TruArray®
Sequence Template Guidelines

LinkZill

Template File Versions

4K Throughput, without standard QC sequences	Fills up to 4,096 sequences	Download: TruArray_4K_wo_QC.xlsx
4K Throughput, with QC sequences	Fills up to 4,000 sequences	Download: TruArray_4K_w_QC.xlsx
65K Throughput, without QC sequences	Fills up to 65,000 sequences	Download: TruArray_65K_wo_QC.xlsx
65K Throughput, with QC sequences	Fills up to 65,536 sequences	Download: TruArray_65K_w_QC.xlsx

File Format

The file is an Excel file with two sheets. You can rename the file, but please do not modify the sheet names.

Oligo_ID_and_Seq

The sheet records the names and sequences of oligonucleotides, containing three columns of information:

Oligo_No	Oligo_ID	Oligo_Seq

- The index for each oligonucleotide.
  0 represents a demo oligo; 1 to 4,096/65,536 represents the sequences to be synthesized.
  Do not modify, add, or delete anything in this column.
- The name of each oligonucleotide,
  equivalent to the content after ">" in FASTA format.
- The sequence of each oligonucleotide,
  provided in the 5' -> 3' direction.

Array_Coord

The sheet sets the coordinates of the oligonucleotides on the chip, containing three columns of information:

Row	Column	Oligo_No

- The row coordinates on the chip,
  typically 1 to 64 or 1 to 256. Do not modify, add, or delete anything in this column.
- The column coordinates on the chip,
  typically 1 to 64 or 1 to 256. Do not modify, add, or delete anything in this column.
- The index number of each oligonucleotide.
  The content entered must already exist in the Oligo_No column of the Oligo_ID_and_Seq sheet.

Filling and Validation Rules

• The Oligo_ID_and_Seq Sheet

Oligo_No	Must be continuous, non-repeating positive integers.
	Should not be modified.
Oligo_ID	If you do not wish to set names, you may leave the entire column blank (IDs will be assigned automatically); however, you **cannot** fill some rows and leave others blank.
	Duplicate **Oligo_IDs** are **not allowed**. If a sequence needs to be synthesized multiple times, please assign multiple coordinates in the **Array_Coord** sheet instead of duplicating the row.
	Allowed characters: Uppercase and lowercase letters (A-Z, a-z), Arabic numerals (0-9), and certain symbols (+-=_.:). Spaces, full-width characters (including Chinese), line breaks, tabs, and other special characters are prohibited.
	Due to limitations in most bioinformatics software, the **first character** of the **Oligo_ID** must be a letter (A-Z, a-z) and cannot be a number or special character.
Oligo_Seq	**Allowed characters**: Letters (A-Z, a-z) and Arabic numerals (0-9).
	Unless there are special requirements, use uppercase **A, C, G, T** for **natural bases**. By default, lowercase letters will be converted to uppercase.
	Uppercase **R, Y, S, W, K, M, B, D, H, V, N** represent **condensed bases**. By default, lowercase letters will be converted to uppercase.
	You may use **N** for **random condensed bases**. However, if you need to synthesize non-N condensed bases (e.g., R, Y, S, W, K, M, B, D, H, V), please contact our customer manager for clarification and confirmation.
	Characters other than A, C, G, T, R, Y, S, W, K, M, B, D, H, V, N (including numbers) may represent **special monomers, specific synthesis recipe, or modification groups**. If required, please contact our customer manager.
	If your **lower- and uppercase letters represent different** monomers or recipes, please contact our customer manager.

• The Array_Coord Sheet

Row	Must be continuous, non-repeating positive integers.
	Should not be modified.
Column	Must be continuous, non-repeating positive integers.
	Should not be modified.
Oligo_No	Must be a positive integer, left blank, or kept as "Blocked for QC Loci".
	Leaving it blank indicates that no oligonucleotide synthesis will be performed at that coordinate.
	Keeping "Blocked for QC Loci" indicates that the coordinate is reserved for synthesizing **quality control sequences**.
	A positive integer represents the synthesis of a custom user sequence from the **Oligo_ID_and_Seq** sheet. This value must exist in the **Oligo_No** column of the **Oligo_ID_and_Seq** sheet, and the corresponding **Oligo_Seq** value for that row must not be empty.

Additional Suggestions and Rules

[1] In the Oligo_ID_and_Seq sheet, each row represents one unique oligonucleotide sequence.
For example, if a user needs to synthesize 1,800 different sequences using a 4K chip with 2 copies of each synthesized at different coordinates on the chip (occupying a total of 3,600 pixels),
they should fill rows with Oligo_No 1 to 1,800 in the Oligo_ID_and_Seq sheet,
and then assign two coordinates (two rows) for each sequence in the Array_Coord sheet,
rather than filling rows with Oligo_No 1 to 3,600 in the Oligo_ID_and_Seq sheet.

[2] The row where Oligo_No is "0" and Oligo_ID is "Demo_Oligo" is an example row. Please do not modify it.
This row is not synthesized and will not appear in the final product.

[3] Sequences that are defined in the Oligo_ID_and_Seq sheet but are not referenced in the Oligo_No column of the Array_Coord sheet will not be synthesized. We recommend that you verify these entries.

[4] In principle, Oligo_Seq should correspond one-to-one with Oligo_ID. A single Oligo_ID can only correspond to one Oligo_Seq.
While different Oligo_IDs corresponding to the same Oligo_Seq are permitted, we recommend verifying your design.

[5] Avoid cases where Oligo_ID is empty while Oligo_Seq contains data.

Product Quality Related Tips

[1] Significant sequence length differences may cause variations in synthesis yield, which can affect the uniformity of hybridization signals and capture efficiency.

[2] If you need to use polyX sequences to normalize sequence length, dT is the recommended base type.

[3] Excessive dA or dG content may negatively impact synthesis quality.

[4] The 3' end of the oligonucleotide is coupled to the chip surface, which may be subject to steric hindrance in some experiments. If you are concerned, you may choose to use a spacer in the inquiry form, typically a polyT sequence with a length of 20 nt.