



# 2023 Product Catalog

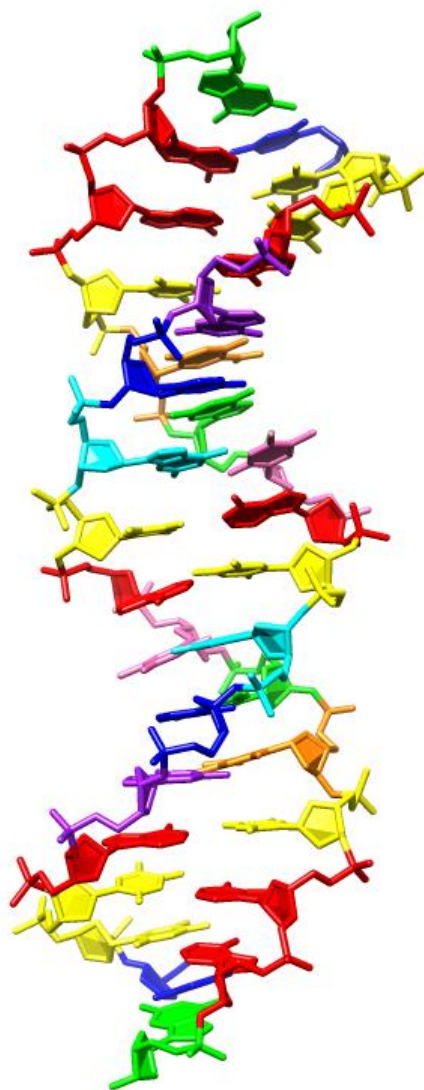
Nucleic acid analogs for:  
DNA sequencing  
Diagnostics  
SNP detection  
Synthetic Biology

[www.firebirdbio.com](http://www.firebirdbio.com)

# Contents

|  |    |
|--|----|
| Reversible terminators   | 4  |
| DNA sequencing, SNP identification, & <i>de novo</i> DNA synthesis     |    |
| AEGIS™   | 8  |
| Artificially Expanded Genetic Information Systems                      |    |
| Orthogonality, cleanliness, and uniformity in nucleic acid analysis    |    |
| SAMRS™   | 17 |
| Self-Avoiding Molecular Recognition Systems                            |    |
| Reducing primer dimers in nucleic acid amplification                   |    |
| Biversals  | 20 |
| Novel bases for binding to degenerate DNA sequences                    |    |
| SNAP-2   | 22 |
| Identifying DNA and RNA molecules when the exact sequence is not known |    |
| Ordering   | 23 |
| References   | 24 |

# Firebird reagents and the origins of life



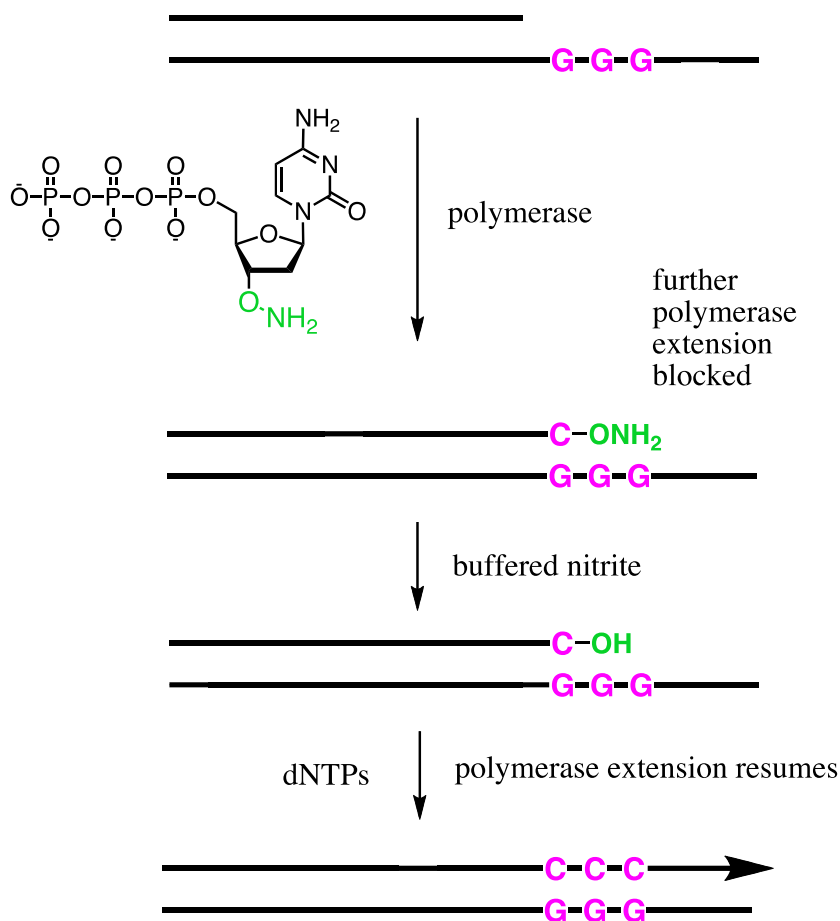
This catalog presents reagents and technologies to aid in the development of new biomedical innovations. Several of the products presented here were developed with the goal of better understanding the features of DNA and RNA that make them the carriers of genetic information for life on earth (Karalkar and Benner, 2018).

The image shown, left, illustrates the crystal structure of a double helix built from an expanded genetic alphabet of eight hachimoji building blocks, G (green), A (red), C (dark blue), T (yellow), B (aqua) P (blue), S (violet), and Z (orange). This hachimoji DNA forms the basis of Firebird. Adopted from Hoshika et al., 2019.

**Reagents in this catalog are sold for research use only. Please inquire for diagnostic or other uses.**

# Reversible Terminators

Firebird has introduced the 3'-ONH<sub>2</sub> reversible terminator as an alternative to the larger 3'-OCH<sub>2</sub>N<sub>3</sub> group (Hutter et al., 2010). The 3'-ONH<sub>2</sub> group is accepted by a variety of polymerases. After incorporation, further primer extension is blocked. The 3'-ONH<sub>2</sub> group is cleaved with buffered aqueous sodium nitrite to regenerate a standard 3'-OH.



3'-ONH<sub>2</sub> reversible terminators can be used in DNA sequencing (Hutter et al., 2010), Oligonucleotide synthesis (Jensen and Davis, 2018, Sarac and Hollenstein, 2019) and SNP analysis (Chen et al., 2010).

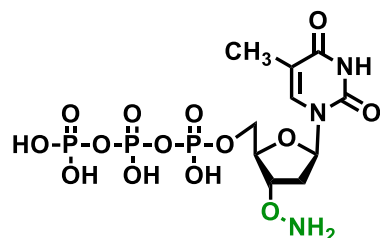
Polymerase variants have been developed that incorporate these terminators with improved efficiency over standard Taq DNA polymerase (Chen et al., 2010):

|             |            |          |
|-------------|------------|----------|
| POL475-400  | 400 units  | \$110.00 |
| POL475-1000 | 1000 units | \$250.00 |

# Reversible Terminators:

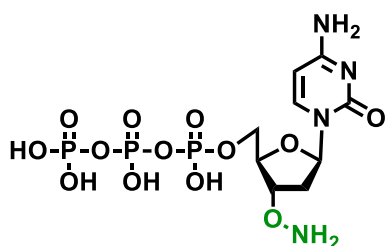
## Ready to Use, Untagged

Firebird offers “ready-to-use” un-tagged reversible terminators with a free 3'-ONH<sub>2</sub> group that can be directly incorporated by various enzymes without further manipulation.



