin-mediated amyloidosis	FDA and EMA approved (2018)
Volanesorsen (Waylivra)	Apolipoprotein C ₃ (apo-CIII) mRNA	2'MOE, PS, 5mC	ASO (RNase H)	Familial chylomicronemia syndrome	EMA approved (2019)
Givosiran (Givlaari)	Aminolevulinatase synthase 1 (ALAS1) mRNA	PS, 2'F, 2'OMe, GalNAc conjugate	siRNA	Acute hepatic porphyria	FDA approved (2019)
Golodirsen (Vyondys 53)	Exon 53 in dystrophin mRNA	PMO	ASO (splicing modulation)	Duchenne muscular dystrophy	FDA approved (2019)

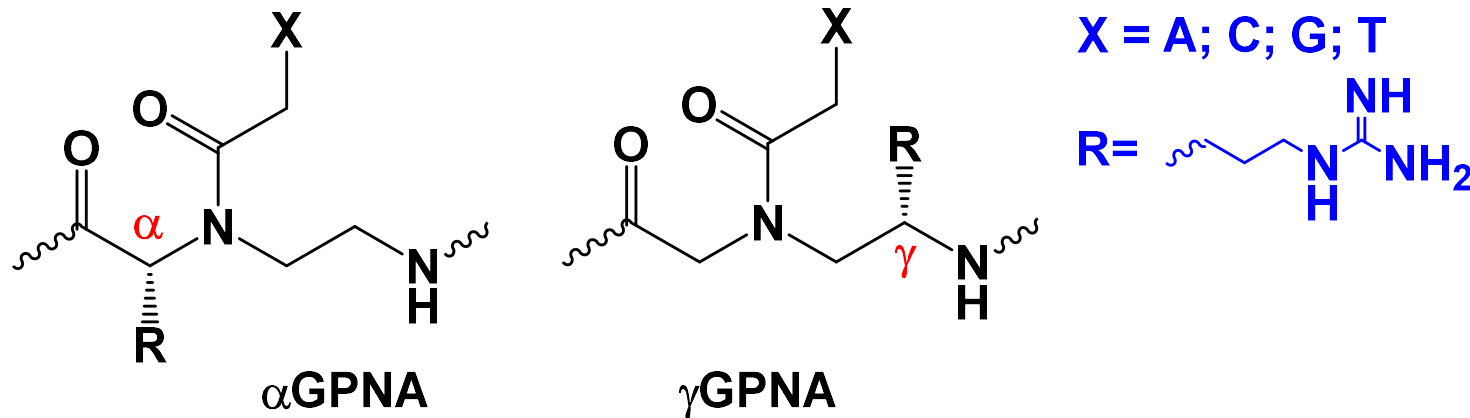
Peptidonucleic acids – functional DNA analogues



PNA – stable *ex vivo*, the backbone detected in cyanobacteria

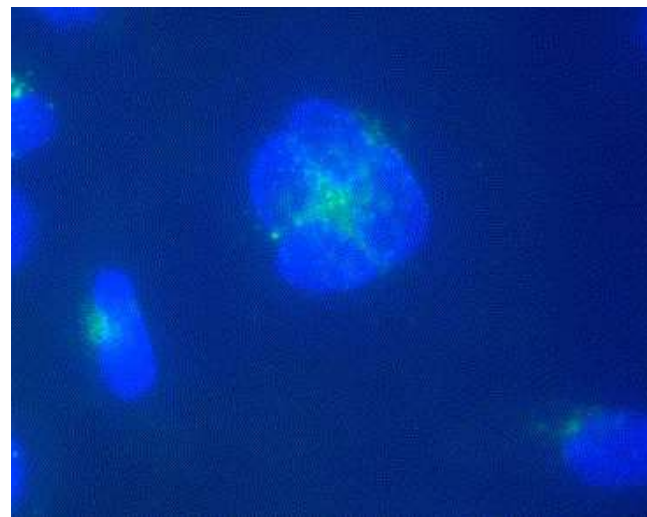
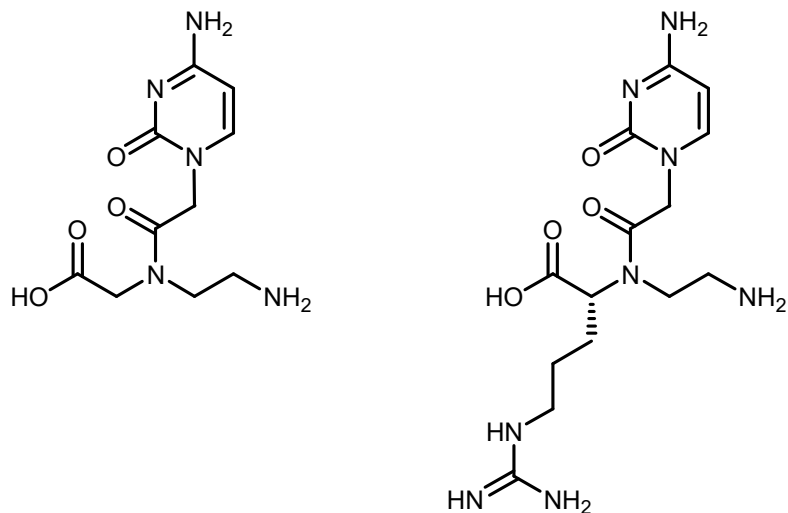
Applications: antigene, antisense agents; fluorescent DNA probes (FISH), anticancer, antiviral, antibacterial, antiparasitic agents; diagnostics, mol. biology

