QUANTO USER GUIDE

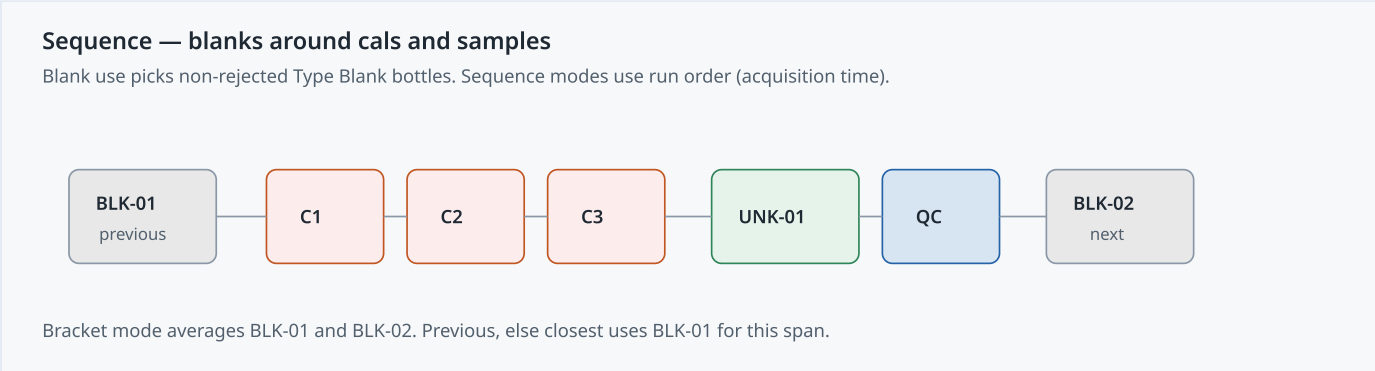
Blank offset

Put blank response on the curve as intercept; Blank use; what you see after Analyze.

Blank offset is a curve setting on the Quant (**Origin**). It uses the blank's *response* as a steady background on the calibration curve.

It does **not** subtract a blank concentration from **NativeConc**. That is a different option — Blank concentration.

Related: both options share the **Blank use** column on the Quants grid. Blank offset works in response space. Blank concentration works after the curve is read, toward NativeConc.



Blanks around calibrations and samples

What it is vs Ignore / Include / Force

Origin	What the fit does
Ignore	Free intercept. Blanks are not used.
Include	Adds a fake (0, 0) point, then fits. Still not a measured blank.
Force	Forces the intercept through zero: `y = m·x` (linear).
Blank offset	Measures blank response `b`, fits the standards after subtracting `b` **through zero**, then puts `b` back: `y = m·x + b`.

A blank is **not** a calibration level. Type **Blank** bottles do not become curve points. Their response (ISTD-normalized when you use ISTD) becomes the intercept.

The unknown keeps its **original** response and is read from the restored curve. If **Blank corr** is also on, Analyze still runs: it keeps Blank offset, skips concentration subtraction (that would correct twice), and writes a warning. See Blank concentration.

When to use it

- The target has a stable background in solvent or matrix blanks.
- You want the curve to sit on that background, not a free intercept or a forced zero.

- You can mark those bottles as Type **Blank** and reject bad ones the same way you reject bad cal points.

