

resDetect™ Trypsin ELISA Kit

Pack Size: 96 tests

Catalog Number: RES-A002

IMPORTANT: Please carefully read this manual before performing your experiment.

For Research Use Only. Not For Use in Diagnostic or Therapeutic Procedures

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【Product Overview】

Trypsin ELISA Kit is used to quantitatively determine trypsin residues during cell culture. It is designed to provide a reliable solution for biological product quality assessment during drug development and CMC quality control stages. It can also be used as a universal detection tool for the quantitative determination of trypsin.

【Assay Principle】

This kit quantifies Trypsin using a sandwich ELISA format. The microplate is pre-coated with an Anti-Trypsin Antibody, which captures Trypsin present in standards and samples. After washing, a Biotin-Anti-Trypsin Antibody is added to bind the captured Trypsin, forming an Antibody-antigen-biotinylated antibody sandwich complex. After washing, a Streptavidin-HRP is added to the plate. Following additional washes, a substrate is added for color development. The reaction is stopped with stop solution, and the color changes from blue to yellow. Absorbance is measured at 450 nm with a 630 nm reference. The absorbance signal is directly proportional to the Trypsin concentration in the sample.

Note: This kit is only suitable for the detection of porcine Trypsin, and Trypsin means porcine Trypsin below.

【Precautions】

1. **For research use only.** Not for use in diagnostic or therapeutic procedures.
2. **Use before the expiration date** indicated on the label.
3. Do not mix or interchange reagents from different lots or kits.
4. If a sample OD exceeds the highest standard dilute the sample with 1×Dilution Buffer and retest.
5. Result variability may arise from operator technique, equipment performance, incubation conditions, or storage/handling. Follow the protocol exactly. The kit is designed to reduce some endogenous interference in biological samples. However, not all potential interfering factors can be eliminated.

【Materials Provided】

Table 1. Materials Provided

ID	Components	Size (96 T)	Format	Storage	
				Unopened	Opened
RES02-C01	Pre-Coated Anti-Trypsin Antibody Microplate	1 plate	Solid	2-8°C	2-8°C
RES02-C02	Trypsin Standard (100 ng/mL)	200 µL	Liquid	2-8°C	2-8°C
RES02-C03	Biotin-Anti-Trypsin Antibody	100 µL	Liquid	2-8°C	2-8°C
RES02-C04	Streptavidin-HRP	5 µg	Powder	2-8°C, Protected from light	-70°C, Protected from light
RES02-C05	1×Dilution Buffer	50 mL	Liquid	2-8°C	2-8°C
RES02-C06	20×Washing Buffer	50 mL	Liquid	2-8°C	2-8°C
RES02-C07	Substrate Solution	12 mL	Liquid	2-8°C, Protected from light	2-8°C, Protected from light
RES02-C08	Stop Solution	7 mL	Liquid	2-8°C	2-8°C

【Storage】

1. Store the unopened kit at 2-8°C upon receipt.
2. Locate the expiration date on the outer packaging and do not use reagents beyond their expiration date.

【Reagents and Consumables / Equipment Required but not Provided】

Table 2. Reagents and Consumables / Equipment Required but not Provided

Items	Specification
Deionized or distilled water	/
Single- or multi-channel micropipettes	Calibrated
Low-retention pipette tips	10 μ L, 100 μ L, 300 μ L, 1000 μ L
Reagent bottle	500 mL
Centrifuge tubes	1.5 mL, 10 mL
Microplate shaker	For 96-well plate shaking
Vortex mixer	/
Timer	/
Incubator	37°C
Microplate reader	Single- or dual- wavelength microplate reader capable of measuring absorbance at 450 nm with a 630 nm reference in 96-well microplates.

【Quick Guide】

Step 1 Preparation of the Standard Curve

Prepare the serial dilutions:

Tubes/Solution Code	Standard Stock Solution	Std.-7	Std.-6	Std.-5	Std.-4	Std.-3	Std.-2	Std.-1
Procedure	19.2 μ L	300 μ L	300 μ L	300 μ L	300 μ L	300 μ L	300 μ L	300 μ L
Solution Conc.	100 ng/mL	3.2 ng/mL	1.6 ng/mL	0.8 ng/mL	0.4 ng/mL	0.2 ng/mL	0.1 ng/mL	0.05 ng/mL
Dilution Buffer Vol.		580.8 μ L	300 μ L	300 μ L	300 μ L	300 μ L	300 μ L	300 μ L

Step 2 Add standards, samples, blank controls and Detection Antibody




Addition: Add 50 μ L of standards, samples, and blank to the designated wells, and then add 50 μ L Biotin-Anti-Trypsin Antibody to each well.