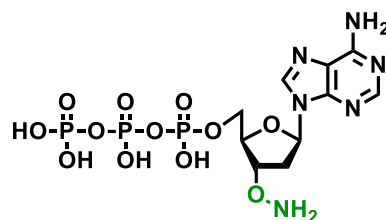
Thymine  
TONH2-171

5 μmoles \$600.00  
50 μmoles \$4200.00



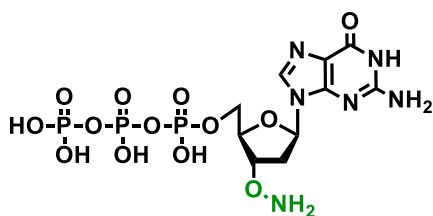
Cytosine  
CONH2-172

5 μmoles \$750.00  
50 μmoles \$5250.00



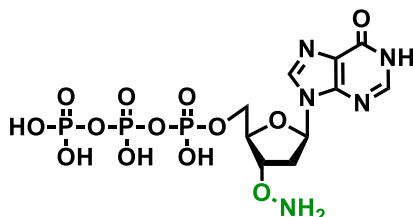
Adenine  
AONH2-173

5 μmoles \$750.00  
50 μmoles \$5250.00



Guanine  
GONH2-174

5 μmoles \$750.00  
50 μmoles \$5250.00



Inosine  
IONH2-175

5 μmoles \$750.00  
50 μmoles \$5250.00

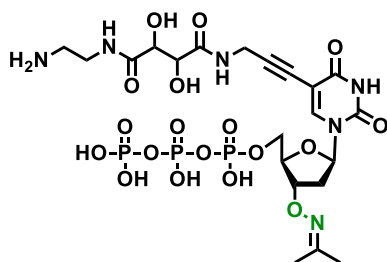
Please inquire for bulk pricing.

# Reversible Terminators:

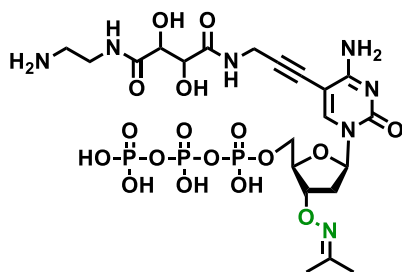
## diol-linked tags

Firebird offers reversible terminators with a 3'-ONH<sub>2</sub> (protected as the acetoxime) and a diol linker carrying a free amino group, to which a tag (fluorescent dye or other moiety) can be attached. The diol can be rapidly cleaved with dilute aqueous periodate.

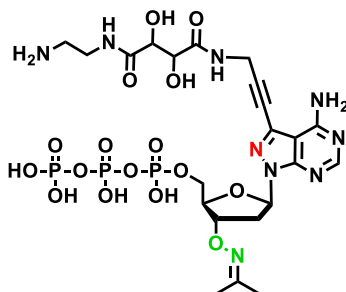
For enzymatic incorporation, the oxime must be deprotected to the free 3'-ONH<sub>2</sub> before use, which can be achieved in situ with buffered aqueous methoxylamine.



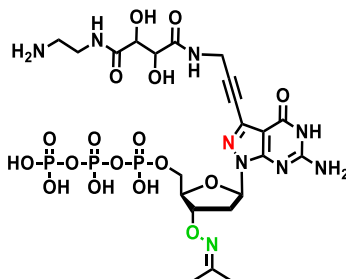
Thymine  
TONH2-DT  
1  $\mu$ mole \$1750.00



Cytosine  
CONH2-DT  
1  $\mu$ mole \$1900.00



Adenine  
7c8n-AONH2-DT  
1  $\mu$ mole \$2200.00



Guanine  
7c8n-GONH2-DT  
1  $\mu$ mole \$2300.00

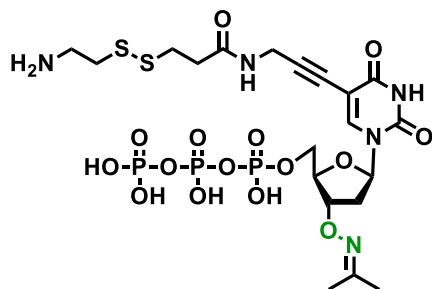
Please inquire for bulk pricing.

*Not available for sequencing applications on certain machines and in certain jurisdictions. Please inquire.*

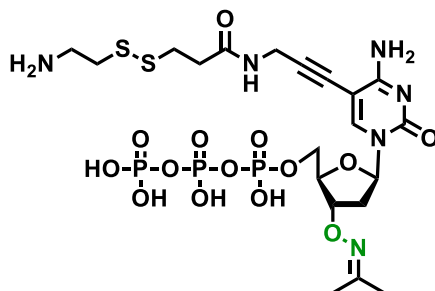
# Reversible Terminators:

## disulfide-linked tags

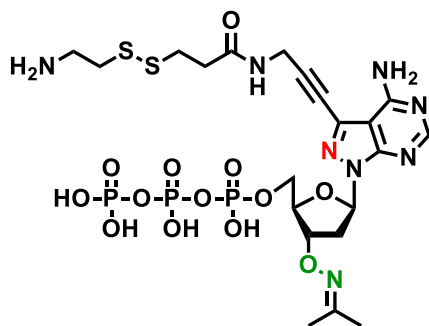
Firebird offers reversible terminators with a 3'-ONH<sub>2</sub> (protected as the acetoxime) and a disulfide linker carrying a free amino group, to which a tag (fluorescent dye or other moiety) can be attached. The disulfide can be rapidly cleaved with phosphine or thiol reagents. For enzymatic incorporation, the oxime must be deprotected to the free 3'-ONH<sub>2</sub> before use, which can be achieved in situ with buffered aqueous methoxylamine.



