

# Comparison and Analysis of In Vitro Apoptosis Assays: Annexin V/PI, Caspase-3/7, TUNEL, and Mitochondrial $\Delta\Psi_m$

Haopeng Wang<sup>1\*</sup>

<sup>1</sup>College of Biological Science,  
University of California, Davis,  
United States of America  
Corresponding author: hapwang@  
ucdavis.edu

## Abstract:

This comparative review integrates evidence from 2015 to 2025 for four prevalent assays--Annexin V/propidium iodide (PI), caspase 3/7 activity, TUNEL, and mitochondrial membrane potential ( $\Delta\Psi_m$ ) dyes--within a cohesive framework encompassing performance, temporal resolution, concordance, and practicality. Core principles, recent advancements, and prevalent pitfalls are delineated alongside mitigations, with particular emphasis on standardized timeframes (6–8 hours and 24 hours) and orthogonal validation.  $\Delta\Psi_m$  and Annexin V/PI usually show early events, caspase 3/7 shows execution phase proteolysis, and TUNEL shows late DNA fragmentation in fixed samples. High content imaging, imaging flow cytometry, bioluminescent no wash formats, and genetically encoded reporters improve the resolution of time and context. The paper summarizes the patterns of concordance against composite standards and shows how trade-offs between throughput, cost, and analytical skill apply to common lab situations. Furthermore, it provides recommendations based on various scenarios to cover aspects such as high-throughput screening, studies of living cell mechanisms, and end-point histology. These recommendations emphasize the importance of clear thresholds/limits, calibration arms, and standardized reporting to make the results more understandable and reproducible.

**Keywords:** Apoptosis Detection; Annexin V/Propidium Iodide (PI); Caspase 3/7 Activity; Mitochondrial Membrane Potential ( $\Delta\Psi_m$ ); TUNEL Assay

## 1 Introduction

Apoptosis is a highly regulated cellular process that is crucial for the development of tissues and the maintenance of homeostasis in the adult body. Its dysregulation can lead to cancer and treatment resistance, the gradual loss of neurons in neurodegenerative diseases, the interaction between pathogens and the host during infections, and toxic consequences related to drug safety. In vitro systems - immortalized cell lines, primary cells, induced pluripotent stem cell-derived cells, tissue and organ models, and co-culture systems - always require reliable results for apoptosis detection to distinguish apoptosis from alternative modes of death and assign it a phenotype, measure the correlation between dose response and time response, depict pathways such as the extrinsic and intrinsic/mitochondrial branches, which are executed in a manner dependent or independent of caspases, and sort candidates in screening plans.

Over the past decade, methodological guidance has converged on three practical principles that motivate a comparative treatment of the most widely used assays. First, purpose driven selection is essential because no single assay captures the full temporal cascade with uniform specificity in all contexts.  $\Delta\Psi_m$  dyes and Annexin V/PI often report early events—mitochondrial depolarization and phosphatidylserine (PS) externalization in the setting of an intact plasma membrane—whereas caspase 3/7 activity marks the execution phase and TUNEL identifies late stage internucleosomal fragmentation in fixed samples [1-12]. Second, standardized time windows and explicit thresholds matter [13-15]. Reporting time matched readouts at 6–8 h and 24 h, coupled with transparent gating and calibration arms—z VAD fmk to test caspase dependence and FCCP/oligomycin to define  $\Delta\Psi_m$  dynamic range—improves cross study comparability and reduces interpretive ambiguity [10-12]. Third, orthogonal confirmation mitigates false positives from transient PS flips, dye photophysics, or DNA nicking in repair contexts, and guards against false negatives in caspase independent apoptosis [13-15].

Technological advances broaden both resolution and context. High content microscopy and imaging flow cytometry enable morphology aware classification and kinetic tracking in heterogeneous populations, strengthening stage specific interpretation [14,16]. Fluorescence lifetime or FRET based caspase sensors and bioluminescent no wash assays reduce handling artifacts and lengthen temporal coverage while maintaining sensitivity and scalability for plate formats [5,6]. Engineered Annexin A5 probes and spectral cytometry expand dynamic range and multiplexing for Annexin V/PI [1,17]. For  $\Delta\Psi_m$ , carefully titrated,

non-quenching TMRE/TMRM protocols increasingly replace legacy JC 1 in quantitative workflows, and methods that directly monitor mitochondrial outer membrane permeabilization (MOMP) add upstream mechanistic precision and closer alignment to causal checkpoints in intrinsic apoptosis [10,18].