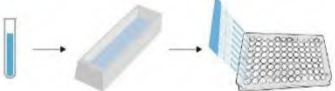
Incubation: Seal the plate and incubate at room temperature with shaking at 400-600 rpm for 1.0 h.


Step 3 Add Streptavidin-HRP



Washing (manual or automated): Discard the liquid. Add 300 μ L of wash buffer, wash 3 times, and tap dry.


Addition: Add 100 μ L to each well.





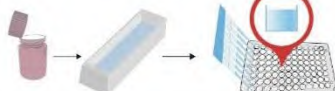
Incubation: Seal the plate and incubate at room temperature with shaking at 400-600 rpm for 30 min, protected from light.


Step 4 Add Substrate Solution



Washing (manual or automated): Discard the liquid. Add 300 μ L of wash buffer, wash 3 times, and tap dry.

Addition: Add 100 μ L to each well.





Incubation: Seal the plate and incubate at room temperature for 20 min, protected from light.

Step 5 Add Stop Solution and Data Recording



Addition: Add 50 μ L of Stop Solution.
Note: The color will change from blue to yellow.



Data Recording: Measure the absorbance at 450 nm with a 630 nm reference within 5 min after adding the stop solution.

【Reagent Preparation】

Bring all reagents to room temperature (20-25°C) before use. Check that each buffer and standard solution is clear and transparent, make sure these solutions are well mixed. If crystals are present in the solution, allow the reagents to equilibrate until the crystals are completely dissolved. If needed, incubate at 37°C for 10-15 minutes to facilitate dissolution.

According to Table 3, reconstitute the provided lyophilized product with ultrapure water to prepare the stock solution. Allow the vial to stand at room temperature for 15 to 30 minutes, then gently pipette up and down to mix. Do not vortex or shake vigorously.

Store the reconstituted stock solution at -70°C. It is recommended to aliquot the stock solution to avoid repeated freeze-thaw cycles. Do not exceed one freeze-thaw cycle.

Note: Due to unavoidable batch-to-batch variability in protein quantification, if lower back-calculation error is desired, users may use the same production batch of the protein as the standard to generate the standard curve for the corresponding residual analysis.

Table 3. Preparation Method

ID	Components	Format (96 T)	Concentration	Reconstituted water Vol.
RES02-C04	Streptavidin-HRP	5 µg	50 µg/mL	100 µL

【Assay Procedure】

1. Preparation of Working Solution

1.1 Preparation of 1×Washing Buffer

Dilute 25 mL of 20×Washing Buffer with ultrapure water or deionized water to a final volume of 500 mL and mix gently.

1.2 Preparation of Biotin-Anti-Trypsin Antibody working solution

Dilute the Biotin-Anti-Trypsin Antibody at 1:100 using 1×Dilution Buffer. Prepare fresh before use.

1.3 Preparation of Streptavidin-HRP working solution

Dilute the Streptavidin-HRP to 0.1 µg/mL using 1×Dilution Buffer. Prepare fresh before use, protected from light.

2. Preparation of the Standard Curve

The Trypsin Standard (RES02-C02) is 100 ng/mL.

2.1 Prepare the highest standard (Std.-7, 3.2 ng/mL)

Dilute 19.2 µL of Trypsin Standard into 580.8 µL of 1×Dilution Buffer. Mix gently and thoroughly.

2.2 Prepare the Serial Dilutions

Add 300 µL of 1×Dilution Buffer to each of the remaining centrifuge tubes. Perform 2-fold serial dilutions starting from Std.-7 to generate the standard curve. Mix thoroughly at each dilution step. 1×Dilution Buffer serves as the zero standard (Blank). The dilution procedure is shown in Figure 1.

Note: For residual analysis, it is recommended to generate the standard curve using standards from the same manufacturer and production lot as the target analyte to minimize measurement variability caused by differences in quantification methods or other supplier-related factors.

Figure 1. Preparation of 2-Fold Serial Dilutions of the Trypsin Standard

Tubes/ Solution Code	Standard stock solution	Std.-7	Std.-6	Std.-5	Std.-4	Std.-3	Std.-2	Std.-1
Procedure	19.2 µL	300 µL	300 µL	300 µL	300 µL	300 µL	300 µL	300 µL
Solution Conc.	100 ng/mL	3.2 ng/mL	1.6 ng/mL	0.8 ng/mL	0.4 ng/mL	0.2 ng/mL	0.1 ng/mL	0.05 ng/mL
Dilution Buffer Vol.		580.8 µL	300 µL	300 µL	300 µL	300 µL	300 µL	300 µL

3. Preparation of Samples (For reference)

Spike recovery experiments are a critical component of ELISA analysis. They are designed to assess potential interference from the sample matrix on target analyte detection and verify the reliability of the assay method. The core principle of this approach is to spike a known quantity of standard material into samples with a pre-determined concentration; recovery is then calculated by comparing the measured signal increment to the theoretical amount of standard added.