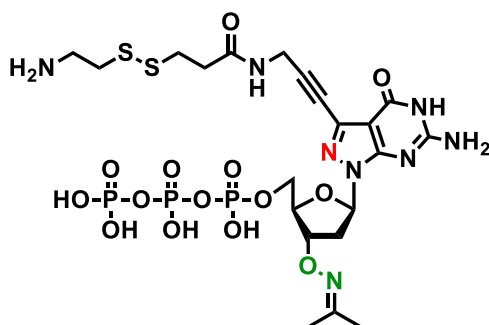
Thymine  
TONH2-ST  
1 μmole \$ 1750.00



Cytosine  
CONH2-ST  
1 μmole \$ 2000.00



Adenine  
7c8n-AONH2-ST  
1 μmole \$ 2400.00



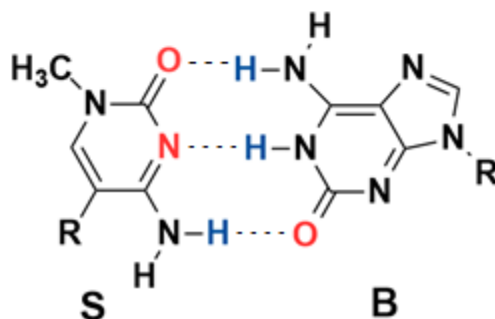
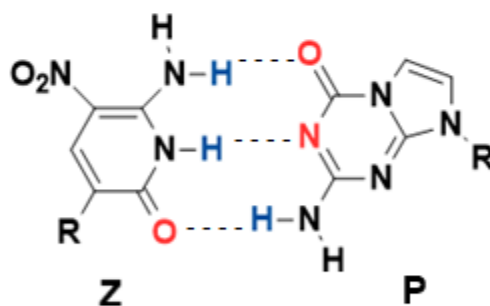
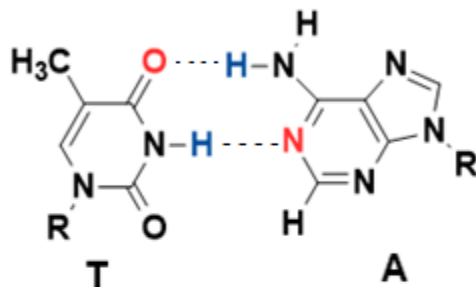
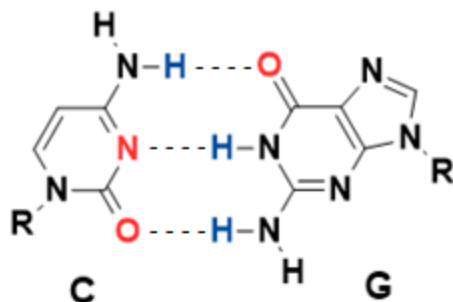
Guanine  
7c8n-GONH2-ST  
1 μmole \$ 2500.00

Please inquire for bulk pricing.

Not available for sequencing applications on certain machines and in certain jurisdictions. Please inquire.

## Artificially Expanded Genetic Information Systems

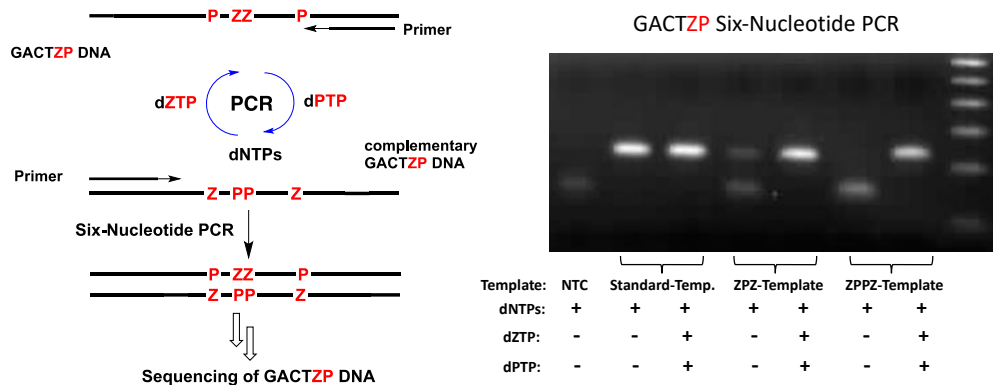
Firebird has created different heterocycles in order to implement additional hydrogen bonding patterns for the Z:P and S:B base pairs as shown below. These base pairs are “orthogonal” to C:G and A:T (Benner, 2004; Hoshika et al., 2019; Sefah et al., 2014; Yang et al., 2006).





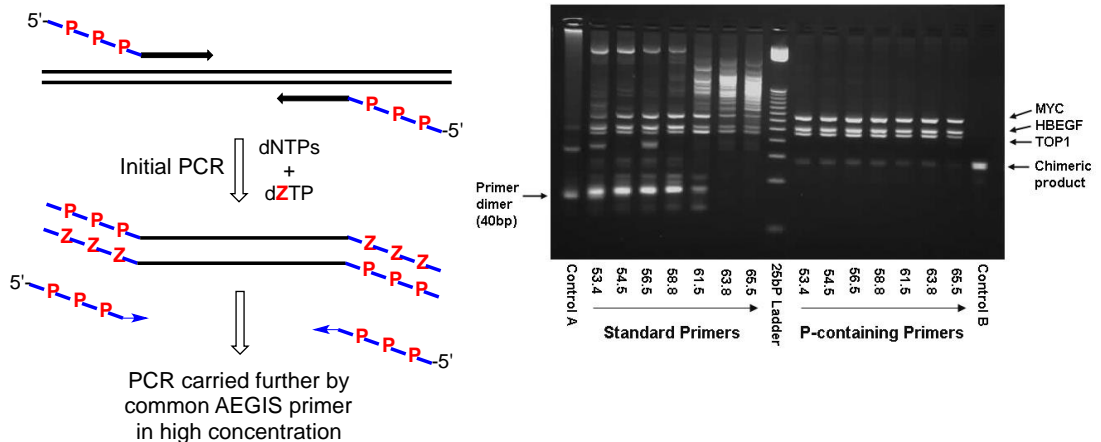
# Using AEGIS: For Ultra-clean Nested PCR

The Z:P pair is retained during PCR amplification, even when present as consecutive base pairs (Yang et al., 2011).



AEGIS-nested primers suppress noise in multiplex PCR (Yang et al., 2010) and support 22-plex PCR to detect RNA viruses (Glushakova et al., 2015a).

"Analyte specific" chimeric primers in low concentration



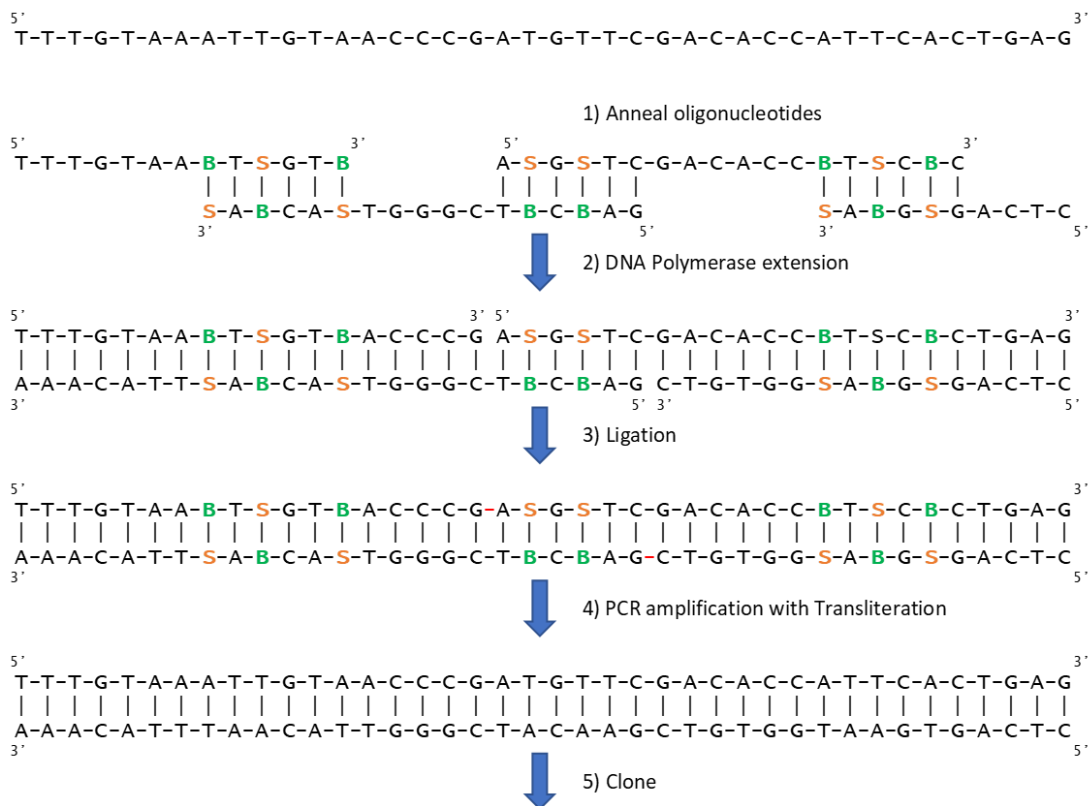
# Using AEGIS:

## Assembling Long DNA Constructs

Adding AEGIS nucleotides to single-stranded oligos increases their information density. This allows clean and rapid hybridization of single stranded DNA unobstructed by hairpins, wandering strands, and non-canonical interactions. Then, using Firebird's "transliteration" technology, the AEGIS nucleotides are cleanly replaced by standard nucleotides giving an entirely natural gene (Bradley and Benner, 2014; Merritt et al., 2014).

An example of this assembly is shown below: S and B residues in the tails of the primers guide specific alignment of the unique sequences at the ends of the primers. The S:B basepair is converted to a T:A basepair during PCR amplification.

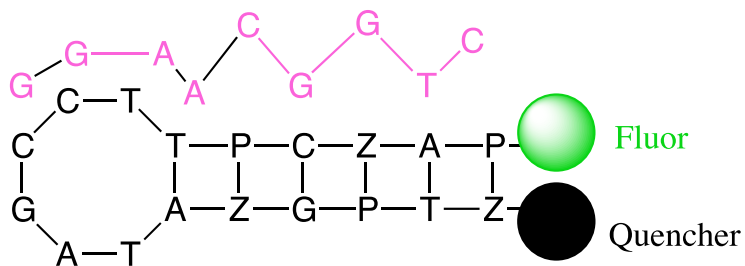
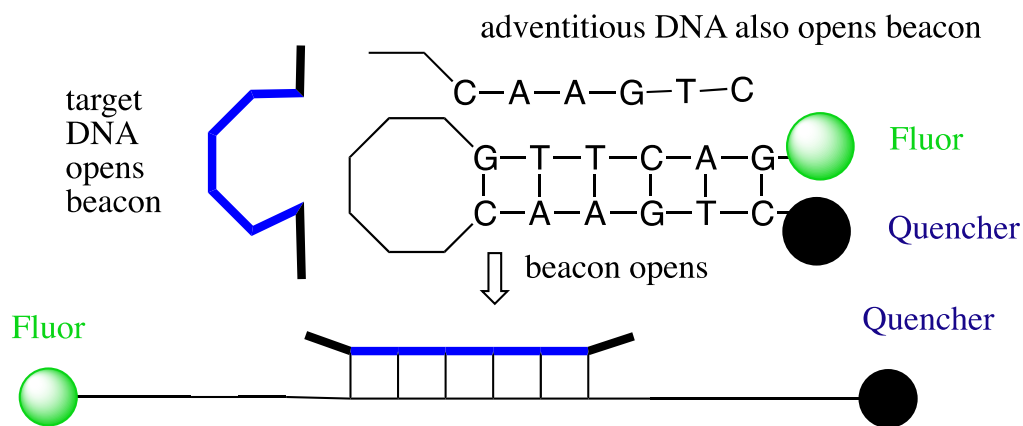
To make the sequence:



# Using AEGIS:

## Molecular Beacons

Adding AEGIS nucleotides to the stems of molecular beacons prevents their being opened by adventitious DNA and RNA in a complex biological sample. This allows beacons to deliver signals in complex biological samples with significantly lower noise (Sheng et al., 2008).



No adventitious DNA can open a beacon that has an AEGIS stem

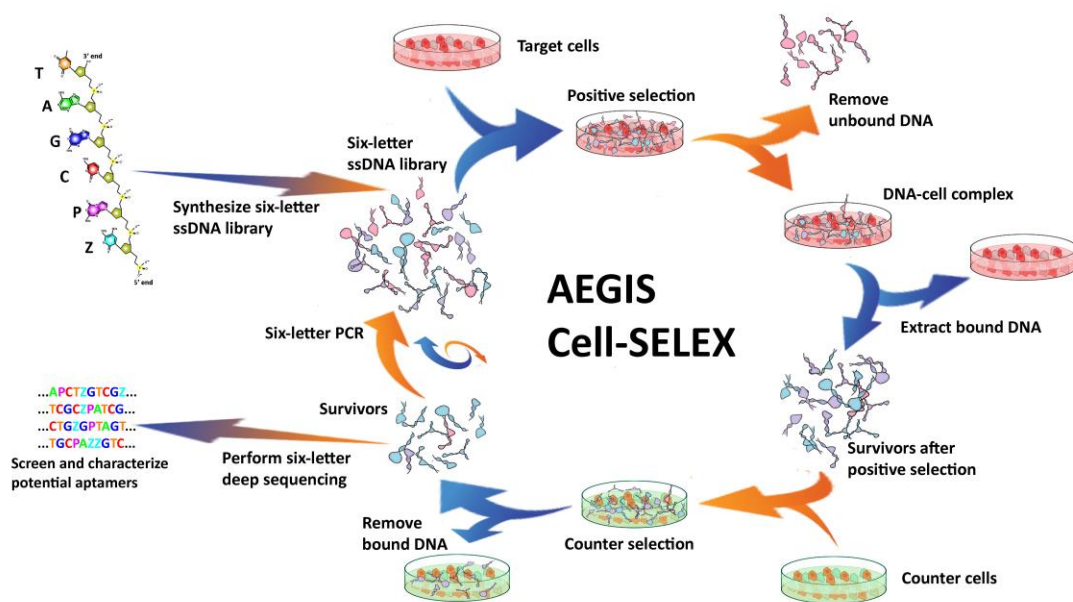
Firebird offers custom-synthesized beacons with a wide range of fluorescent dyes and quenchers. Please inquire.

# AEGIS:

## Increasing Aptamer Diversity

The dP and dZ bases increase the chemical repertoire of nucleic acids for aptamer selections (Biondi et al., 2016; Sefah et al., 2014; Zhang et al., 2015, 2016). Of special note is the NO<sub>2</sub> group present on dZ.

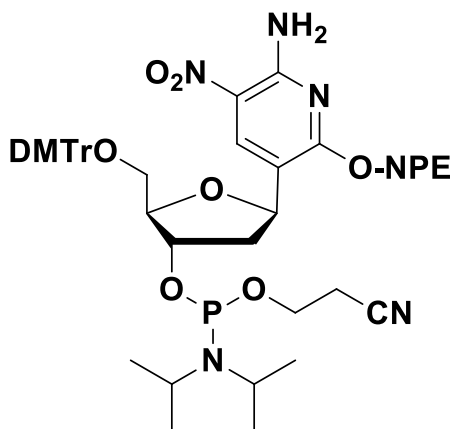
The figure below shows one application of AEGIS for the selection of aptamers specific to a cell surface protein on a cancer cell (Zhang et al., 2016).



