PTMScan® Succinyl-Lysine Motif [Succ-K] Kit

1 Kit (10 assays)

Description: PTMScan® Technology employs a proprietary methodology from Cell Signaling Technology for peptide enrichment by immunoprecipitation using a specific bead-conjugated antibody in conjunction with liquid chromatography (LC) tandem mass spectrometry (MS/MS) for quantitative profiling of post-translational modification (PTM) sites in cellular proteins. These include phosphorylation (PhosphoScan®), ubiquitination (Ubiscan®), acetylation (AcetylScan®), and methylation (MethylScan®), among others. PTMScan® enables researchers to isolate, identify and quantitate large numbers of post-translationally modified cellular peptides with a high degree of specificity and sensitivity providing a global overview of PTMs in cell and tissue samples without preconceived biases about where these modified sites occur. For more information on PTMScan® services, please visit www.cellsignal.com/services/index.html.

Background: Lysine is subject to a wide array of regulatory post-translational modifications due to its positively charged ε-amino group side chain. The most prevalent of these are ubiquitination and acetylation, which are highly conserved among prokaryotes and eukaryotes (1,2). Acyl group transfer from the metabolic intermediates acetyl-, succinyl-, malonyl-, glutaryl-, butyryl-, propionyl-, and crotonyl-CoA all neutralize lysine's positive charge and confer structural alterations affecting substrate protein function. Lysine acetylation is catalyzed by histone acetyltransferases, HATs, using acetyl-CoA as a cofactor (3). Deacylation is mediated by histone deacetylases, HDACs 1-11, and NAD-dependent Sirtuins 1-7. Some sirtuins have little to no deacetylase activity, suggesting that they are better suited for other acyl lysine substrates (5).

Sirt 5 is a predominantly mitochondrial desuccinylase and demalonylase (5,6), in the absence of a known succinylltransferase, succinylation is likely driven by the concentration of succinyl-CoA and intracellular pH and is subject to metabolic fluctuations (7,8). Protein succinylation is especially prevalent among mitochondrial metabolic proteins and bacteria, further solidifying the evolutionary link between mitochondria and prokaryotes. It often occurs at lysine residues that are alternatively acetylated or ubiquitinated. More than a thousand lysine succinylation sites were identified on hundreds of proteins including glutamate dehydrogenase (15 sites), malate dehydrogenase, citrate synthase, carnabovyl phosphate synthase 1, and histone proteins (9).

License/Use Restrictions: Use of CST Motif Antibodies within certain methods (e.g., U.S. Patent No. 7,198,896 & 7,300,753) may require a license from CST. For information regarding academic licensing terms please have your technology transfer office contact CST Legal Department at CST_ip@cellsignal.com. For information regarding commercial licensing terms please contact CST Pharma Services Department at ptmscan@cellsignal.com.

Storage: Antibody beads supplied in IAP buffer containing 50% glycerol. Store at -20°C. Do not aliquot the antibody.

Directions for Use: Cells are lysed in a urea-containing buffer, cellular proteins are digested by proteases, and the resulting peptides are purified by reversed-phase solid-phase extraction. Peptides are then subjected to immunofluorescence purification using a PTMScan® Motif Antibody conjugated to protein A agarose beads. Unbound peptides are removed through washing, and the captured PTM-containing peptides are eluted with dilute acid. Reversed-phase purification is performed on microlites to desalt and separate peptides from antibody prior to concentrating the enriched peptides for LC-MS/MS analysis. CST recommends the use of PTMScan® IAP Buffer #9993 included in the kit. A detailed protocol and Limited Use License allowing the use of the patented PTMScan® method are included with the kit.

The chart shows the relative category distribution of proteins with succinylated lysine residues identified from peptides generated from a PTMScan® LC-MS/MS experiment of mouse liver tissue using PTMScan® Succinyl-Lysine Motif [Succ-K] Immunoaffinity Beads.
A. Solutions and Reagents

Reagents Not Included:
1. HEPES (Sigma, H-4334)
2. Sodium pyrophosphate (Sigma, S-6422)
3. β-glycerophosphate (Sigma, G-9691)
4. Urea, Sequential grade (Thermo Scientific, 29700)
5. Sodium orthovanadate (Thermo Scientific, S-5008)
6. Iodoacetamide (Sigma, I-1425)
7. Dithiotreitol (DTT) (Cell Signaling Technology, 7016)
8. Trypsin-TPCK (Worthington, LS-037/4)
9. Trypsin (Promega, V5113)
10. Lysyl Endopeptidase, LysC (Wako, 129-02541)
11. Trifluoroacetic acid (TFA), Sequential grade (Thermo Scientific, S-2800)

NOTE: Prepare solutions for cell lysis (Section I), Sep-Pak purification (Section II), and IP enrichment (Section III) with reverse osmosis deionized (RODI) or equivalent grade water. Prepare solutions using HPLC grade water (Burdick and Jackson water) for the peptide concentration steps (Section IV and V).