3.1 Pretreatment of Test Samples

Serially dilute the test samples with 1×Dilution Buffer to ensure that the analyte concentration falls within the detection range of the standard curve and to reduce potential matrix interference. The dilution scheme is shown in Table 4.

Table 4. Preparation Method

Sample ID	Volume(μ L)	1×Dilution Buffer(μ L)	Total volume(μ L)	Final Dilution Ratio	Diluted Sample ID
Test sample	150	150	300	2	Test sample-1
Test sample-1	150	150	300	4	Test sample-2

Note: 1) The required dilution factor may vary depending on the sample matrix and should be optimized for each sample type.

2) Perform serial dilutions carefully to ensure accuracy. It is recommended that the dilution factor for any single step does not exceed 10-fold, as excessive dilution may affect assay accuracy.

3.2 Preparation of Spiking Working Solution

Based on the expected sample concentrations, dilute the standard to an appropriate concentration for the spiking working solution using 1×Dilution Buffer. Prepare the spiking solution freshly before use.

Note: The final concentration of analyte in the spiked samples should fall within the linear detection range of the assay to avoid inaccurate results caused by values outside the assay range.

3.3 Preparation of Spiked Samples

Mix the test samples prepared in Step 3.1 with either the spike working solution or 1×Dilution Buffer at a 1:1 (v/v) ratio to prepare spiked and unspiked samples, respectively. Mix thoroughly. The dilution scheme is shown in Table 5.

Note: To minimize procedural variation, ensure that the sample volume, diluent or spike volume, mixing method, incubation time, and incubation temperature are identical for both spiked and unspiked samples.

Table 5. Preparation Method

Sample ID	Group	Volume(μ L)	1×Dilution Buffer(μ L)	Spiking working solution(μ L)	Total volume(μ L)	Final Dilution Ratio
Test sample	Unspiked	150	150	0	300	2
Test sample	Spiked	150	0	150	300	2
Test sample-1	Unspiked	150	150	0	300	4
Test sample-1	Spiked	150	0	150	300	4
Test sample-2	Unspiked	150	150	0	300	8
Test sample-2	Spiked	150	0	150	300	8

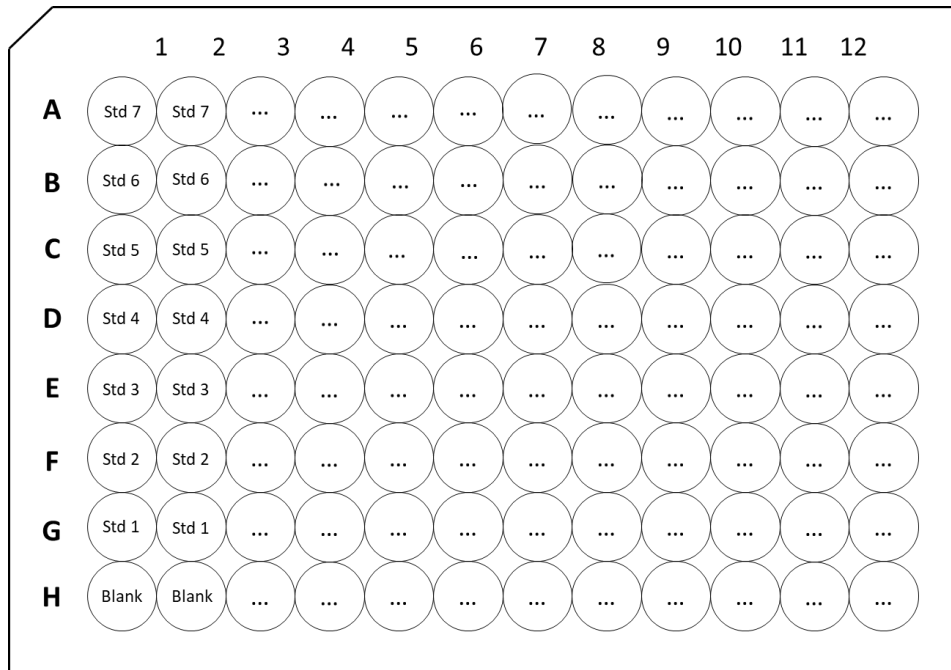
4. Addition of Samples

Add 50 µL serially diluted standards, test samples and spiked samples to the appropriate wells. For Blank Control wells, please add 50 µL 1×Dilution Buffer. Then add 50 µL Biotin-Anti-Trypsin Antibody (1:100 dilution) to each well. Shake gently to mix.