Within this landscape, the present review offers a structured comparison designed for common laboratory scenarios. Section 2 summarizes the principles, strengths, and vulnerabilities of each assay family; Section 3 formalizes evaluation axes—performance, temporal resolution, concordance with composite standards, and practicality—and synthesizes findings from studies that report explicit time points, thresholds, controls, and cross assay comparisons [13-15]. Section 4 provides scenario based recommendations for high throughput discovery, live cell mechanistic studies, and endpoint histology, and closes with a forward looking outlook centered on multimodal automation, minimum information reporting, and open benchmarks.

## 2 Overview of Mainstream Assays

### 2.1 Annexin V/PI

For principle & readout, Annexin V binds externalized PS in a  $Ca^{2+}$ -dependent manner, while PI enters cells with compromised membranes to stain DNA [1-3]. Two-parameter analysis partitions viable (Annexin-/PI-), early apoptotic (Annexin+/PI-), late apoptotic/secondary necrotic (Annexin+/PI+), and primary necrotic (Annexin-/PI+) [1-3]. Imaging flow adds morphology-aware features (blebbing, nuclear condensation) to refine classification [14,16].

Regarding operational dependencies, free  $Ca^{2+}$  must be present; chelators such as EDTA reduce sensitivity. Compensation, voltage settings, and reproducible gate placement materially affect specificity and cross-study comparability. Annexin concentration and incubation time should be titrated in the actual matrix because serum proteins and ionic strength alter binding kinetics.

Regarding common confounders & mitigations, transient PS externalization during activation, mechanical shear during harvest, and ionic/temperature shifts inflate early apoptosis calls. Gentle handling,  $Ca^{2+}$  containing buffers, time-matched untreated controls, and transparent gate documentation mitigate such artifacts. Because late apoptotic cells may lose Annexin epitopes or fragment, combining with PI and morphology avoids misclassification [1-3]

Regarding recent advances, spectral cytometry improves separation in multiplex panels; engineered Annexin A5 probes extend dynamic range and enable no-wash live-cell monitoring; imaging flow supports trajectory analysis

when paired with caspase reporters [16,17].

For practical notes, use EDTA free dissociation; titrate Annexin/PI; include a necrosis control (e.g., mild detergent or heat shock) to anchor the Annexin-/PI+ quadrant; archive compensation matrices and representative dot plots for reproducibility [1-3].

## 2.2 Caspase 3/7 activity

For principle & readout, DEVD using fluorogenic or chemiluminescent substrates and genetically encoded reporters measures executioner caspase activity [4-6]. Luminescent formats offer elevated sensitivity and a broad dynamic range, accommodating 96–384-well plates, rendering them suitable for high-throughput screening.

Regarding complementary strategies, FLICA chemicals enable covalent, activity-dependent labeling in intact cells for microscopy or flow cytometry, facilitating single-cell resolution and co-staining (e.g., Annexin or  $\Delta\Psi_m$ ) to stage events [4,12].

Regarding specificity limits & mitigations, caspase-independent apoptosis results in false negatives, while off-target proteases and probe instability lead to erroneous positives. Adding z-VAD-fmk rescue arms, morphological confirmation, and time-matched Annexin strengthens inference. Normalizing to cell number or ATP content accounts for cytotoxicity-induced loss and plate edge effects.

Regarding recent advances, fluorescence lifetime and FRET sensors measure caspase activity in living cells with less background noise. Bioluminescent no-wash devices reduce disturbances and allow for continuous monitoring [5,6].

For practical notes, report the concentration of the substrate, the time of incubation, and the settings for the reader. Check for linearity and signal stability, and set positive thresholds based on vehicle distributions and known inducers.

## 2.3 TUNEL

For principle & readout, TUNEL labels 3' OH DNA ends generated during internucleosomal cleavage and is suited to endpoint analysis in fixed cells and tissues [7-9]. Signal

colocalizes with nuclear condensation/fragmentation and often with cleaved PARP or active caspase 3 in canonical apoptosis.

Regarding confounders & mitigations, severe necrosis, autolysis, or intense DNA repair can generate TUNEL positivity; over permeabilization inflates background [7-9]. Gentle fixation, DNase treated positives, strict negatives (–TdT), and triangulation with membrane or caspase readouts are recommended [7-9]. For tissues and 3D cultures, optical clearing and careful sampling frames reduce edge bias.

For practical notes, find the best way to fix and permeabilize cells to preserve morphology and ensure probe access. Report the thresholding method, display typical fields, and think about using multiplex immunostaining to give spatial context.