# AEGIS:

## dZ and dP Phosphoramidites

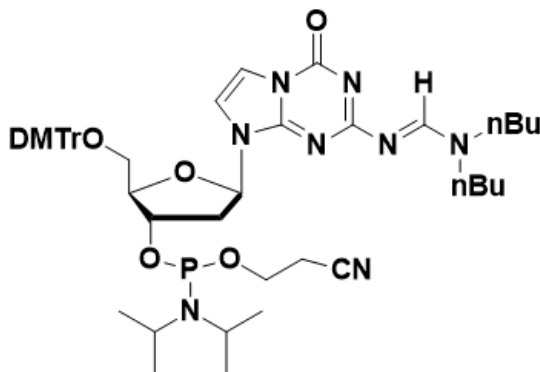
### dZ Phosphoramidite



Hydrogen bonding pattern: Z  
Sugar: 2'-Deoxyribose  
Heterocycle: Nitropyridine  
Linear Formula  $C_{48}H_{55}N_6O_{11}P$   
Mol Weight 922.96

Cat. No. dZ-PA-101  
100 mg \$ 720.00  
1 gram \$5760.00

### dP Phosphoramidite



Hydrogen bonding pattern: P  
Sugar: 2'-Deoxyribose  
Heterocycle: Imidazotriazine  
Linear Formula  $C_{49}H_{65}N_8O_7P$   
Mol Weight 909.08

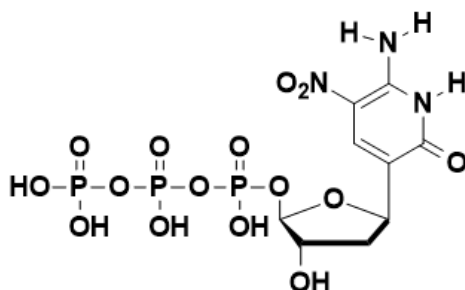
Cat. No. dP-PA-102  
100 mg \$ 850.00  
1 gram \$6800.00

(Yang et al., 2006)  
Please inquire for bulk pricing

Oligonucleotides are available that contain dZ and dP.  
Please inquire for availability of ribonucleoside derivatives.

## dZ and dP Triphosphates

### dZ Triphosphate



Hydrogen bonding pattern: Z

Sugar: 2'-deoxyribose

Heterocycle: Nitropyridine

Linear Formula  $C_{10}H_{16}N_3O_{15}P_3$

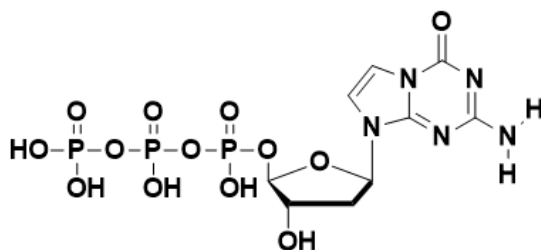
Mol Weight 511.17

Cat. No. dZTP-101

1  $\mu$ mole \$ 400.00

5  $\mu$ moles \$ 1600.00

### dP Triphosphate



Hydrogen bonding pattern: P

Sugar: 2'-deoxyribose

Heterocycle: Imidazotriazine

Linear Formula  $C_{10}H_{16}N_5O_{13}P_3$

Mol Weight 493.15

Cat. No. dPTP-201

1  $\mu$ mole \$ 420.00

5  $\mu$ moles \$ 1680.00

(Yang et al., 2007)

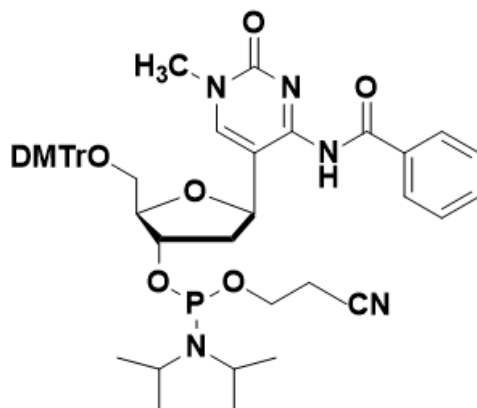
Please inquire for bulk pricing.

Please inquire for availability of ribonucleoside derivatives.

# AEGIS:

## dS and dB Phosphoramidites

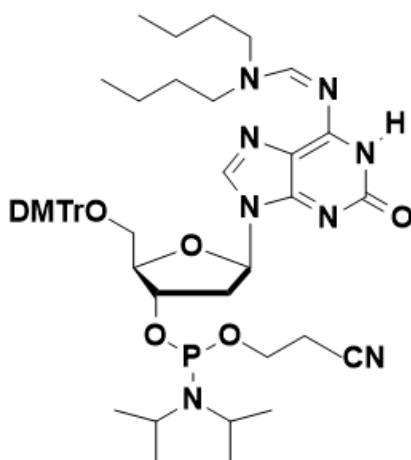
### dS Phosphoramidite



Hydrogen bonding pattern: S  
Sugar: 2'-Deoxyribose  
Heterocycle: Pseudo-C  
Linear Formula  $C_{47}H_{54}N_5O_8P$   
Mol Weight 847.93

Cat. No. dS-PA-104S  
100 mg \$ 720.00  
1 gram \$5760.00

### dB Phosphoramidite



Hydrogen bonding pattern: B  
Sugar: 2'-Deoxyribose  
Heterocycle: Purine  
Linear Formula  $C_{49}H_{68}N_7O_7P$   
Mol Weight 898.08

Cat. No. dB-PA-103P  
100 mg \$ 600.00  
1 gram \$4800.00

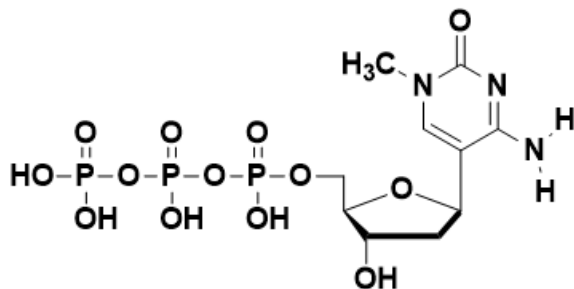
Please inquire for bulk pricing.

Oligonucleotides are available that incorporate dS and dB.  
Please inquire for availability of ribonucleoside derivatives.