Stock Solutions:
1. HEPES, pH 8.0 (200mM): Dissolve 23.8 g HEPES in approximately 450 ml water, adjust to pH 8.0 with 5 M NaOH, and bring to a final volume of 500 ml. Filter through a 0.22 μm filter. Store at 4°C for up to six months.
2. Sodium pyrophosphate: Make 50X stock (125 mM): 1.1 g/50 ml. Store at 4°C for up to six months.
3. β-glycerophosphate: Make 1000X stock: 22 g/100 ml. Divide into 100 μl aliquots and store at -20°C.
4. Sodium orthovanadate: Make 100X stock: 1.84 g/100 ml. Sodium orthovanadate must be depolymerized (activated) according to the following protocol:
   a. For a 100 ml solution, fill up with water to approximately 90 ml. Adjust the pH to 10.0 using 1 M NaOH with stirring. At this pH, the solution will be yellow.
   b. Boil the solution until it turns colorless and cool to room temperature (put on ice for cooling).
   c. Adjust the pH to 10.0 and repeat step 2 until the solution remains colorless and the pH stabilizes at 10.0 (usually it takes two rounds). Adjust the final volume to 100 ml with water.
5. Dithiotreitol (DTT): Make 1.25 M stock: 19.25 g/100 ml. Divide into 200 μl aliquots. Store at -20°C for up to one year. Thaw one aliquot for each experiment, do not refreeze thawed vial.
6. Trypsin-TPCK (Worthington): Store dry powder for up to 2 years at -80°C. Seal the cap of the trypsin-TPCK container with parafilm to avoid collecting moisture, which can lead to degradation of the reagent. Prepare 1 mg/ml stock in 1 mM HCl. Divide into 1 ml aliquots and store at -20°C. Do not use up to six months.
7. Lysyl Endopeptidase (LysC): Store dry powder up to 2 years at -80°C. Seal the cap of the LysC container with parafilm to avoid collecting moisture, which can lead to degradation of the reagent. Prepare 5 mg/ml stock in 20 mM HEPES pH 8.0. Divide into single use aliquots, store at -80°C for up to one year.

I. Cell Lysis and Protein Digestion

A. Solutions and Reagents

NOTE: Prepare solutions with RODI or equivalent grade water.

1. Urea Lysis Buffer: 20 mM HEPES pH 8.0, 9 M urea, 1 mM sodium orthovanadate, 2.5 mM sodium pyrophosphate, 1 mM β-glycerophosphate.

NOTE: The Urea Lysis Buffer should be prepared fresh prior to each experiment. Do not include protease inhibitors.

NOTE: Dissolving urea is an endothermic reaction. Urea Lysis Buffer preparation can be facilitated by placing a stir bar in the beaker and by using a warm (not hot) water bath on a stir plate. 9 M Urea is used so that upon lysis, the final concentration is approximately 8 M. The urea lysis buffer should be used at room temperature. Placing the urea lysis buffer on ice will cause the urea to precipitate out of solution.

2. DTT solution (1.25 M) (see stock solutions for preparation)
3. Iodoacetamide solution: Dissolve 95 mg of iodoacetamide in water to a final volume of 5 ml. After weighing the powder, store the dark and add water only immediately before use. The iodoacetamide solution should be prepared fresh prior to each experiment.

B. Preparation of Cell Lysate, Suspension Cells

1. Grow approximately 1–2 x 10^6 cells for each experimental condition (enough cells to produce approximately 10–20 mg of soluble protein).
2. Harvest cells by centrifugation at 130 x g, for 5 min at room temperature. Carefully remove supernatant, wash cells with 20 ml of cold 1x PBS, centrifuge, remove PBS wash, and add 10 ml Urea Lysis Buffer (room temperature) to the cell pellet. Pipet the slurry up and down a few times (do not cool lysate on ice as this may cause precipitation of the urea).
3. If desired, the PTMScan® protocol may be interrupted at this stage. The harvested cells can be frozen and stored at -80°C for several weeks.
4. Using a microtip, sonicate lysate at 15 W output with 3 bursts of 15 sec each. Cool on ice for 1 min between each burst. Clear the lysate by centrifugation at 20,000 x g for 15 min at room temperature and transfer the protein extract (supernatant) into a new tube.