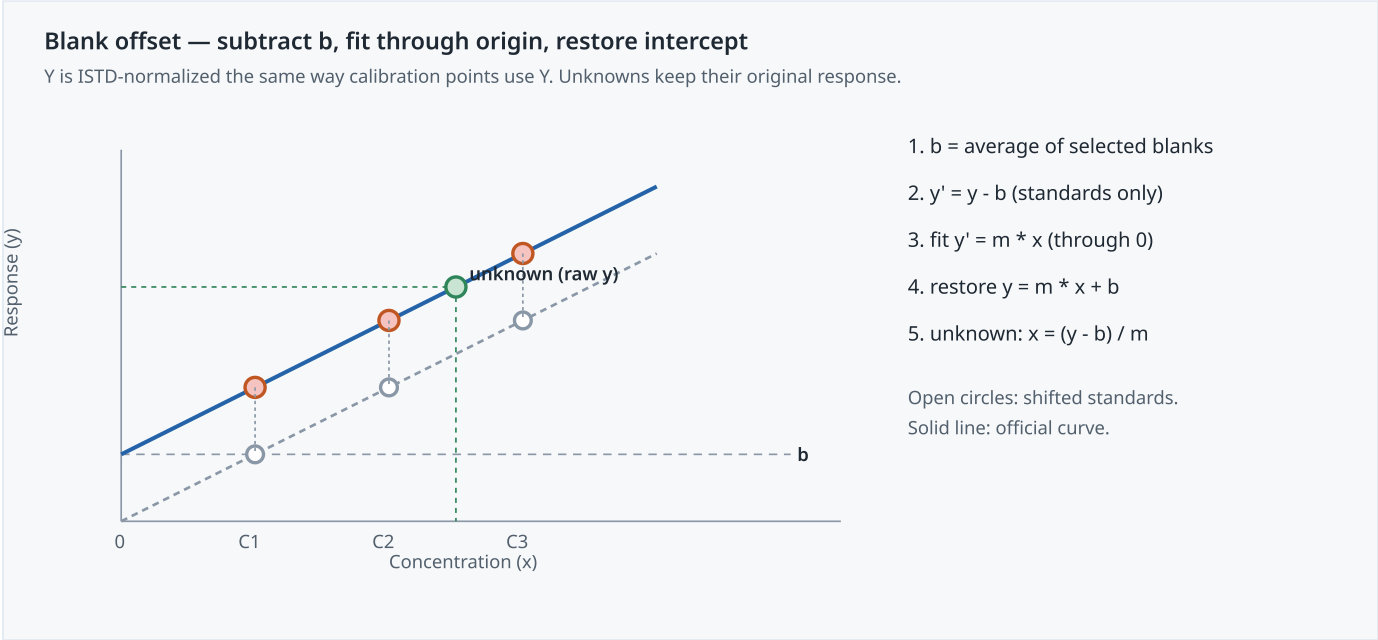
On the Quants grid: set **Origin** = **Blank offset**, then set **Blank use** to choose which blanks supply `b`.

What Analyze does (step by step)

Response Y is ISTD-normalized the same way as calibration points (`y = response / istdY`; for ESTD, `istdY = 1`).

1. Collect **non-rejected** Type **Blank** bottles (see Blank use).
2. `b` = average of those blank `y` values. If none (or Blank use = **None**), `b = 0` — same slope as Force. A **Warnings** entry records that fallback.
3. For each calibration standard on the curve: subtract `b` from its `y`.
4. Fit the active model **through the origin** on those shifted standards (linear, quadratic, or power). Average response factors and ln fits cannot use Blank offset.
5. Put the intercept back: effective curve `y = m·x + b` (or the quadratic / power form with intercept `b`).
6. For unknowns, QC, and other samples: use the **original** `y` and read concentration from the restored curve. Linear example: `x = (y − b) / m`.

Negative amounts clamp to 0, same as other origins.



Response plot: blank level, shifted standards, restored line, unknown on raw y

Blank use (which blanks)

Only **non-rejected** Type **Blank** bottles contribute — same idea as clearing **Use** on a cal point. Type **Solvent** is **not** a blank source.

A bottle is skipped when:

- the sample is rejected, or
- that Quant's result is rejected, or
- the blank has no usable (finite, non-negative) response.

Blank use	Selection
None	No blanks. `b = 0`. No measured intercept.
Average (CalGroup)	Average of eligible blanks in the **same CalGroup** as the curve. Unlabeled samples share the default group.
Average (overall)	Average of eligible blanks in the **whole batch**, all CalGroups.
Previous, else closest	The blank before the bracket span in run order; if none, the closest blank. Stays inside the CalGroup.
Bracket (previous + next)	Average of the blank before and after the span. One side is enough if the other is missing; if both are missing, same fallback as Previous, else closest. Stays inside the CalGroup.

The **span** is the run-time range of that bracket's calibration points and the samples that curve quantitates.

Use **Average (CalGroup)** or a sequence mode when groups should keep their own blanks. Use **Average (overall)** when one set of blanks should serve every group.

Rejected blanks never enter `b`.

After Analyze: what you see

Each calibration bracket stores:

- **Blank b** — the intercept `b` (response used on the curve)
- **Blank use** — how the blanks were picked
- **Blanks used** — sample names (or file names) that contributed

Those columns are on the calibration and result grids. Every concentration from that curve shows the **same** blank list: one `b` per bracket, not a different blank per unknown.

Method editor

On the **Quants** grid:

1. **Origin** → **Blank offset**
2. **Blank use** → how to pick blanks (shared with Blank concentration when **Blank corr** is checked)

ISTD Quants stay on average response factors and do not use Blank offset.

What this is not

- Not a zero-concentration calibration level.
- Not Include (fake origin) or Force (intercept exactly 0).
- Not subtraction of a blank *concentration* from NativeConc — that is Blank concentration.

Next: Blank concentration, ESTD, ISTD, bracketing, method design.