Structural modifications of the PNA - α GPNA, γ GPNA



- GPNA: Alkylguanidinium residues (Arg side chains)
- enhanced water solubility
- **cell permeability** (analogous to oligoarginine CPPs)
- α position \leftarrow *D*-arginine
- γ position \leftarrow *L*-arginine

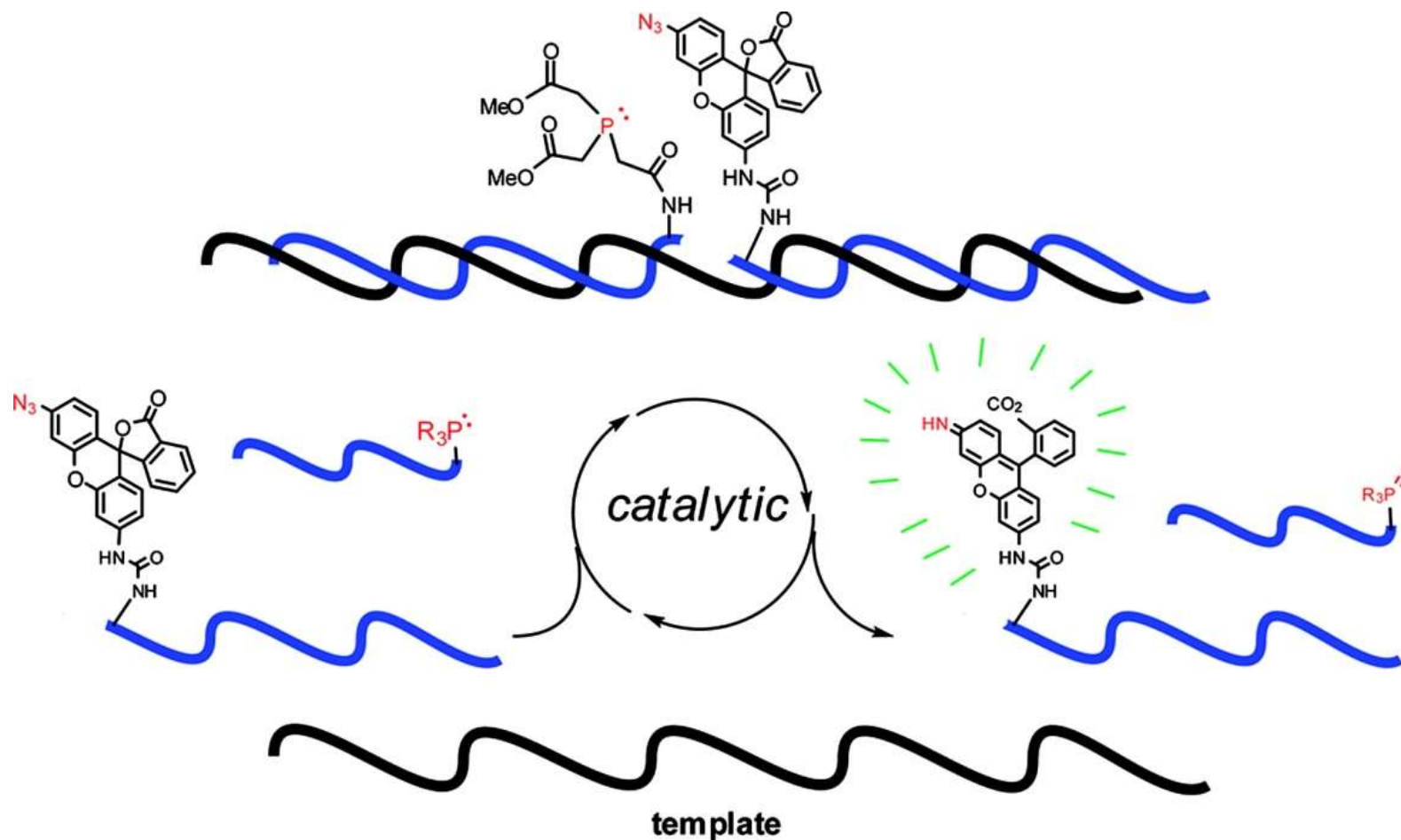
Cell-penetrating α GPNA



HeLa cells incubated with 1 μ M GPNA (FITC-^DCC^DAC^DCT^DCT^DGC^DCA^DAC^DGG^DGT-NH₂) for 16 h, Fixed, stained with DAPI. Nuclei (blue), GPNA (green).