Note: 1) It is recommended to run all standards and samples in duplicate wells.

2) It is recommended to use the example plate layout shown in Figure 2 to record the positions of standards and samples.

Figure 2. Recommended Plate Layout for Standards and Samples



5. Incubation

Seal the plate with microplate sealing film. Incubate at room temperature on a microplate shaker set to 400-600 rpm for 1.0 hour.

6. Washing

Carefully remove the plate sealer and discard the liquid from the wells. Add 300 µL of 1×Washing Buffer to each well and soak for 10 seconds. Aspirate or decant the buffer. Repeat for a total of three washes. After the final wash, invert the plate and blot dry on absorbent paper.

7. Addition of Streptavidin-HRP

Add 100 µL Streptavidin-HRP working solution (0.1 µg/mL) to each well. Prepare the working solution fresh before use.

8. Incubation

Seal the plate with microplate sealing film. Incubate at room temperature on a microplate shaker set to 400-600 rpm for 30 minutes, protected from light.

9. Washing

Repeat step 6.

10. Substrate Reaction

Add 100 µL Substrate Solution to each well. Seal the plate and incubate at room temperature for 20 minutes, protected from light.

11. Reaction Termination

Add 50 µL of Stop Solution to each well. Gently tap the plate to ensure thorough mixing.

Note: The color in the wells will change from blue to yellow.

12. Data Recording

Measure the absorbance at 450 nm with a 630 nm reference within 5 minutes after adding the stop solution.

Note: Subtracting the OD_{630nm} value from the OD_{450nm} value helps reduce background interference.

【Calculation of Results】

1. Calculate the mean absorbance of duplicate wells for each standard and sample.
2. Generate the standard curve by plotting the standard concentrations on the x-axis and the absorbance values on the y-axis. Fit the curve using a four-parameter logistic (4-PL) model. The coefficient of determination (R²) should be ≥ 0.9900.
3. Determine the concentrations of the samples and spiked samples from the standard curve. Multiply the calculated concentrations by the appropriate dilution factors.
4. Calculation of spiked recovery (%)

$$\text{Recovery Rate (\%)} = \frac{\text{Concentration Spiked Sample} - \text{Concentration Unspiked Sample}}{\text{Concentration Control Spike}} \times 100\%$$

If the spike recovery falls outside the range of 75%-125%, this may indicate matrix interference affecting the ELISA assay. In such cases, optimize sample pre-treatment (e.g., additional dilution) before retesting.

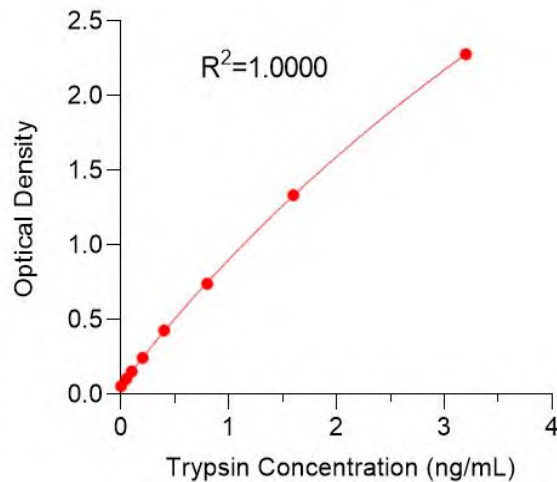
5. Detection Range

The assay detection range is 0.05 ng/mL-3.2 ng/mL. Samples with concentrations above the upper limit of the calibration curve should be reported as >3.2 ng/mL or diluted appropriately and reanalyzed to fall within the linear range. Samples with concentration below the lower limit of calibration curve should be reported as <0.05 ng/mL.

【Typical Data】

A standard curve must be generated for each microplate in every experiment. Absolute OD values may vary depending on the laboratory, operator, and equipment used. The example data provided below for reference only.

Standard Num.	Standard (ng/mL)	Average
Standard 7	3.2	2.280
Standard 6	1.6	1.337
Standard 5	0.8	0.742
Standard 4	0.4	0.431
Standard 3	0.2	0.247
Standard 2	0.1	0.156
Standard 1	0.05	0.105
Standard 0	0	0.058



【Sensitivity】

The minimum detectable concentration (MDC) of Trypsin is 0.033 ng/mL. The MDC was determined by calculating the mean optical density (OD) of 20 zero-standard replicates, adding two standard deviations (mean+2SD), and converting the resulting OD value to concentration using the standard curve.

