




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# Cell lysis and gel electrophoresis for protein analysis of HeLa cells (Provisional unformatted)

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## ABSTRACT

Here, we present multiple protocols used for biochemical analysis of protein expression and association. First, we used a simple lysis technique to determine the efficiency of an siRNA knockdown. Then, we modified two previously published methods for assaying co-precipitation of p62 and NEMO with magnetic beads conjugated to a GFP-trap molecule. In the first, we pulled down EGFP-NEMO in control or mitochondrial-damaged conditions, and in the second, we pulled down EGFP-Ubiquitin in p62<sup>-/-</sup> cells with expression of wild-type p62 or a dysfunctional mutant. Since p62 is known to form multimers, we used specialized buffers to preserve those putative interactions. We were able to reproduce results published previously by pulling down EGFP-Ubiquitin in p62-expressing cells. However, interestingly, we did not find evidence that NEMO interacts with p62 in the soluble fraction, or via ubiquitin chains generated in basal conditions. These studies demonstrated that NEMO recruitment to damaged mitochondria occurs in specific circumstances, and NEMO co-localization with p62 is also dependent on multiple factors.

## PROTOCOL CITATION

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## CREATED

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- 1 - This protocol was developed to analyze protein expression and enrichment in cell culture, including HeLa-M cells and HeLa p62<sup>-/-</sup> cells
- 2 - Option 2 was modified from a protocol used in Turco et al, Molec. Cell, 2019
- 3 - Option 3 was modified from a protocol used in Wurzer et al, eLife, 2015 Materials
- 4 -
- 5 5 mL capped tubes (Millipore Sigma, EP022364120)
- 6 - Cell scrapers
- 7 - Liquid nitrogen
- 8 -
- 9 5 mL Lo-Bind capped tubes (Eppendorf, 022431081)

- 10 - 10% acrylamide gels with desired number of wells (make or purchase) Reagents For all Options
- 11 - 1X Phosphate buffered saline (PBS)
- 12 - 2% bovine serum albumin (BSA) (Fisher Scientific, BP1605-100) for Option 2
- 13 - 10% sodium dodecyl sulfate solution (SDS) (Invitrogen, 15553-035)
- 14 - Protease and phosphatase inhibitors
- 15 o Leupeptin (10 mg/mL = 1000X)
- 16 o DTT (1M = 1000X)
- 17 o Pepstatin A (1 mg/mL = 1000X)
- 18 o TAME (10 mg/mL = 1000X)
- 19 o PMSF (100mM = 100X)
- 20 - 4X Denaturing buffer (DB) [900 uL (4% SDS, 50% glycerol, 125 mM Tris HCl, pH 6.8, 0.2% w/v Orange G) + 100 uL beta-mercaptoethanol (BME)]

- 21 - Methanol
- 22 - 4X Running buffer (RB)
- 23 - 1X Tris buffered saline (TBS)
- 24 - 1X TBS with 0.1% Tween (BIO-RAD, 1706531) (TBST)
- 25 - Running Buffer (RB) (250 mL 4X RB + 750 mL water + 10 mL 10% SDS)
- 26 - Transfer buffer (125 mL 4X RB + 775 mL water +  
27 mL methanol + 500 uL 10% SDS + 560 uL BME)
- 28 - PVDF membranes
- 29 - REVERT 700 Total Protein Stain (LICOR, 926-11021)
- 30 - REVERT Wash Buffer (6.7% w/v glacial acetic acid, 30% v/v methanol in water)

- 31 - REVERT Reversal Buffer (0.1 M NaOH, 30% v/v methanol in water)
- 32 - Desired primary antibodies
- 33 - LICOR secondary antibodies such as donkey anti-mouse 800 (926-32212) and donkey anti-rabbit 680 (926-68073)
- 34 - TrueBlack buffer (Biotium, 23013B-1L)
- 35 - EveryBlot buffer (BIO-RAD, 12010020) Specialized buffers and other reagents
- 36 - RIPA buffer (Option 1) Reagent stock concentration final concentration volume of stock (for 10 mL) Tris-HCl (pH 8.0)
- 37 M
- 38 mM
- 39 uL EDTA
- 40 mM
- 41 mM