NOTE: Centrifugation is performed at room temperature to prevent urea from precipitating out of solution.

NOTE: Lysate sonication fragments DNA and reduces sample viscosity. Ensure that the sonicator tip is submerged in the lysate. If the sonicator tip is not submerged properly, it may induce foaming and degradation of your sample.

C. Preparation of Cell Lysate, Adherent Cells

1. Grow 1–2 x 10^6 cells for each experimental condition (enough cells to produce approximately 10–20 mg of soluble protein). The cell number corresponds to approximately 10 x 150 mm culture dishes (depending on the cell type), grown to 70–80% confluence. Prepare solutions with RODI or equivalent grade water.
2. Harvest all 10 x 150 mm culture dishes for one sample, remove media from the first dish by decanting, and let stand in a tilted position for 30 seconds so the remaining medium flows to the bottom edge. Remove the remainder of the medium at the bottom edge with a P-1000 micropipetor. Rinse each dish with 5 ml of cold PBS. Remove PBS as described above.
3. Add 10 ml of Urea Lysis Buffer (at room temperature) to the first dish, scrape the cells into the buffer, and let the dish stand in tilted position after scraping the buffer to the bottom edge of the tilted dish. Remove the medium from the second dish as above. Transfer the lysate buffer from the first dish to the second dish using a 10 ml pipette, then fill the first dish with the lid on for 30 sec and remove remaining buffer from the dish and collect. Scrape cells from the second dish and repeat the process until the cells from all the dishes have been scraped into the lysate buffer. Collect all lysate in a 50 ml conical tube.

NOTE: DO NOT place Urea Lysis Buffer or culture dishes on ice during harvesting. Harvest cells using Urea Lysis Buffer at room temperature. During lysing, the buffer becomes viscous due to DNA released from the cells.

4. The yield will be approximately 9–12 ml lysate after harvesting all the culture plates.
5. If desired, the PTMScan® protocol may be interrupted at this stage. The cell lysis can be frozen and stored at -80°C for several weeks.
6. Using a microtip, sonicate lysate at 15 W output with 3 bursts of 15 sec each. Cool on ice for 1 min between each burst. Clear the lysate by centrifugation at 20,000 x g for 15 min at room temperature and transfer the protein extract (supernatant) into a new tube.

NOTE: Lysate sonication fragments DNA and reduces sample viscosity. Ensure that the sonicator tip is submerged in the lysate. If the sonicator tip is not submerged properly, it may induce foaming and degradation of your sample.

D. Reduction and Alkylation of Proteins

1. Add 1/278 volume of 1.25 M DTT to the cleared cell supernatant (e.g. 36 µl of 1.25 M DTT for 10 ml of protein extract), mix well and place the tube into a 50°C incubator for 30 min.
2. Cool the solution on ice briefly until it has reached room temperature.
3. Add 1/10 volume of iodoacetamide solution to the cleared cell supernatant, mix well, and incubate for 15 min at room temperature in the dark.

E. Protease Digestion

1. Dilute 4-fold with 20 mM HEPES pH 8.0 to a final concentration of approximately 2 M urea, 20 mM HEPES, pH 8.0. For example, add 30 ml 20 mM HEPES pH 8.0 for 10 ml of lysate.

To view an updated protease digestion reference table, please visit http://www.cellsignal.com/services/ptmscan_kits.html

NOTE: LysC-digested material, a second protease digestion is required after the C18 tip purification of enriched peptides (see the protocol after C18 tip Purification). A secondary trypsin digestion is also recommended for enriched methylated tryptic peptides.

NOTE: Alternative proteases such as GluC, chymotrypsin, and others can be used in addition to the protease treatments outlined in the reference table to expand the coverage of modified peptides from each Motif Antibody. When considering the use of additional protease treatments it should be compatible with the respective Motif Antibody not cleaving residues within the designated sequence motif. Protease treatments that generate larger proteolytic peptides may not be ideal if the resulting peptides do not ionize well in the mass spectrometer.