## 2.4 $\Delta\Psi_m$ (TMRE/TMRM, JC 1)

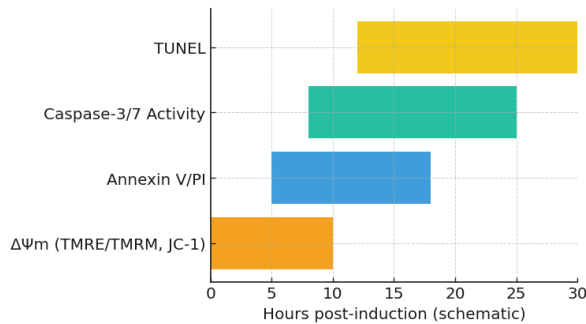
For principle & readout, potentiometric dyes quantify mitochondrial depolarization that often precedes caspase activation in intrinsic apoptosis [10-12]. TMRE/TMRM at non-quenching concentrations provide linear single-channel quantitation; JC-1 is ratiometric but aggregation prone and less quantitative [10-12].

Regarding calibration, artifacts & mitigations, FCCP titration defines the depolarized floor; oligomycin tests ATP synthase coupled contributions [10,12]. Photobleaching, dye self-quenching at high concentration, and non-equilibrium loading are recurrent issues; standardized, non-quenching protocols mitigate them. Pairing  $\Delta\Psi_m$  with caspase reporters aligns mitochondrial and execution events and clarifies kinetics [10-12].

Regarding mechanistic extensions, direct MOMP reporters and cytochrome c release assays add upstream mechanistic anchors and help interpret  $\Delta\Psi_m$  changes when electron transport inhibition or metabolic remodeling complicate polarization states [10,18].

For practical notes, validate dynamic range in every cell system; minimize illumination; specify dye concentration/loading time; document temperature and medium composition.

As a temporal reference point, see Figure 1 for typical detection windows used for staging across this review.



**Fig. 1. Typical detection windows for in vitro apoptosis assays (Picture credit: Original).**

### 3 Comparative Analysis

#### 3.1 Corpus and inclusion

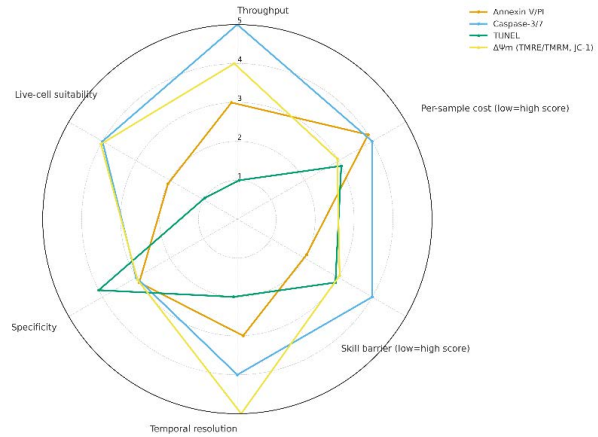
This synthesis emphasizes in vitro studies from 2015 to 2025 that report explicit time points, thresholds, controls, or cross assay comparisons enabling standardized evaluation. Methods/protocol papers are retained when they provide gating/compensation strategies, inhibitor arms (z VAD fmk), or  $\Delta\Psi_m$  calibration details (FCCP/oligomycin) [10-12]. A structured extraction template captures model system, perturbation identity/dose/schedule, assay parameters, control arms, time points (including the canonical 6–8 h and 24 h windows), thresholds/gates, analytical modality, and adjudication standards.

#### 3.2 Evaluation metrics

**Performance:** Sensitivity/specificity are interpreted relative to composite standards (e.g., morphology + Annexin quadrants) or consensus across orthogonal assays [13-15]. **Temporal resolution:** Early (6–8 h) vs late ( $\approx 24$  h or longer) windows map to biological sequence from mitochondrial events and PS externalization to caspase execution and DNA fragmentation.

**Concordance:** Agreement is analyzed within time matched pairs and against composites; discordance is traced to kinetic offsets (e.g.,  $\Delta\Psi_m$  loss prior to caspase activation), pathway dependence (e.g., caspase independent apoptosis), or technical factors (e.g.,  $\Delta\Psi_m$  quenching, poor compensation) [1-12].

**Practicality:** Throughput (plate vs single cell cytometry), per sample cost, instrument access, and required analytical skill (compensation, kinetic imaging) shape method selection. Figure 2 provides a qualitative practicality profile across assays.