# AEGIS:

## dS and dB Triphosphates

### dS Triphosphate



Hydrogen bonding pattern: S

Sugar: 2'-deoxyribose

Heterocycle: Pseudo-C

Linear Formula  $C_{10}H_{18}N_3O_{13}P_3$

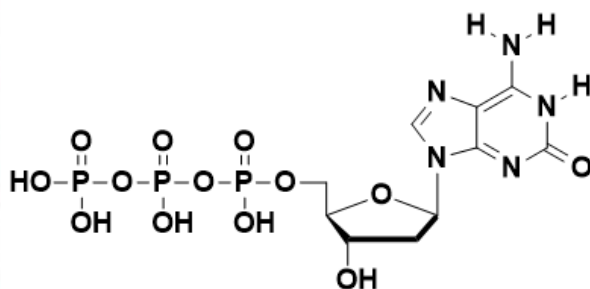
Mol Weight 481.18

Cat. No. dSTP-401S

1  $\mu$ mole \$ 400.00

5  $\mu$ moles \$ 1600.00

### dB Triphosphate



Hydrogen bonding pattern: B

Sugar: 2'-deoxyribose

Heterocycle: Purine

Linear Formula  $C_{10}H_{16}N_5O_{13}P_3$

Mol Weight 507.18

Cat. No. dBTP-301P

1  $\mu$ mole \$ 400.00

5  $\mu$ moles \$ 1600.00

Please inquire for bulk pricing.

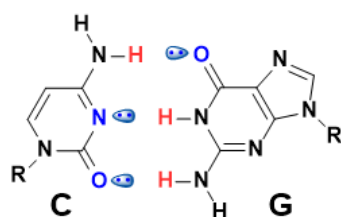
Please inquire for availability of ribonucleoside derivatives.



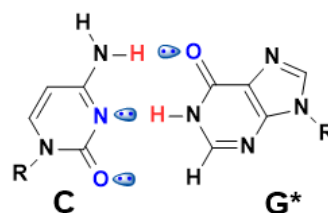
# Self Avoiding Molecular Recognition System

Nucleic acid amplification reactions suffer from the formation of off-target amplification products. This problem increases with the number of primers in the reaction. It mainly occurs because of primer-primer interactions. Thus, selectively removing hydrogen bonding units from the primer bases results in *self-avoiding* DNA primers that can be added to enable and improve multiplexed PCR (Hoshika et al., 2010).

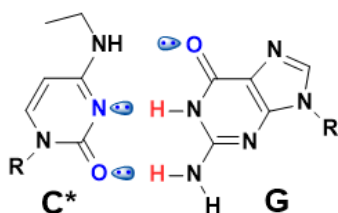
As shown below, SAMRS bases, indicated with a \*, can base pair with standard bases (in the target or amplicon) but not with other SAMRS bases.



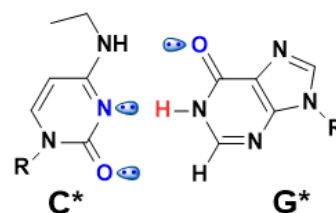
3 H bonds



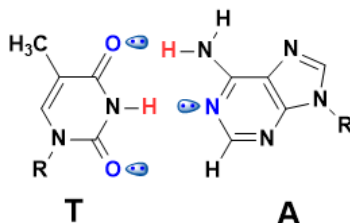
2 H bonds



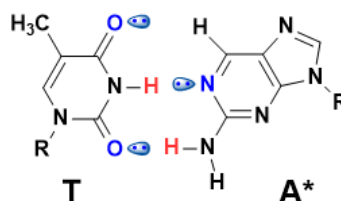
2 H bonds



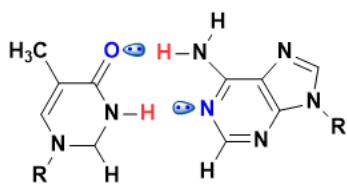
1 H bonds



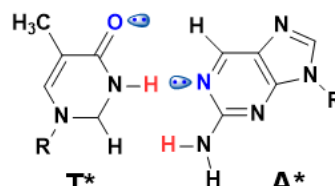
2 H bonds



2 H bonds



2 H bonds



1 H bonds

# SAMRS:

## Design Rules

General rules for placement of SAMRS bases into primers used in PCR and other amplification techniques. Upper case letters indicate the standard base, lower case letters indicate the SAMRS base.

1. Recommended lengths are 20-35 nts. SAMRS bases should be utilized in the first 4, (up to 8), positions at the 3' end of the oligonucleotide but not in the very first 3' base.
2. Between two and four SAMRS bases should be used per oligonucleotide, with two or three SAMRS modifications being preferred.
3. The SAMRS t base has not demonstrated as much reduction in primer dimer formation so it is preferable to substitute a, g or c rather than t when given a choice.
4. Avoid using SAMRS bases in a string of three and four consecutive identical bases. For example: ggg, ccc, aaa, ttt, gggg, cccc, aaaa, and tttt are to be avoided.
5. Separate SAMRS bases with standard bases, for example: gGg, cCc, aAa, and tTt.
6. If the 3'-end of an oligo is standard A or T, the second base should also be a standard base, followed by two or three SAMRS modifications.

(Benner et al., 2015; Glushakova et al., 2015a, 2015b; Hoshika et al., 2010; Sharma et al., 2014; Yang et al., 2015 and unpublished data)

*As with all primer designs, Firebird makes no guarantee as to the performance of oligonucleotides made by following these rules.*

# SAMRS:

## Phosphoramidites

t\* phosphoramidite

1 g      \$ 1050

10 g     \$ 8220

a\* phosphoramidite

1 g      \$ 655

10 g     \$ 5340

c\* phosphoramidite

1 g      \$ 394

10 g     \$3150

g\* phosphoramidite

1 g      \$ 110

10 g     \$ 880

Oligonucleotides are available that incorporate the SAMRS bases.

SAMRS can be combined with AEGIS in oligos to get highly multiplexed and highly clean PCR, as well as isothermal amplification. Please inquire.

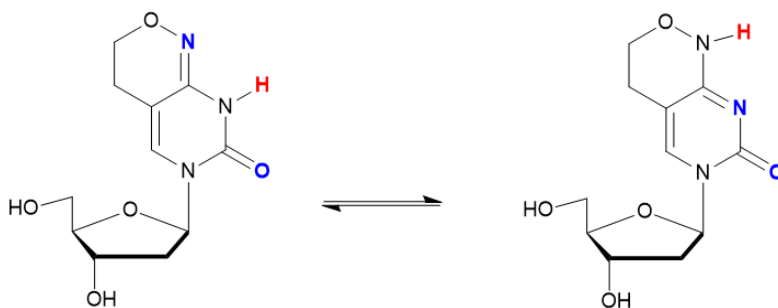


# Biversal™ Nucleotides

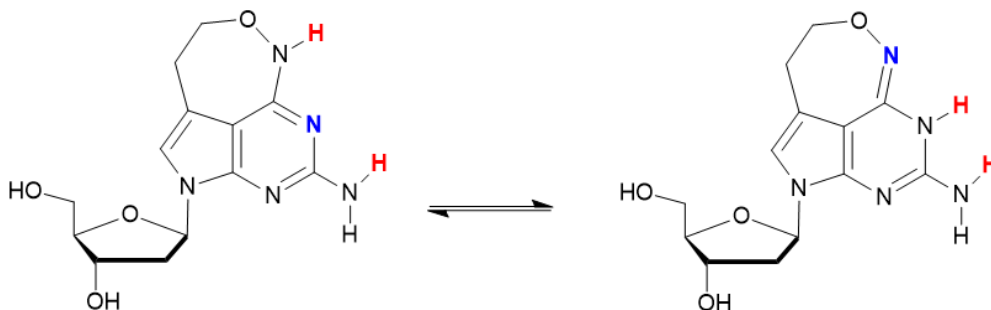
The divergence present in pathogen genomes makes it difficult or impossible to design a single probe or primer that is the exact complement of all possible target sequences. In practice this is handled using degenerate or “universal bases” (e.g. inosine).

