

**Primer design for DNA sequencing.v1**

1. **Obtain the target DNA sequence** from your source or online, and save it in a word file. Print a hard copy of the sequence.
2. **Use T7 and Sp6 primers** if these sequences flank your sequence in the plasmid.
3. **Pick up a 20-bp sequence** at about 500 bp into your full sequence and paste to the query box of “Nucleotide base codes”at: [www.basic.northwestern.edu/biotools/oligoalc.html](http://www.basic.northwestern.edu/biotools/oligoalc.html).
4. Click the “Calculate” button to obtain the resulting calculation information. You should move your oligonucleotide sequence upstream and downstream this site to make sure that the temperature of “Salt Adjusted” is about **60°C and the GC content is about 50%**.
5. Click the button of “**Check self-complementarity**” to make sure no potential hairpin formation and self-complementarity.
6. **Repeat step 4 and 5** around the sites of 1kb, 1.5kb and so on for additional primers to cover all the whole sequence.
7. Login at [www.idtdna.com/Home/Home.aspx](http://www.idtdna.com/Home/Home.aspx) using the username “zhenyan” and the password to order the primers. **Order your primers** as instructed. You should use the PO number to pay the charge.
8. **Print the receipt**. File everything in two places in Zhen Yan’s office: Oligo folder and Gene folder.
9. **Spin down the primers** for 30 seconds at full speed and then resuspend the oligoes in TE buffer at 200  $\mu\text{M}$  as a stock when the oligoes are received,. **Dilute** 20  $\mu\text{l}$  in 380  $\mu\text{l}$  of TE buffer (final concentration 10  $\mu\text{M}$ ) as working stock and store in X oligo-box at 4°C. Store the 200  $\mu\text{M}$  stock at -20°C. Log the primer information in the database (Yan’Office\Yan data\Database\YanLabDatabase). Please fill in the complete information.