F. Trypsin Digestion

1. Add 1/100 volume of 1 mg/ml Trypsin-TPCK (Worthington, LS037/4) stock in 1 mM HCl to digest overnight at room temperature with mixing.
2. Analyze the lysate before and after digest by SDS-PAGE to check for complete digestion.
3. Continue through the Sep-Pak, IAP, and C18 tip protocols prior to LC-MS analysis of enriched peptides.

G. LysC Digestion

1. Prepare 5 mg/ml stock solution of LysC in 20 mM HEPES pH 8.0. Aliquot for single use and store at -80°C.
2. Add LysC solution to peptides at 1:250 (w/w). For 20 mg sample, use 20 mg + 250 µg x 1 µL/µg = 16 µL LysC and digest overnight at room temperature.
3. Analyze the lysate before and after digest by SDS-PAGE to check for complete digestion.
4. Continue through the Sep-Pak, IAP, and C18 tip protocols before conducting the SECONDARY DIGESTION with trypsin (see end of protocol). Trypsin Digestion of Enriched LysC or Methylated Peptides.
II. Sep-Pak® C₁₈ Purification of Lysate Peptides

NOTE: Purification of peptides is performed at room temperature on 0.7 ml Sep-Pak columns from Waters Corporation, WAT051010.

NOTE: Sep-Pak® C₁₈ purification uses reversed-phase (hydrophobic) solid-phase extraction. Peptides and lipids bind to the chromatographic material. Large molecules such as DNA, RNA, and most protein, as well as hydrophobic molecules such as many small metabolites are separated from peptides using this technique. Peptides are eluted from the column with 40% acetonitrile (MeCN) and separated from lipids and proteins, which elute at approximately 60% MeCN and above.

NOTE: About 20 mg of protease-digested peptides can be purified from one Sep-Pak column. Purify peptides immediately after proteolytic digestion.

A. Solutions and Reagents

1. 20% trifluoroacetic acid (TFA): Add 1 ml of IAP buffer to the beads, mix by inverting tube 5 times, centrifuge for 30 sec at 2,000 x g, and transfer the peptide solution into the vial containing motif antibody beads. Pipet sample directly on top of the beads at the bottom of the tube to ensure immediate mixing. Avoid creating bubbles upon pipetting.

B. Acidification of Digested Cell Lysate

NOTE: Before loading the peptides from the digested sample on the column, they must be acidified with TFA for efficient peptide binding. The acidification step helps remove fatty acids from the digested peptide mixture.

1. Add 1/20 volume of 20% TFA to the digest for a final concentration of 1% TFA. Check the pH by spotting a small amount of peptide sample on a pH strip (the pH should be under 3). After acidification, allow precipitate to form by letting sample stand for 15 min on ice.

2. Centrifuge the acidified peptide solution for 15 min at 1,780 x g at room temperature to remove the precipitate. Transfer peptide-containing supernatant into a new 50 ml conical tube without precipitating the material.

C. Peptide Purification

NOTE: Application of all solutions should be performed by gravity flow.

1. Connect a 10 cc syringe (remove plunger) to the SHORT END of the Sep-Pak column.

2. Pre-wet the column with 5 ml 100% MeCN.

NOTE: Each time solution is applied to the column, air bubbles form in the junction where the 10 cc syringe meets the narrow inlet of the column. These must be removed with a gel-loading tip placed on a 1.7 ml Eppendorf tube, otherwise the solution will not flow through the column efficiently. Always check for appropriate flow.

2. Wash sequentially with 1 ml, 3 ml, and 6 ml of Solvent A (0.1% TFA).

3. Load acidified and cleared digest (from previous step) from a new 1.7 ml Eppendorf tube to save at -80°C for future use. Flow-through material can be used for subsequent IAPs.

D. Procedure

1. Centrifuge the tube containing lyophilized peptide for 5 minutes at 2,000 x g at room temperature to collect all material for dilution in IAP buffer. Add 1.4 ml IAP buffer. Resuspend pellets mechanically by pipetting repeatedly with a P-1000 micropipettor taking care not to introduce excessive bubbles into the solution. Transfer solution to a 1.7 ml Eppendorf tube.