**Fig. 2. Practicality profile across assays (qualitative schematic; higher is better) (Picture credit: Original).**

#### 3.3 Comparative findings

$\Delta\Psi_m$  and Annexin V/PI often exhibit discernible changes within 6–8 hours following robust intrinsic inducers (e.g., staurosporine) [1,12].  $\Delta\Psi_m$  loss frequently occurs prior to Annexin-positive in several cell types, aligning with mitochondrial priming and MOMP [10,18]. The activity of caspase-3/7 connects early and late windows; it may be seen in strong models after 6–8 hours and is generally higher after 24 hours. [4-6]. TUNEL-positive usually builds up at least 24 hours after the event, showing how fragmentation and clearing work downstream [7-9].

The specificity of Annexin V/PI depends on  $\text{Ca}^{2+}$  buffers, careful handling, and stable gate positioning. Transient PS flips and chelation artifacts are common problems. [1-3]. Caspase readouts might not detect apoptosis that doesn't depend on caspases, and they could be messed up by off-target proteases or probe decay. Using z-VAD-fmk rescue and morphology can help resolve this. TUNEL gives false positives in necrosis and repair, hence DNase+ and rigorous –TdT controls are very important [7-9].  $\Delta\Psi_m$  tests are susceptible to dye aggregation, quenching, and photobleaching; non-quenching TMRE/TMRM settings and FCCP/oligomycin titrations normalize the dynamic range [10-12].

In early windows, there is a better match between  $\Delta\Psi_m$  loss and Annexin positivity. In late windows, there is a better match between caspase activity and TUNEL. [7-12]. Deviations often exhibit mechanistic diversity; for instance,  $\Delta\Psi_m$  collapse occurs without caspase activation in the presence of metabolic toxins, or caspase-positive/Annexin-negative intermediates mani-fest during rapid execution [10-12].

Plate-based caspase assays provide the best sensitivity and throughput and are the most cost-effective.  $\Delta\Psi_m$  imaging,

on the other hand, balances throughput with mechanistic knowledge but needs careful calibration. Standard Annexin V/PI requires access to a cytometer and knowledge of how to compensate for it. Imaging flow makes things clearer but slows down throughput. TUNEL has lower throughput but is very useful for fixed samples and spatial multiplexing [1,14].

These trade-offs are shown in effective pipelines: HTS

prefers screening for caspase first, then staging for Annexin, and finally selective  $\Delta\Psi_m$  calibration. live-cell mechanism investigations use calibrated  $\Delta\Psi_m$  with kinetic caspase reporters and planned Annexin snapshots. Endpoint histology uses TUNEL with multiplex immunostaining [7-12]. Table 1 shows practical comparison and recommended controls.

**Table 1. Practical comparison and recommended controls**

Assay	Primary event measured	Typical informative window	Strengths	Common pitfalls	Recommended controls
Annexin V/PI	PS externalization with membrane integrity	Early (3–12 h) and late ( $\geq 12$ h) staging	Widely available; quadrant classification; pairs with morphology	Transient PS flips; chelation; shear-induced artifacts; compensation errors	$\text{Ca}^{2+}$ buffers; gentle handling; necrosis positive control; transparent gates [3], [2], [1]
Caspase3/7	Executioner proteolysis	6–24 h (inducer dependent)	High sensitivity; scalable plates; kinetic nowash options	Caspaseindependent apoptosis; offtarget proteases; probe decay	zVADfmk rescue; morphology/Annexin corroboration; normalization [4], [6], [5]
TUNEL	DNA fragmentation (3'OH ends)	$\geq 24$ h (endpoint)	Spatial context in fixed samples; multiplex immunostaining	Necrosis/repair positivity; overpermeabilization	DNase+ and -TdT controls; gentle fixation; parallel Annexin/caspase [7], [8], [9]
$\Delta\Psi_m$ (TMRE/TMRM, JC1)	Mitochondrial depolarization	1–12 h (often precedes caspase)	Early, mechanismleaning; quantitative with TMRE/TMRM	Dye aggregation/quenching; photobleaching; nonequilibrium loading	FCCP/oligomycin calibration; nonquenching protocols; minimized illumination [10], [12]

## 4 Recommendations and Outlook

### 4.1 Scenario based pipelines

#### 4.1.1 High throughput screening (HTS)

Use a caspase 3/7 bioluminescent primary assay to detect a broad set of apoptosis linked perturbations with high sensitivity in 96–384 well format [4-6]. Predefine positivity thresholds using vehicle distributions and a canonical inducer. Validate a representative subset by Annexin V/PI to stage cells and flag necrosis; include  $\Delta\Psi_m$  calibration (FCCP/oligomycin) to prioritize mechanism leaning hits [1,12]. Add z VAD fmk rescue to test caspase dependence and normalize signals to cell number or ATP to control for cytotoxic loss. Record Z' factor and plate maps to ensure assay robustness across lots.