P. Zhou, A. Dragulescu-Andrasi, B. Bhattacharya, H. O'Keefe, P. Vatta,
J. J. Hyldig-Nielsen and D. H. Ly *Bioorg. Med. Chem. Lett.* **2006**, *16*, 4931
A. Dragulescu-Andrasi, S. Rapireddy, G. He, B. Bhattacharya, J. J. Hyldig-Nielsen,
B. G. Zon, and D. H. Ly *J. Am. Chem. Soc.* **2006**, *128*, 16104

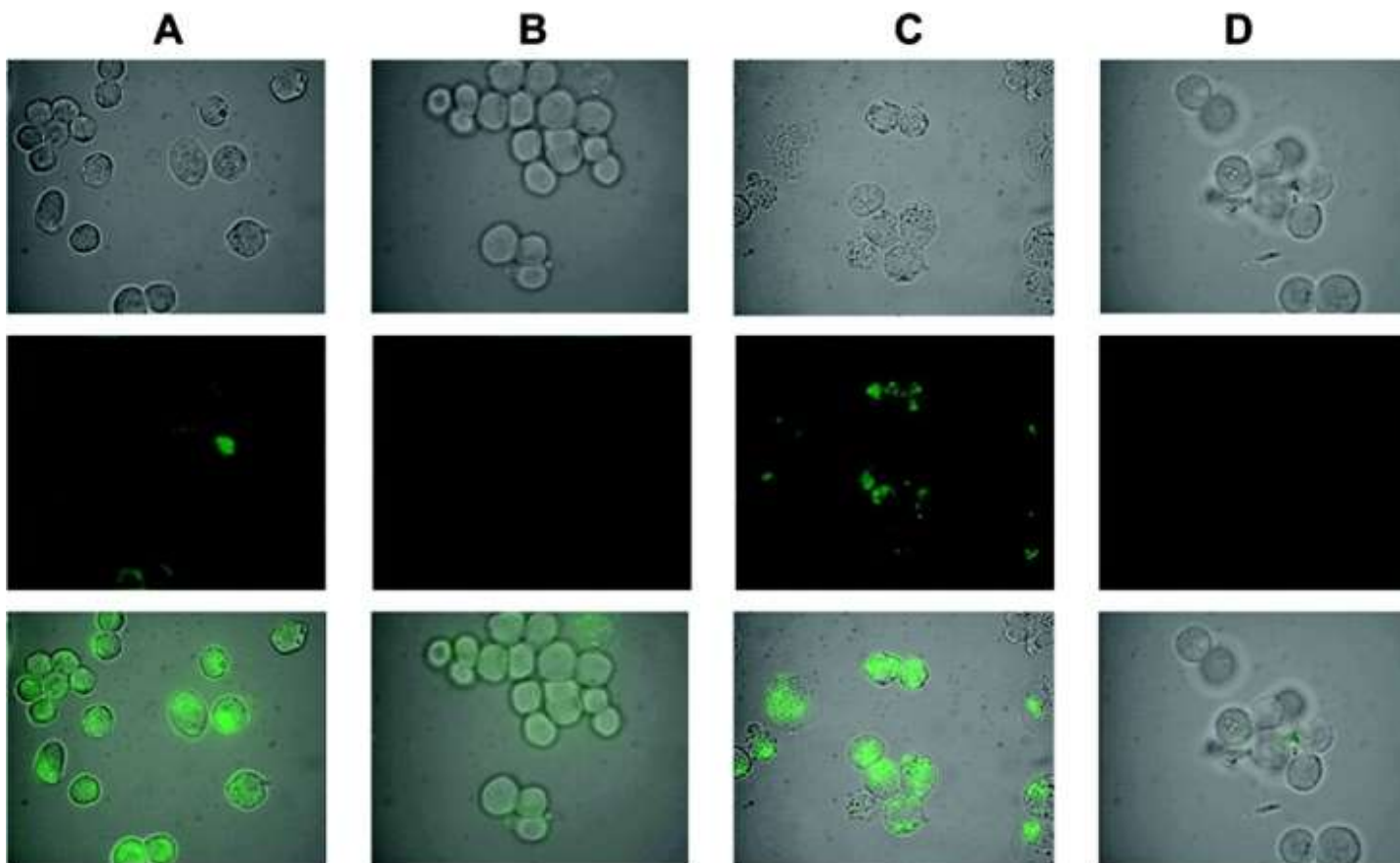
Cell-penetrating α GPNA for *in vivo* catalytic oligonucleotide sensing



Z. Pianowski, N. Winssinger *Chem. Comm.* **2007**, 37, 3820-3822
Z. Pianowski et al. *J. Am. Chem. Soc.* **2009**, 131, 6492-6497