Firebird scientists have created two “biversals”™. Each exists in two tautomeric forms that provide alternate hydrogen bonding patterns. This allows the pyrimidine biversal to pair with either guanine or adenine and the purine biversal to pair with either thymine or cytosine. These bases provide a new alternative to the existing methods of handling divergent sequences for both PCR amplification and SNP detection (Yang et al., 2018).

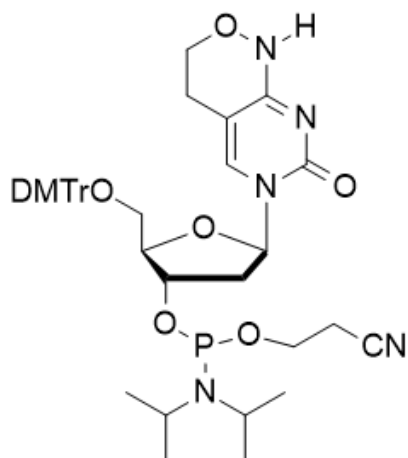
Tautomeric forms of the Pyrimidine biversal:



Tautomeric forms of the Purine biversal:



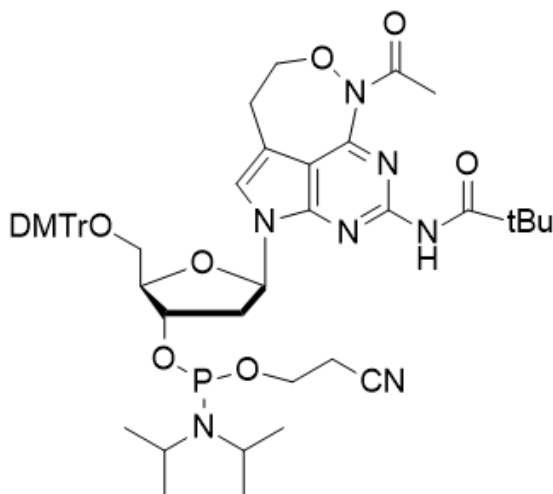
# Biversal: Phosphoramidites



Pyrimidine biversal  
phosphoramidite  
Linear Formula  $C_{41}H_{50}N_5O_8P$   
Mol Weight 771.84

Cat No. Pyr-BiVer

|        |         |
|--------|---------|
| 100 mg | \$ 500  |
| 1 gram | \$ 4000 |



Purine biversal  
phosphoramidite  
Linear Formula  $C_{50}H_{62}N_7O_9P$   
Mol Weight 936.04

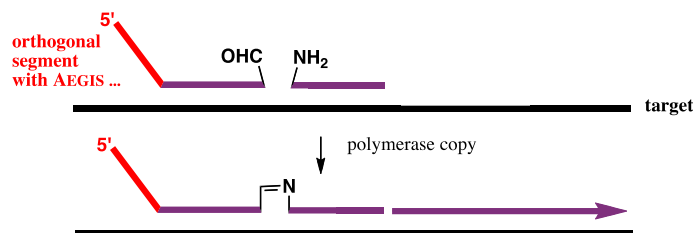
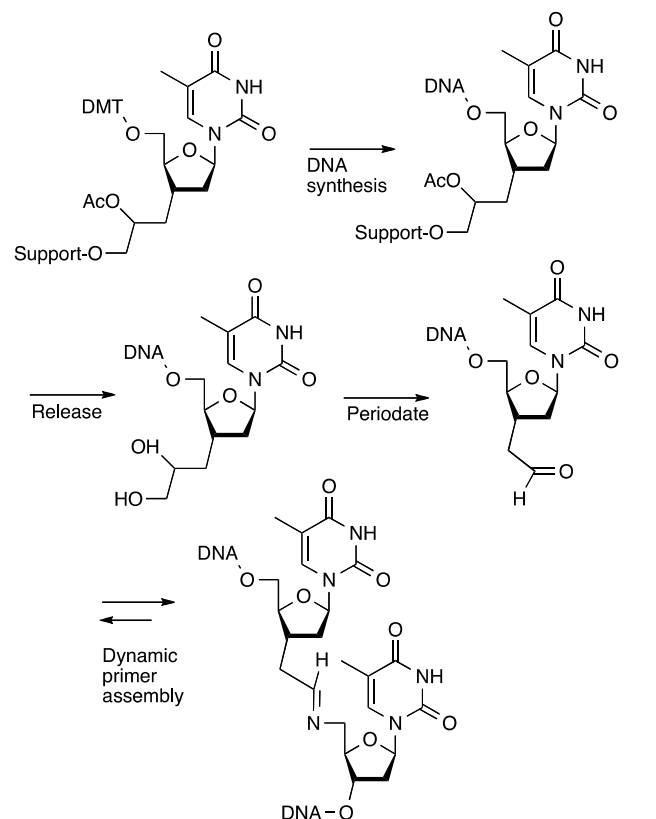
Cat No. Pur-BiVer

|        |         |
|--------|---------|
| 100 mg | \$ 2850 |
| 1 gram | Inquire |

Firebird sells oligonucleotides that contain the purine and pyrimidine biversals. Please inquire.

# SNAP2™ Oligonucleotides: Priming with High Specificity

Specific DNA priming requires oligonucleotides with complementarity of  $\geq 16$  nucleotides but the ability to discriminate against single mismatches. Dynamic assembly of a primer on a template can provide this (Leal et al., 2006).



Controlled pore glass with aldehyde precursor  
SNAP2T\_HJK001  
100 mg      \$600.00

Firebird sells phosphoramidites, oligos and libraries with SNAP2 ends. Please inquire.

SNAP2 primers are not to be confused with Snap-Tag® and other registered trademarks of New England BioLabs.

# Purchasing, Shipping and Handling

## Contact

### Orders

By email: [orders@firebirdbio.com](mailto:orders@firebirdbio.com)

By telephone: (386) 418-0347  
9:00 - 5:00 Eastern Time

### Technical inquiries

[support@firebirdbio.com](mailto:support@firebirdbio.com)

*Reagents and enzymes are shipped at the customer's expense, on dry ice as appropriate.*