42 uL EGTA

43 mM

44 mM

45 uL Triton X-100 10% 1%

46 uL DOC 5%

47 50%

48 uL SDS 10%

49 10%

50 uL NaCl

51 M

52 mM

53 uL Water - -

54 mL

55 - Lysis Buffer-A (Option 2) Reagent Final conc For 10 mL

56 M HEPES/KOH

57 mM pH 7.5

58 uL

59 M Sorbitol

60 mM

61 5 mL

62 mM EGTA

63 5 mM

64  $\mu$ L

65 M Mg-Acetate

66 mM

67  $\mu$ L ddH<sub>2</sub>O

68 92 mL

69 - PBS with 0.1% TWEEN (PBST) for Option 2

70 - Wash Buffer (Option 3) Reagent Final conc For 20 mL

71 M Tris-Cl

72 mM, pH 7.4



73    uL    100% Glycerol    10%

74    mL

75    M NaCl

76    mM

77    uL    ddH<sub>2</sub>O

78    0.6 mL

79    -    Lysis Buffer-B (Option 3)    Reagent    Final conc    For 5 mL    Master buffer

80    mM, pH 8.0

81    975 mL    100% NP-40 (IGEPAL)

82    5%

83    uL

- 84 - Pierce BCA Assay (ThermoFisher, 23225) for Option 1
- 85 - GFP-Trap Magnetic Particles (Chromotek M-270) for immuno-precipitations Equipment
- 86 - vacuum apparatus
- 87 - end-on-end rotating apparatus
- 88 - refrigerated centrifuge
- 89 - magnetic rack (for GFP-Trap particle precipitation)
- 90 - rockers at room temperature (R.T.) and at 4C
- 91 - Plate reader (such as BioTex Synergy Mx)
- 92 - Odyssey CLx membrane scanner (LI-COR, 9140)
- 93 - ImageStudio software (LI-COR)

- 94 - Heat source to 95 C
- 95 - Gel electrophoresis apparatus (BIO-RAD)
- 96 - Membrane transfer apparatus (BIO-RAD)
- 97 - Excel Before start
- 98 - The start point for this protocol is after cells grown on 3.5 cm, or 10 cm dishes have been transfected with relevant constructs for 18-24 hours and treated with appropriate small molecules or vehicles
- 99 - For 3.5 cm dishes, follow transfection procedures enumerated in imaging protocols.
- 100 - Chill all reagents on ice
- 101 - Add protease and phosphatase inhibitors to 1X to each lysis buffer immediately before use Step-by-step Wash cells
- 102 - Aspirate media from dishes
- 103 - Wash samples quickly x2 with ice cold PBS
- 104
  - o Note: Can stop after washes by scraping cells with the second wash of PBS into 1.5 mL tube, spin down at 2.4G, 3min, 4 degrees. Aspirate PBS and snap-freeze tubes in liquid

nitrogen. If frozen, add respective lysis buffer and inhibitors and let thaw on ice 10 min before proceeding Option 1: Standard lysis with RIPA Note: We used this protocol to assess depletion of p62 in HeLa-M cells after siRNA treatment and imaging NEMO recruitment. Samples were collected from 35 mm imaging dishes.

- 105 - Add
- 106 uL RIPA + inhibitors to dish and scrape cells into 1.5 uL tube, OR add buffer to thawed sample and resuspend by pipetting
- 107 - Rotate resuspended sample on end-over-end machine at 4 degrees for 20 min
- 108 - Spin at top speed (17 G), 4 degrees, 20 min
- 109 - Remove supernatant as Lysis and keep on ice or store at -80 C
- 110 - Measure protein concentration with Pierce BCA assay by adding 25 uL sample or BSA standard to each well in duplicate and 200 uL Reagent A+B. Incubate 37 C for 30 min then measure absorbance on a plate reader
- 111 o Note: it is likely necessary to dilute samples 1:4 or more to measure within the range of the assay.
- 112 - Add 1/3 volume of 4X DB to remaining Lysis or a measured fraction of sample and heat 95 C for 5 min
- 113 - Proceed to gel electrophoresis Option 2: Co-IP EGFP-NEMO for p62 association assay in AntA/OligA or vehicle conditions
- 114 - The samples for this assay are: A) EGFP-vector + veh, B) EGFP-vector + AntA/OligA, C) EGFP-NEMO + veh, and D) EGFP-NEMO + AntA/OligA. Start with 3x 10 cm dish per condition

for one biological replicate

- 115 - 18-24 hr before collection, transfect 3 ug Parkin and 1.5 ug EGFP-NEMO (or vector), to 70-80% confluent cells on each dish
- 116 - it is best to plan collection times such that each is collected and snap frozen ~10 min apart. Then all snap frozen samples can be processed simultaneously from that step Lysis with heavy fraction isolation
- 117 - Scrape and combine like samples into 800 uL PBS, transfer to 1.5 mL tube
- 118 - Spin
- 119 min, 2 G, at 4 C
- 120 - Aspirate PBS and snap freeze in liquid nitrogen
- 121 - Add
- 122 uL LB-A with inhibitors to each frozen sample
- 123 - Pipet to resuspend
- 124 - Incubate on ice 10 min