【Precision】

1. Intra-assay Precision

Three samples of known concentration were tested ten replicates within a single plate to evaluate intra-assay precision.

2. Inter-assay Precision

Three samples of known concentration were tested in ten independent assays to evaluate inter-assay precision.

	Intra-assay Precision			Inter-assay Precision		
Sample (ng/mL)	3.2	0.5	0.05	3.2	0.4	0.05
n	10	10	10	10	10	10
Mean (ng/mL)	3.003	0.486	0.057	3.188	0.401	0.052
SD	0.173	0.019	0.002	0.017	0.008	0.003
CV (%)	5.8	3.9	3.5	0.5	2.0	5.0

【Recovery】

Five samples at different concentration levels were evaluated to determine the spike recovery of the assay.

Sample Conc.(ng/mL)	3.2	2.5	0.5	0.1	0.05
n	10	10	10	10	10
Mean (ng/mL)	3.003	2.434	0.486	0.105	0.057
SD	0.173	0.071	0.019	0.002	0.002
CV (%)	5.8	2.9	3.9	1.9	3.5
Recovery (%)	93.8	97.4	97.2	105.0	114.0

【Specificity】

Specificity 1: High, medium, and low concentrations of trypsin were spiked into MDCK (2.8×10^6 cells/mL), HEK293 (4×10^6 cells/mL), CHO (2×10^6 cells/mL), and Vero (3.6×10^6 cells/mL) samples, and the trypsin recovery rate was used as the specific validation index.

Sample	MDCK			HEK293			CHO			Vero		
Cells Conc.(cells/mL)	2.8×10^6			4×10^6			2×10^6			3.6×10^6		
Dilution Factor	2			2			2			2		
Spiked (ng/mL)	3.2	0.5	0	3.2	0.5	0	3.2	0.5	0	3.2	0.5	0
Mean (ng/mL)	3.25	0.55	0	2.86	0.47	0	2.82	0.38	0	2.74	0.41	0
Recovery (%)	102	110	/	89	85	/	88	77	/	86	81	/

Specificity 2: It was proved that there was no cross with bovine trypsin.

【Interfering Substances】

Spike a known concentration of Trypsin standard into the buffer. A recovery of 80%–120% is considered acceptable, indicating no significant matrix interference. For specific matrices or buffers, recovery should be verified to determine the optimal dilution factor.

Trypsin		
Matrix	Recovery (%)	Dilution Factor
20 mM L-histidine with 0.1% (w/v) PF68, pH6.0	101	2
20 mM L-histidine with 0.4% (w/v) Tween-80, pH6.0	96	2
1×PBS, pH7.3	81	2
1×PBS, pH7.3 with 11% Trehalose	83	2
20 mM L-histidine, pH6.0	96	2
50 mM Tris, 100mM Glycine, pH7.5	92	2
100 mM Tris, 20mM Sodium citrate, pH7.5	89	2
20 mM L-histidine 10% trehalose, pH6.0	89	2
50 mM Na Acetate, pH3.5	91	2
25 mM Phosphate, pH7.5	83	4
100 mM Glycine, pH3.5	92	2
100 mM Tris citrate, pH7.5	95	2

【Troubleshooting Guide】

Problem	Cause	Solution
Low signal	a. Kit components were not equilibrated to room temperature before use; b. Insufficient reconstitution time for lyophilized components.	a. Remove the kit from 2-8 °C storage in advance and allow all reagents to fully equilibrate to room temperature before starting the assay; b. After adding reconstitution buffer, allow lyophilized components to stand for at least 15 minutes and mix gently before use.
Poor assay reproducibility	a. Improper storage of reagents after opening; b. In consistent timing during sample dilution or pipetting.	a. Store reagents strictly according to the instructions in this manual; b. Plan the experimental workflow in advance and properly schedule assay timing.
High background	a. Insufficient washing; b. Excessive incubation temperature or prolonged substrate development time; c. Reagent contamination.	a. Increase soak time during wash steps and ensure the plate is thoroughly blotted dry after final wash; b. Strictly follow the operating procedures described in the manual; c. Use clean reagents and consumables, and maintain a clean experimental environment.
Edge effects	Uneven temperature distribution across the plate.	Ensure uniform incubation temperature and avoid stacking plates during incubation.
Good standard curve but no detectable signal in samples	a. Interfering substances present in the samples; b. Target analyte concentration below the assay detection.	a. Optimize sample dilution to minimize matrix interference; b. Use a higher-sensitivity assay if lower analyte levels are expected.