# References

- Benner, S.A. (2004). Chemistry. Redesigning genetics. *Science* 306, 625–626.
- Benner, S.A., Kim, H.-J., Merritt, K.B., Yang, Z., McLendon, D.C., Hoshika, S., and Hutter, D. (2015). Next-generation DNA in pathogen detection, surveillance, and CLIA-waivable diagnostics. *SPIE Digital Library* 9490, 94900K-94900K – 6.
- Biondi, E., Lane, J.D., Das, D., Dasgupta, S., Piccirilli, J.A., Hoshika, S., Bradley, K.M., Krantz, B.A., and Benner, S.A. (2016). Laboratory evolution of artificially expanded DNA gives redesignable aptamers that target the toxic form of anthrax protective antigen. *Nucleic Acids Res.* 44, 9565–9577, PMID: PMC5175368.
- Bradley, K.M., and Benner, S.A. (2014). OligArch: A software tool to allow artificially expanded genetic information systems (AEGIS) to guide the autonomous self-assembly of long DNA constructs from multiple DNA single strands. *Beilstein J Org Chem* 10, 1826–1833, PMID: PMC4142867.
- Chen, F., Gaucher, E.A., Leal, N.A., Hutter, D., Havemann, S.A., Govindarajan, S., Ortlund, E.A., and Benner, S.A. (2010). Reconstructed evolutionary adaptive paths give polymerases accepting reversible terminators for sequencing and SNP detection. *Proc. Natl. Acad. Sci. U.S.A.* 107, 1948–1953, PMID: PMC2804741.
- Glushakova, L.G., Bradley, A., Bradley, K.M., Alto, B.W., Hoshika, S., Hutter, D., Sharma, N., Yang, Z., Kim, M.-J., and Benner, S.A. (2015a). High-throughput multiplexed xMAP Luminex array panel for detection of twenty two medically important mosquito-borne arboviruses based on innovations in synthetic biology. *J. Virol. Methods* 214, 60–74, PMID: PMC4485418.
- Glushakova, L.G., Sharma, N., Hoshika, S., Bradley, A.C., Bradley, K.M., Yang, Z., and Benner, S.A. (2015b). Detecting respiratory viral RNA using expanded genetic alphabets and self-avoiding DNA. *Anal. Biochem.* 489, 62–72, PMID: PMC4733849.
- Hoshika, S., Chen, F., Leal, N.A., and Benner, S.A. (2010). Artificial genetic systems: self-avoiding DNA in PCR and multiplexed PCR. *Angew. Chem. Int. Ed. Engl.* 49, 5554–5557, PMID: PMC6027612.
- Hoshika, S., Leal, N.A., Kim, M.-J., Kim, M.-S., Karalkar, N.B., Kim, H.-J., Bates, A.M., Watkins, N.E., SantaLucia, H.A., Meyer, A.J., et al. (2019). Hachimoji DNA and RNA: A genetic system with eight building blocks. *Science* 363, 884–887, PMID: PMC6413494.



# References

- Hutter, D., Kim, M.-J., Karalkar, N., Leal, N.A., Chen, F., Guggenheim, E., Visalakshi, V., Olejnik, J., Gordon, S., and Benner, S.A. (2010). Labeled nucleoside triphosphates with reversibly terminating aminoalkoxyl groups. *Nucleosides Nucleotides Nucleic Acids* 29, 879–895, PMID: PMC3858015.
- Jensen, M.A., and Davis, R.W. (2018). Template-Independent Enzymatic Oligonucleotide Synthesis (TiEOS): Its History, Prospects, and Challenges. *Biochemistry* 57, 1821–1832.
- Karalkar, N.B., and Benner, S.A. (2018). The challenge of synthetic biology. *Synthetic Darwinism and the aperiodic crystal structure*. *Curr Opin Chem Biol* 46, 188–195.
- Leal, N.A., Sukeda, M., and Benner, S.A. (2006). Dynamic assembly of primers on nucleic acid templates. *Nucleic Acids Res.* 34, 4702–4710, PMID: PMC1635275.
- Merritt, K.K., Bradley, K.M., Hutter, D., Matsuura, M.F., Rowold, D.J., and Benner, S.A. (2014). Autonomous assembly of synthetic oligonucleotides built from an expanded DNA alphabet. Total synthesis of a gene encoding kanamycin resistance. *Beilstein J Org Chem* 10, 2348–2360, PMID: PMC4222377.
- Sarac, I., and Hollenstein, M. (2019). Terminal Deoxynucleotidyl Transferase in the Synthesis and Modification of Nucleic Acids. *Chembiochem* 20, 860–871.
- Sefah, K., Yang, Z., Bradley, K.M., Hoshika, S., Jiménez, E., Zhang, L., Zhu, G., Shanker, S., Yu, F., Turek, D., et al. (2014). In vitro selection with artificial expanded genetic information systems. *Proc. Natl. Acad. Sci. U.S.A.* 111, 1449–1454, PMID: PMC3910645.
- Sharma, N., Hoshika, S., Hutter, D., Bradley, K.M., and Benner, S.A. (2014). Recombinase-based isothermal amplification of nucleic acids with self-avoiding molecular recognition systems (SAMRS). *Chembiochem* 15, 2268–2274.
- Sheng, P., Yang, Z., Kim, Y., Wu, Y., Tan, W., and Benner, S.A. (2008). Design of a novel molecular beacon: modification of the stem with artificially genetic alphabet. *Chem. Commun. (Camb.)* 5128–5130, PMID: PMC2763601.

# References

- Yang, Z., Hutter, D., Sheng, P., Sismour, A.M., and Benner, S.A. (2006). Artificially expanded genetic information system: a new base pair with an alternative hydrogen bonding pattern. *Nucleic Acids Res.* 34, 6095–6101, PMCID: PMC1635279.
- Yang, Z., Sismour, A.M., Sheng, P., Puskar, N.L., and Benner, S.A. (2007). Enzymatic incorporation of a third nucleobase pair. *Nucleic Acids Res.* 35, 4238–4249, PMCID: PMC1934989.
- Yang, Z., Chen, F., Chamberlin, S.G., and Benner, S.A. (2010). Expanded genetic alphabets in the polymerase chain reaction. *Angew. Chem. Int. Ed. Engl.* 49, 177–180, PMCID: PMC3155763.
- Yang, Z., Chen, F., Alvarado, J.B., and Benner, S.A. (2011). Amplification, mutation, and sequencing of a six-letter synthetic genetic system. *J. Am. Chem. Soc.* 133, 15105–15112, PMCID: PMC3427765.
- Yang, Z., McLendon, C., Hutter, D., Bradley, K.M., Hoshika, S., Frye, C.B., and Benner, S.A. (2015). Helicase-Dependent Isothermal Amplification of DNA and RNA by Using Self-Avoiding Molecular Recognition Systems. *Chembiochem* 16, 1365–1370, PMCID: PMC4489552.
- Yang, Z., Kim, H.-J., Le, J.T., McLendon, C., Bradley, K.M., Kim, M.-S., Hutter, D., Hoshika, S., Yaren, O., and Benner, S.A. (2018). Nucleoside analogs to manage sequence divergence in nucleic acid amplification and SNP detection. *Nucleic Acids Res.* 46, 5902–5910, PMCID: PMC6159519.
- Zhang, L., Yang, Z., Sefah, K., Bradley, K.M., Hoshika, S., Kim, M.-J., Kim, H.-J., Zhu, G., Jiménez, E., Cansiz, S., et al. (2015). Evolution of functional six-nucleotide DNA. *J. Am. Chem. Soc.* 137, 6734–6737, PMCID: PMC4500535.
- Zhang, L., Yang, Z., Le Trinh, T., Teng, I.-T., Wang, S., Bradley, K.M., Hoshika, S., Wu, Q., Cansiz, S., Rowold, D.J., et al. (2016). Aptamers against Cells Overexpressing Glypican 3 from Expanded Genetic Systems Combined with Cell Engineering and Laboratory Evolution. *Angew. Chem. Int. Ed. Engl.* 55, 12372–12375, PMCID: PMC5554412.