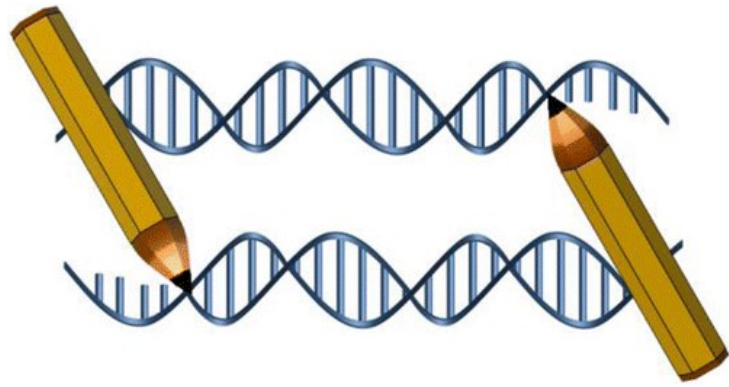
Cell-penetrating α GPNA for *in vivo* catalytic oligonucleotide sensing

Inside living cells

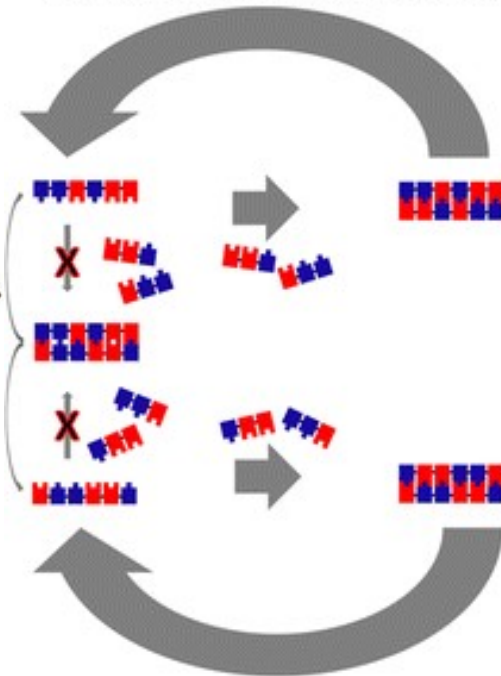


A, B – controls (+/-) **C** – matching PNA **D** – mismatched PNA

Abiotic self-replication

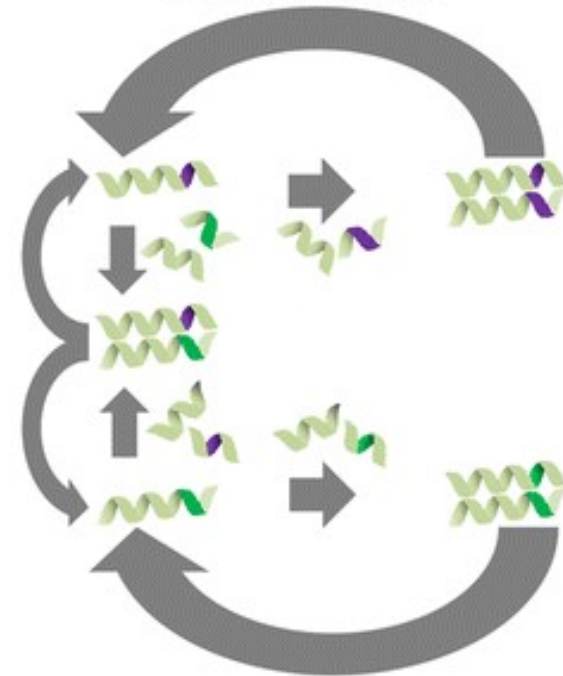


A. Darwinian/nucleic acid replicator



Cross-replication
disfavored

B. Peptide replicator

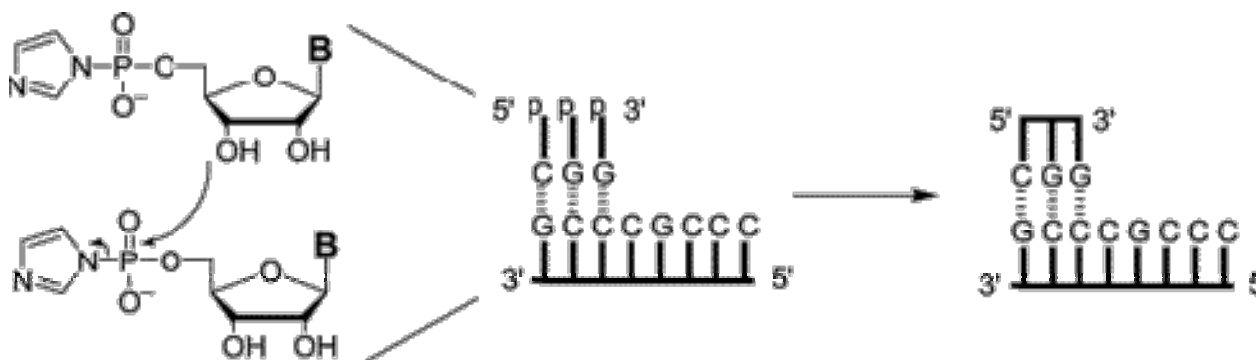
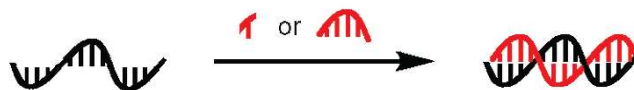