NOTE: After dissolving the peptide, check the pH of the peptide solution by spotting a small volume on pH indicator paper (the pH should be close to neutral), or no lower than 6.0. In the rare case that the pH is more acidic (due to insufficient removal of TFA from the peptide under sub-optimal conditions of lyophilization), titrate the peptide solution with 1 M Tris base solution that has not been adjusted for pH. 5-10 μl is usually sufficient to neutralize the solution.

2. Clear solution by centrifugation for 5 min at 10,000 x g at 4°C in a microcentrifuge. The insoluble pellet may appear considerable. This will not pose a problem since most of the peptide will be soluble. Cool on ice.

3. Centrifuge the vial of antibody-bead slurry at 2,000 x g for 30 sec and remove all buffer from the beads. Wash antibody beads five times with 1 ml of 1X PBS. Centrifuge 2,000 x g after each wash. Resuspend beads in 40 μl PBS in the provided vial.

4. Transfer the peptide solution into the vial containing motif antibody beads. Pipet sample directly on top of the beads at the bottom of the tube to ensure immediate mixing. Avoid creating bubbles upon pipetting.

5. Tighten the cap on the vial. Seal the top of the vial with parafilm to avoid leakage. Incubate on a rotator for 2 hr at 4°C.

6. Centrifuge at 2,000 x g for 30 sec and transfer the supernatant with a P-1000 micropipettor to a labeled Eppendorf tube to save at -80°C for future use. Flow-through material can be used for subsequent IAPs.

NOTE: Some Phenol Red pH indicator may remain (it co-elutes during the Sep-Pak® C₁₈ purification of peptides) and color the peptide solution yellow. This coloration has no effect on the immunofinity purification step.

7. Perform all subsequent wash steps at 2-4°C. For all the washes except the final wash, avoid removing the last few microliters, since this may cause inadvertent removal of the beads.

8. Add 1 ml of IAP buffer to the beads, mix by inverting tube 5 times, centrifuge for 30 sec at 2,000 x g, and remove supernatant with a P-1000 micropipettor.

9. Repeat step 7 once for a total of TWO IAP buffer washes.

NOTE: All steps from this point forward should be performed with solutions prepared with Burdick and Jackson or other HPLC grade water.

10. Add 1 ml chilled HPLC water to the beads, mix by inverting tube 5 times, centrifuge for 30 sec at 2,000 x g, and remove supernatant with a P-1000 micropipettor.

11. Repeat step 9 two times for a total of THREE water washes. During the last water wash, the tube may need to be shaken while inverting in order to ensure efficient mixing.

NOTE: After the last wash step, remove supernatant with a P-1000 micropipettor as before, then centrifuge for 5 sec at 2,000 x g to remove fluid from the tube walls, and carefully remove all remaining supernatant with a gel loading tip attached to a P-200 micropipettor.

12. Add 55 μl of 0.15% TFA to the beads, tap the bottom of the tube several times (do not vortex), and let stand at room temperature for 10 min, mixing gently every 2-3 min.

NOTE: In this step, the post-translationally modified peptides of interest will be in the eluent.

13. Centrifuge 30 sec at 2,000 x g in a microcentrifuge and transfer supernatant to a new 1.7 ml Eppendorf tube.

14. Add 50 μl of 0.15% TFA to the beads, and repeat the centrifugation/elution step. Combine both eluents in the same 1.7 ml tube. Briefly centrifuge the eluent to pellet any remaining beads and carefully transfer eluent to a new 1.7 ml tube taking care not to transfer any beads.

IV. Concentration and Purification of Peptides for LC-MS Analysis

NOTE: We recognize there are many other routine methods for concentrating peptides using commercial products such as ZipTip® and C₁₈ tips (see below) that have been optimized for peptide desalting/concentration. Regardless of the particular method, we recommend that the method of choice be optimized for recovery and be amenable for peptide loading capacities of at least 10 μg.

C₁₈ tips: Thermo Scientific, part number SP201
ZipTip®: EMD Millipore, catalog number ZTC185960

III. Immunoaffinity Purification (IAP)

A. Solutions and Reagents

NOTE: Prepare solutions with RODI or equivalent grade water. Trifluoroacetic acid should be of the highest grade. All percentage specifications for solutions are vol/vol.

