

ECHO DNA Thermodynamics (<https://www.dnaform.com/devel/echo/thermodynamics>)にアクセスする。

### ECHO/DNA Thermodynamics

Please enter oligonucleotide sequence below.

- ECHO with thiazole orange doubly labeled thymidine (described as Z (T<sup>E</sup> in the paper below)) only.
- Different lines are treated as different oligonucleodies.
- ECHO and Reverse complementary DNA sequences must be the same size.
- Mis-match base pair one-base next to Z(T<sup>E</sup>) can not be calculated properly yet.

ECHO Sequences (using Z for T<sup>E</sup>) (5'→3') :      Reverse Complement DNA Sequences (5'→3') :

① 計算したいEprobeの塩基配列をコピーする。  
蛍光標識したいTをZに置き換える。

→

↑

② クリック

③ 相補鎖が表示される。

Temperature:  ° C

[Na<sup>+</sup>] =  M (typical PCR: 0.05M, typical SmartAmp: 0.01 M)

[Mg<sup>++</sup>] =  M (typical PCR: 0.0015M, typical SmartAmp: 0.008 M)

[ECHO] = [DNA] =  μM

④ クリック

\*PCRの反応条件(温度、ナトリウム、マグネシウム)を入力。  
通常は60°C、[Na+]=0.05M、[Mg++]=0.0015M、  
[ECHO]=[DNA]=0.05もしくは0.04uM

Users of the ECHO/DNA Thermodynamics page are requested to cite:

Kimura,Y., Hanami,T., Tanaka,Y., de Hoon,M.J.L., Soma,T., Harbers,M., Lezhava,A., Hayashizaki,Y. and Usui,K. [Effect of Thiazole Orange Doubly Labeled Thymidine on DNA Duplex Formation](#). Biochemistry, 51, 6056-6067 (2012).

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## Tm計算例(5'-GGCTAGZCGATCGAATGC-3'のTm予測)

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- Mis-match base pair one-base next to Z(T<sup>E</sup>) can not be calculated properly yet.

ECHO Sequences (using Z for T<sup>E</sup>) (5'→3') :  
 GGCTAGZCGATCGAATGC

Reverse Complement DNA Sequences (5'→3') :  
 GCATTCGATCGaCTAGCC

Temperature: 60 ° C  
 [Na<sup>+</sup>] = 0.05 M (typical PCR: 0.05M, typical SmartAmp: 0.01 M)  
 [Mg<sup>++</sup>] = 0.0015 M (typical PCR: 0.0015M, typical SmartAmp: 0.008 M)  
 [ECHO] = [DNA] = 0.05 μM

DNA/DNA = チアゾールピンク標識の場合の予測Tm値 (▼)  
 ECHO/DNA (by fluorescence) = チアゾールオレンジ標識の場合の予測Tm値 (▼)

⑤ 予測結果が表示される。

$\Delta H$ [kcal/mol],  $\Delta S$ [cal/mol/K],  $\Delta G_{60}$ [kcal/mol],  $\alpha$  (the fraction of double-stranded DNA),  $T_M$ [° C]

Sequence	DNA/DNA					ECHO/DNA					ECHO/DNA (by fluorescence)				
	$\Delta H$	$\Delta S$	$\Delta G_{60}$	$\alpha$	$T_M$	$\Delta H$	$\Delta S$	$\Delta G_{60}$	$\alpha$	$T_M$	$\Delta H$	$\Delta S$	$\Delta G_{60}$	$\alpha$	$T_M$
5'-GGCTAGZCGATCGAATGC-3' 3'-CGATCaGCTAGCTTAGC-5'	-143.0	-400.0	-10.1	0.093	55.6	-126.0	-341.0	-12.5	0.61	61.2	-156.0	-428.0	-13.6	0.8	63.3

Users of the ECHO/DNA Thermodynamics page are requested to cite:  
 Kimura,Y., Hanami,T., Tanaka,Y., de Hoon,M.J.L., Soma,T., Harbers,M., Lezhava,A., Hayashizaki,Y. and Usui,K. [Effect of Thiazole Orange Doubly Labeled Thymidine on DNA Duplex Formation](#). Biochemistry, 51, 6056-6067 (2012).

# フルマッチとミスマッチのTm値予測例

フルマッチ(上側がEprobe配列、下側が相補鎖)  
 5' GGCTAGZCGATCGAATGC 3'  
 3' CCGATCaGCTAGCTTACG 5'

ミスマッチ(上側がEprobe配列、下側がミスマッチを含む相補鎖)  
 5' GGCTAGZCGATCGAATGC 3'  
 3' CCGATCaGC**G**AGCTTACG 5'

## ECHO/DNA Thermodynamics

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- Different lines are treated as different oligonucleotides.
- ECHO and Reverse complementary DNA sequences must be the same size.
- Mis-match base pair one-base next to Z(T<sup>E</sup>) can not be calculated properly yet.

ECHO Sequences (using Z for T<sup>E</sup>) (5'→3') :

```
GGCTAGZCGATCGAATGC
GGCTAGZCGATCGAATGC
```

①Eprobeの配列 (5'→3'方向)を入力

Reverse Complement DNA Sequences (5'→3') :

```
GCAATTCGATCGaCTAGCC
GCATTCGATCGaCTAGCC
```

②相補鎖の配列(5'→3'方向)を入力  
 上段:フルマッチ、下段:ミスマッチ

↑  
 ここは押さないでください。

Temperature: 60 ° C

[Na<sup>+</sup>] = 0.05 M (typical PCR: 0.05M, typical SmartAmp: 0.01 M)

[Mg<sup>2+</sup>] = 0.0015 M (typical PCR: 0.0015M, typical SmartAmp: 0.008 M)

[ECHO] = [DNA] = 0.05 μM

Calculate ← ③クリック

④予測結果が表示される(上段:フルマッチ、下段:ミスマッチ)。

$\Delta H$ [kcal/mol],  $\Delta S$ [cal/mol/K],  $\Delta G_{60}$ [kcal/mol],  $\alpha$ (the fraction of double-stranded DNA),  $T_m$ [° C]

Sequence	DNA/DNA					ECHO/DNA					ECHO/DNA (by fluorescence)				
	$\Delta H$	$\Delta S$	$\Delta G_{60}$	$\alpha$	$T_m$	$\Delta H$	$\Delta S$	$\Delta G_{60}$	$\alpha$	$T_m$	$\Delta H$	$\Delta S$	$\Delta G_{60}$	$\alpha$	$T_m$
5'-GGCTAGZCGATCGAATGC-3' 3'-CCGATCaGCTAGCTTACG-5'	-143.0	-400.0	-10.1	0.093	55.6	-126.0	-341.0	-12.5	0.61	61.2	-156.0	-428.0	-13.6	0.8	63.3
5'-GGCTAGZCGATCGAATGC-3' 3'-CCGATCaGC <b>G</b> AGCTTACG-5'	-129.0	-360.0	-9.32	0.031	53.1	-112.0	-301.0	-11.7	0.41	58.9	-142.0	-388.0	-12.7	0.66	61.7

Users of the ECHO/DNA Thermodynamics page are requested to cite:

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