Cross-replication
allowed

(A) For nucleic acids replicators, templating is based on base pairing, so the formation of a mutant template is rare. Once formed, the mutant replicator forms a competing replication cycle. (B) For a peptide replicator, templating is less exact, so the formation of a mutant template is common. The mutant template can catalyze formation of mutant progeny or parental progeny, and the two species form a mutualistic network.

Meyer AJ, Ellefson JW, Ellington AD. *Acc Chem Res.* 2012 45(12):2097-2105.

Nonenzymatic templated nucleic acid synthesis – monomer/short oligomer



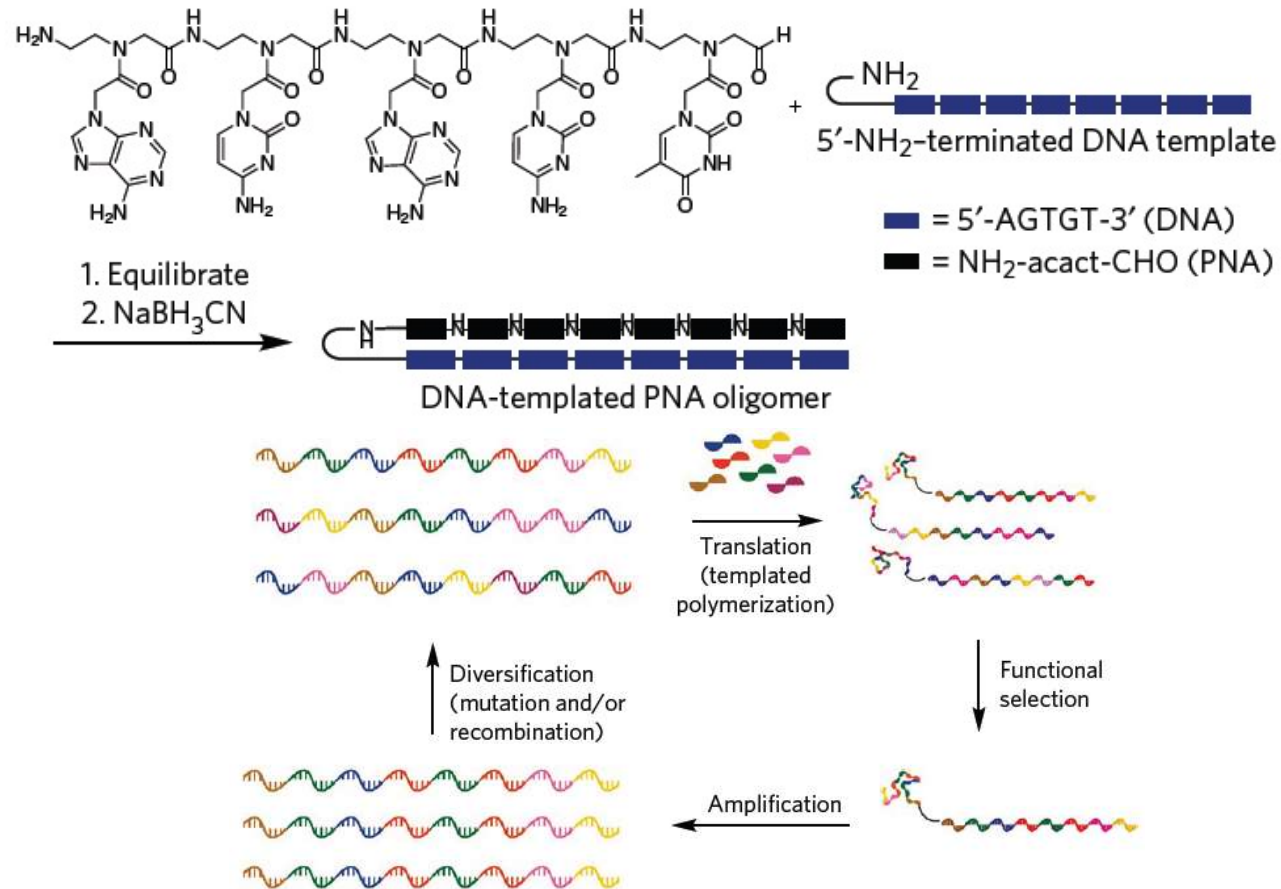
Problems:

- very slow reactions
- limited range of templates (mostly C-rich)
- poor regioselectivity (2'-5' linkages, predominant in some cases)
- 3'-aminonucleotides perform better, but undergo intramolecular cyclizations as side reaction