#### 4.1.2 Live cell dynamics & mechanism

Combine calibrated  $\Delta\Psi_m$  (TMRE/TMRM at non quench-

ing concentrations) with genetically encoded or no wash caspase reporters; schedule Annexin snapshots at key milestones to capture membrane reorganization [10-12]. Include FCCP/oligomycin and z VAD fmk control arms to validate dynamic range and dependence [10,12]. Imaging flow or high content time lapse supports morphology aware trajectories and estimation of time to event distributions (e.g., time from  $\Delta\Psi_m$  loss to caspase activation, and from caspase activation to Annexin positivity) [10,14]. Pre register analysis rules for cells exiting the field of view or dividing during acquisition.

#### 4.1.3 Endpoint/fixed (2D/3D cultures, tissues)

Endpoint/fixed (2D/3D cultures, tissues). Employ TUNEL in conjunction with multiplex immunostaining (cleaved PARP, active caspase 3) to establish spatial context; validate findings with Annexin or caspase readouts in parallel cells where necrosis or substantial repair is anticipated [7-9]. For 3D organoids, use optical clearing and light sheet imaging where you can. Report sample frames to reduce



edge bias and measure apoptosis gradients.

## 4.2 Minimum information reporting checklist (MIA)

Model identity (species/line/passage), culture conditions, perturbation identity/purity/dose/schedule and solvent, assay parameters (sources/lots, dye/reagent concentrations, incubation/loading times, buffer composition including  $\text{Ca}^{2+}$  for Annexin), control & calibration arms (z VAD fmk; FCCP/oligomycin; DNase+/-TdT), acquisition/analysis details (instrument, spectral settings, compensation, thresholds with representative plots/images, blinding), time windows ( $\geq 1$  early and  $\geq 1$  late point), normalization (cell number/ATP/protein), adjudication standard (composite criteria), and data availability (raw images/FCS files and analysis scripts where allowed) [7-10].

## 4.3 Methodological caveats and mitigations

Avoid single assay determinism; disclose batch effects and instrument drift; document  $\Delta\Psi\text{m}$  non quenching conditions and FCCP curves; archive Annexin gate placement and compensation; include z VAD fmk and morphology for caspase; document fixation/permeabilization and DNase+/-TdT controls for TUNEL; report illumination dose and phototoxicity checks for imaging workflows [7-12].

## 4.4 Future directions

Multimodal automation that synchronizes  $\Delta\Psi\text{m}$ , caspase activity, Annexin positivity, and morphology at single cell resolution will clarify state transitions and inter cell variability [10-12]. Open benchmark datasets with harmonized thresholds will enable quantitative concordance maps and rigorous power analyses for study design. Emerging methods that directly track MOMP and non canonical effectors, combined with standardized sharing of raw data and scripts, can transform purpose driven guidance into reusable decision support and shorten iteration cycles [18].

# 1 Conclusion

This analysis brings together what each common in vitro apoptosis test assesses, when the results are useful, where mistakes are most likely to happen, and what protections work best to prevent those mistakes.  $\Delta\Psi\text{m}$  dyes and Annexin V/PI capture early events suited for triage and staging; caspase 3/7 indexes execution and scaled easily for screening; TUNEL gives late-stage confirmation with spatial context in fixed samples. A consistent pattern emerges across studies: aligning measurements to standardized

windows (an early 6–8 h check and a  $\approx 24$  h endpoint), reporting explicit thresholds/gates and calibration arms, and corroborating results with orthogonal readouts materially improve interpretability and reproducibility. In practice, technique selection can be aligned with prevalent objectives and limitations. Caspase-first pipelines with selective Annexin confirmation and tailored  $\Delta\Psi\text{m}$  calibration help high-throughput discovery by putting mechanism-relevant hits at the front of the list while keeping costs down. Live cell mechanistic studies benefit from calibrated  $\Delta\Psi\text{m}$ , kinetic caspase reporters, and planned Annexin photos to recreate trajectories from mitochondrial dysfunction to membrane rearrangement. Endpoint assessments in 2D/3D cultures or tissues utilize TUNEL with multiplexing, while safeguarding against necrosis and repair artifacts with suitable controls. Looking ahead, multimodal automation, open concordance benchmarks, and community adoption of minimum information reporting can turn purpose-driven guidance into decision support that can be used again and over again. This will make people more confident in apoptosis-centric inference in discovery and mechanistic biology.

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