1. Materials Provided in the PTMScan Kit: 10X IAP buffer; dilute with RODI or equivalent water to 1X concentration before use. Store 1X buffer up to one month at 4°C.
V. Concentration and Purification of Peptides for LC-MS on StageTip

A. Solutions and Reagents

NOTE: Prepare solutions with Burdick and Jackson water or other HPLC grade water. Organic solvents (trifluoroacetic acid, acetonitrile) should be of the highest grade. Pierce™ Trifluoroacetic Acid (TFA), Sequencing grade (Thermo Scientific, 28903) and Pierce™ Acetonitrile (ACN), LC-MS Grade (Thermo Scientific, 51101) are recommended.

1. Solvent C (0.1% trifluoroacetic acid, 50% acetonitrile): add 0.1 ml trifluoroacetic acid to 40 ml HPLC water, then add 50 ml acetonitrile, adjust the final volume to 100 ml with HPLC water.
2. Solvent D (0.1% trifluoroacetic acid): add 0.1 ml trifluoroacetic acid to 50 ml HPLC water, adjust the final volume to 100 ml with HPLC water.
3. Solvent E (0.1% trifluoroacetic acid, 40% acetonitrile): add 0.1 ml trifluoroacetic acid to 30 ml HPLC water, then add 40 ml acetonitrile, adjust the final volume to 100 ml with HPLC water.

NOTE: Organic solvents are volatile. Tubes containing small volumes of these solutions should be prepared immediately before use and should be kept capped as much as possible, because the organic components evaporate quickly.

B. Procedure

1. Equilibrate the C18 tip by passing 50 μl of Solvent C through (once) followed by 50 μl of Solvent D two times.
2. Load sample by passing IP eluent through the C18 tip. Load IAP eluent in two steps using 50 μl in each step.
3. Wash the C18 tip by passing 55 μl of Solvent D through two times.
4. Elute peptides off the C18 tip by passing 10 μl of Solvent E through two times. Pool the resulting eluent.
5. Dry down the C18 tip eluent from the second C18 tip purification in a vacuum concentrator (Speed-Vac) and redissolve the peptides in an appropriate solvent for LC-MS analysis such as 5% acetonitrile, 0.1% TFA.

VI. Trypsin Digestion of Enriched LysC or Methylated Peptides

NOTE: Trypsin digestion of enriched LysC or methylated tryptic peptides is recommended for all basophilic and methylation-specific motif antibodies.

1. Prepare fresh 1 M ammonium bicarbonate stock solution.
2. Prepare digestion buffer, 50 mM ammonium bicarbonate containing 5% acetonitrile.
3. Dilute a stock solution of sequencing grade trypsin (Promega) with digestion buffer from 0.4 μg/μl to a final concentration of 25 ng/μl.
4. Resuspend the dried, LysC digested or tryptic methylated peptides generated from the C18 tip concentration protocol above with 10 μl of trypsin solution (25 ng/μl, 250 ng total). Vortex 3 times to redissolve the peptides and microfuge the sample to collect peptides/trypsin solution at the bottom of the microfuge tube as the final step.
5. Incubate the solution at 37°C for 2 hr.
6. After trypsin digestion, add 1 μl of 5% TFA to the digest solution. Vortex to mix and briefly centrifuge to collect peptide solution at the bottom of the microfuge tube.
7. Transfer the acidified peptide solution to a newly conditioned C18 tip, rinse the 0.5 ml Eppendorf tube once with 40 μl of 0.1% TFA, and apply the rinse solution to the C18 tip.
8. Perform the C18 tip desalting of the peptide digest and elute the peptides into an Eppendorf tube, HPLC autosampler vial insert, or 96-well plate. Dry purified peptides under vacuum prior to LC-MS analysis (as described above).
PTMScan® IAP Buffer (10X)

**Store at**: -20°C

0.6 ml

**Description**: PTMScan® IAP Buffer is used to reconstitute lyophilized peptides prior to immunoaffinity purification (IAP).

**Directions for Use**: Thaw 10X PTMScan® IAP buffer at room temperature or at 37°C. Ensure all contents are dissolved as some components may have precipitated upon freezing. If necessary, dissolve by shaking gently. Before use, dilute with Milli-Q or equivalently purified H₂O to 1X buffer (e.g., pipet 0.5 ml 10X IAP buffer from the vial into 4.5 ml H₂O).

**Solutions and Reagents**: 1X Buffer Components:
- 50 mM MOPS/NaOH pH 7.2
- 10 mM Na₂HPO₄
- 50 mM NaCl

**Storage**: Store at -20°C. Prepared 1X IAP Buffer can be stored up to one month at 4°C.