Lohrmann, R.; Orgel, L. E. *Tetrahedron* **1978**, *34*, 853

A. Silverman, E. Kool *Chem. Rev.* **2006**, *106*, 3775

Templated nucleic acid synthesis – short oligomer coupling

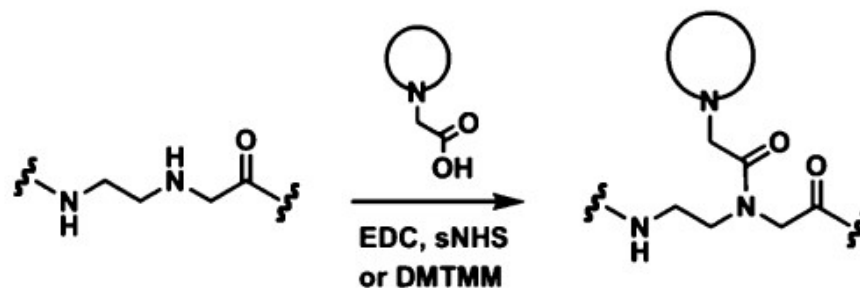
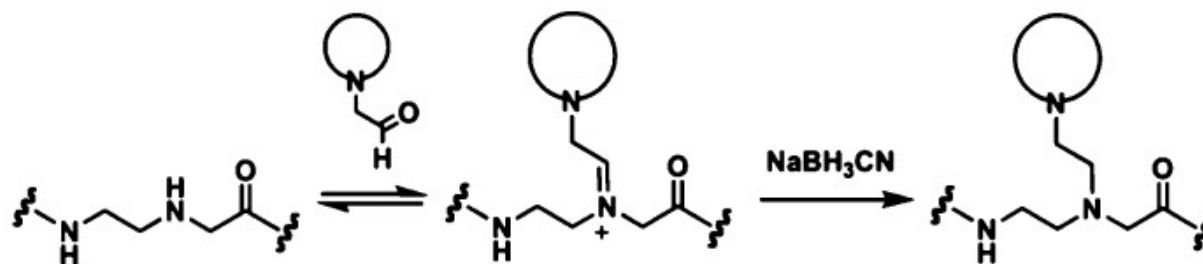


Limitations:

- slightly distorted backbone (amine instead of amide backbone every 5 bases)
- only carefully designed pentamers work – limiting the diversity for functional selection

Brudno Y, Birnbaum ME, Kleiner RE, Liu DR. *Nature Chem. Biol.* **2010**, *6*, 148-155.

Templated nucleic acid synthesis – base filling



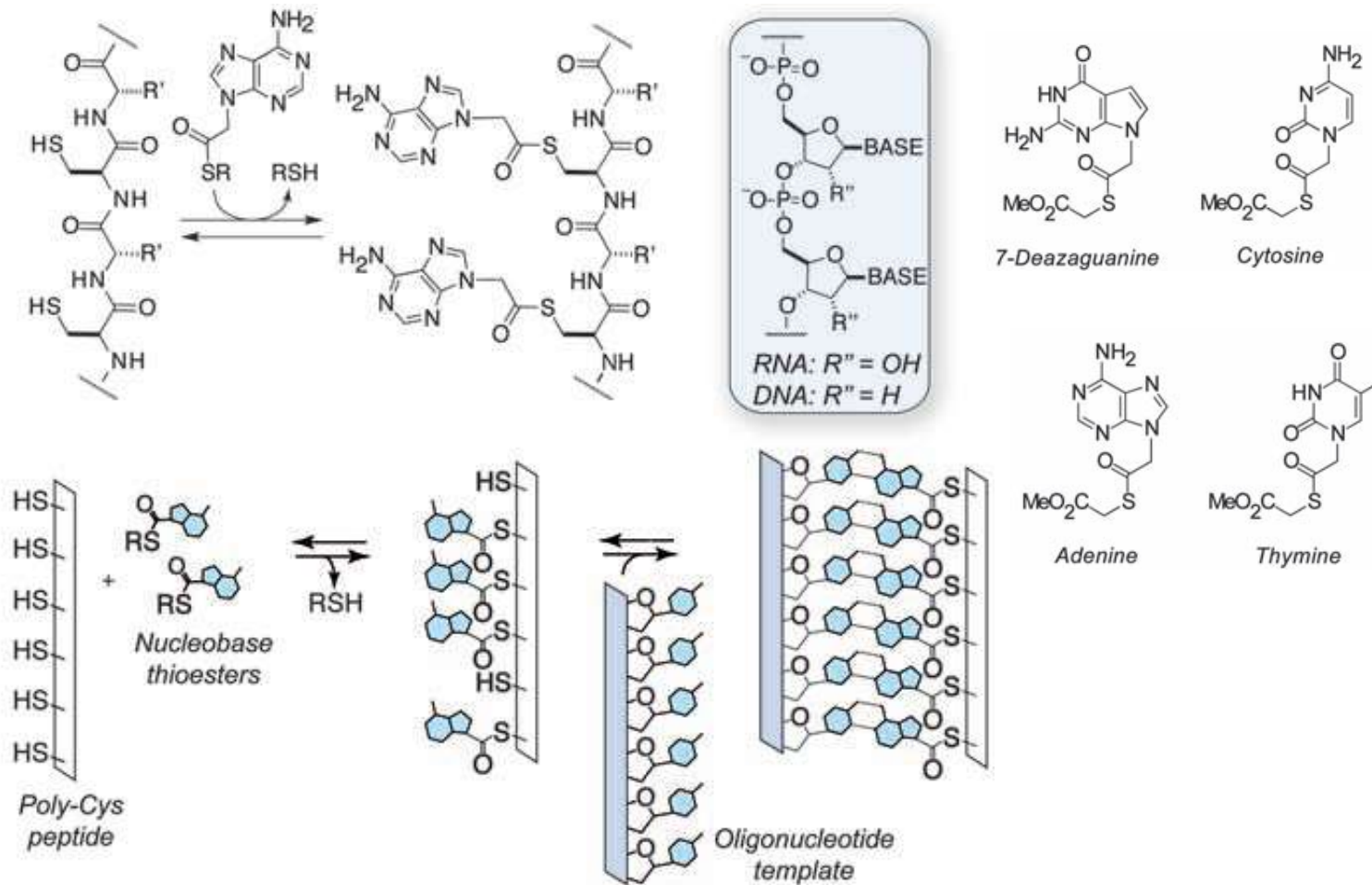
Advantages:

- no cross-reactivity
- selectivity increased by proximity of the reaction to the hybridization site

Limitations:

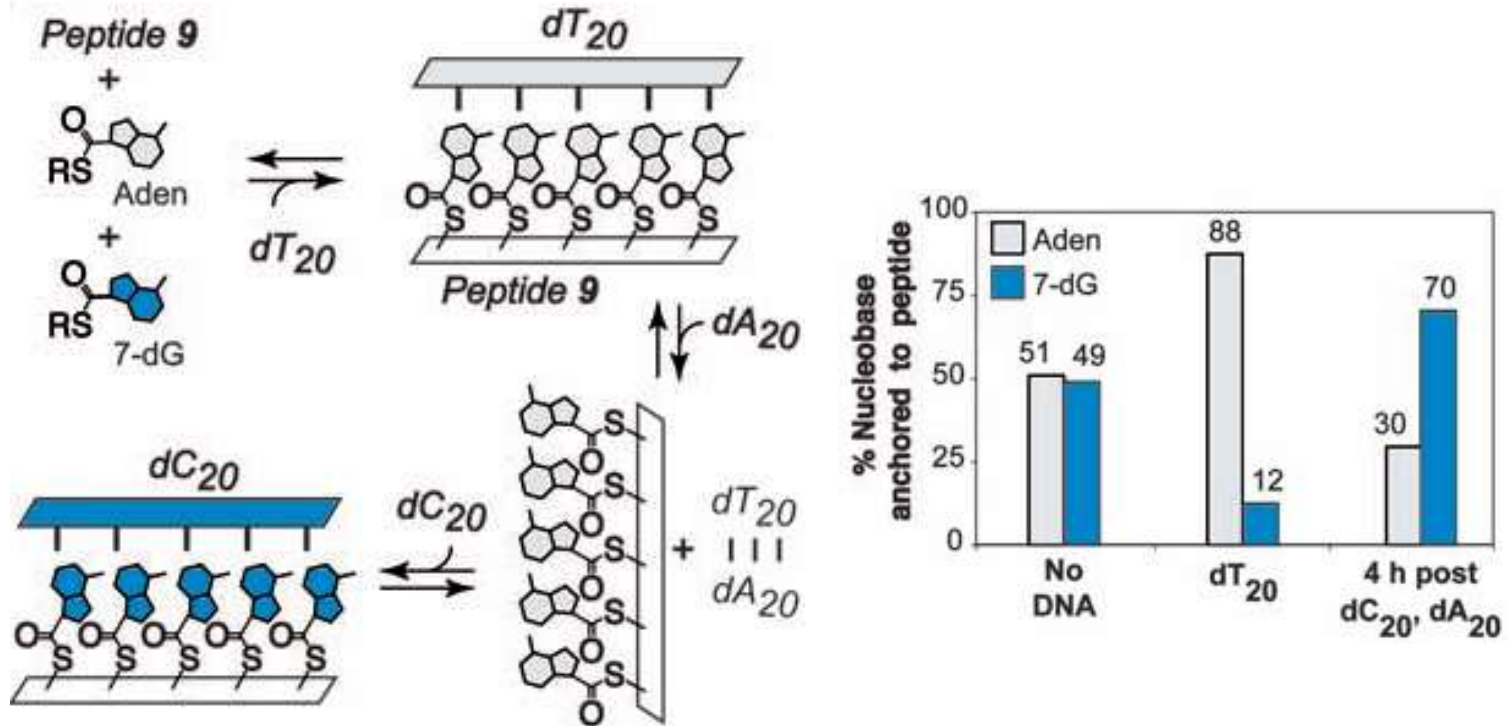
- single or double abasic sites (most efficient inside of the chain)
- Aldehydes give better yields and accuracy, but worse hybridization of the product

A polyamide responsive to selection pressure



Ura Y, Beierle J, Leman L, Orgel LE, Ghadiri MR. *Science* **2009**, 325, 73-77.

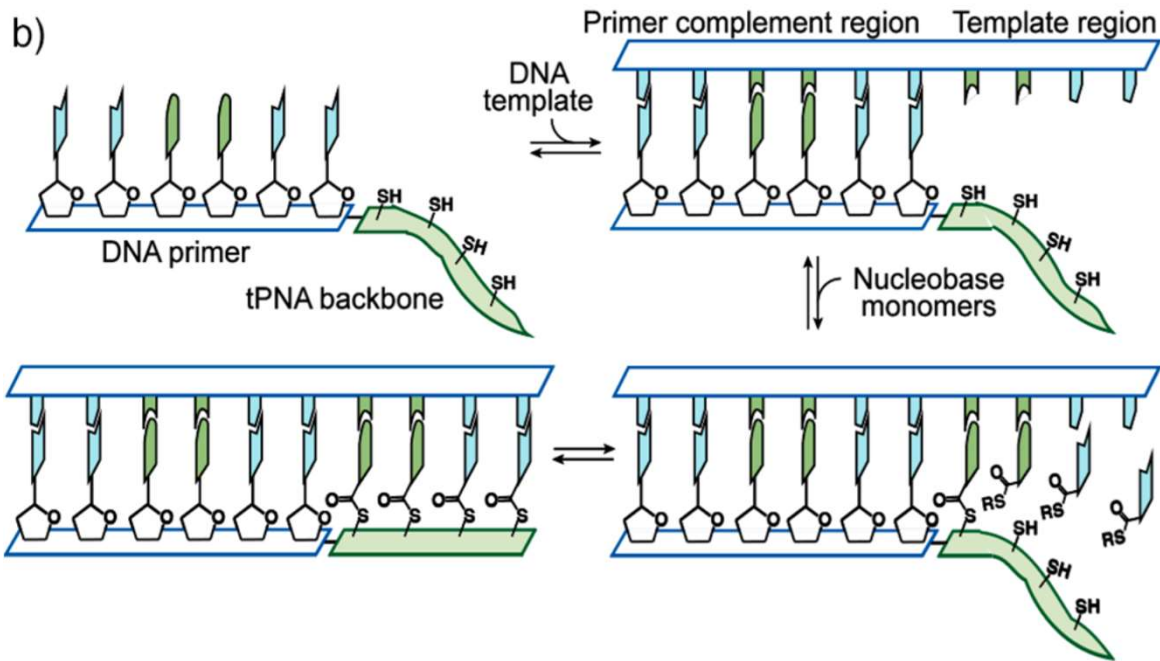
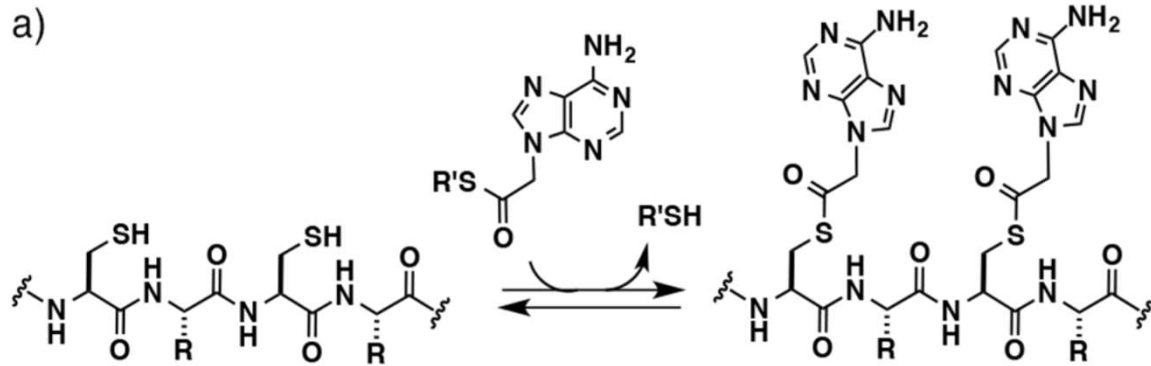
A polyamide responsive to selection pressure



Dynamic polymer responsive to template changes with high fidelity

Ura Y, Beierle J, Leman L, Orgel LE, Ghadiri MR. *Science* **2009**, 325, 73-77.

Templated Self-Assembly of Dynamic Peptide Nucleic Acids



The DNA primer region affords a high level of control over the location and register of the tPNA backbone in relation to the template strand.

Artificial genetic polymers