- 125 - centrifuge at 1000g, 5 min, 4 degrees
- 126 - Transfer sup. (Cytosol) to a new tube
- 127 - Centrifuge again at top speed, 10 min, 4 degrees
- 128 - Save pellet as Heavy Fraction if desired and resuspend in 50 uL 1X DB Prep IP beads
- 129 - Mix GFP-Trap beads by swirling and gently pipetting to break up accumulations
- 130 - aliquot 25 uL bead slurry into LoBind tubes (one for each condition)
- 131 - Remove supernatant from beads by inserting the tube in a magnetic rack and carefully aspirating clear solution
- 132 - Resuspend beads in 500 uL cold PBST
- 133 - Insert to magnetic rack and remove PBST wash
- 134 - Block beads in 2% BSA (in water) for 1 hr at 4 degrees with end-over-end rotation
- 135 - wash 2X with 500 uL r.t. PBST

- 136 - wash 1X with 500 uL LB-A
- 137 - Allow magnets to collect beads for up to 5 min Bead capture
- 138 - Add
- 139 uL Cytosol to bead tube, rotate end-over-end gently for 1 hr, 4 degrees (save the rest of Cytosol for Input)
- 140 - Remove supernatant by magnet (up to 5 min) and save as Flow Through
- 141 - Wash 3X with 500 uL R.T. PBS (no TWEEN) (can save these washes)
- 142 - for the last wash, transfer beads and wash to a new tube
- 143 o Note: optional if using Lo-bind tubes
- 144 - Remove sup from last wash and resuspend in ~90 uL 1X DB with rough mixing (vortex, pipetting), then heat 95 C for 5 min
- 145 - Magnetize 5 min and save sup as Eluate

- 146 - Add 1/3 volume of 4X DB to Input and Flow Through and heat 95 C for 5 min
- 147 - Proceed to gel electrophoresis Option 3: Co-IP GFP-Ubiquitin for p62 and NEMO association assay
- 148 - The samples for this assay are in p62<sup>-/-</sup> Hela cells: A) EGFP-vector + mCherry-vector, B) EGFP-vector + mCherry-p62, C) EGFP-Ubiquitin + mCherry-vector, D) EGFP-Ubiquitin + mCherry-p62, and E) EGFP-Ubiquitin + mCherry-p62-ΔPB1. Start with 2x 10 cm dish per condition for one biological replicate
- 149 - 18-24 hr before collection, transfect 3 ug Parkin and EGFP-Ubiquitin (or vector), 1.5 ug NEMO, and 2-2.5 ug mCherry-p62 (or vector) to 70-80% confluent cells in each dish
- 150 - Note: it is best to plan collection times such that each is collected and snap frozen ~10 min apart. Then all snap frozen samples can be processed simultaneously from that step
- Lysis
- 151 · Combine samples by scraping cells into 600 uL LB-B with inhibitors and transfer to 1.5 mL tube
- 152 · Incubate on ice, 15 min
- 153 · Centrifuge at 16,100 g (16.1 G), 13 min, 4 degrees
- 154 · Transfer sup. to a new tube as Lysis Prep IP beads
- 155 · Mix GFP-Trap beads by swirling or gently pipetting to break up accumulations and aliquot 10 uL into LoBind tubes (one for each condition)
- 156 · Remove supernatant from beads by inserting the tube in a magnetic rack and carefully



aspirating clear solution

- 157 · Resuspend beads in 500 uL r.t. Wash Buffer
- 158 · Insert to magnetic rack and remove wash
- 159 · Repeat for a total of 2 washes
- 160 · wash 1X with 500 uL LB-B
- 161 · Allow magnets to collect beads for up to 5 min    Bead capture
- 162 · Add 500 uL Lysed sample to bead tube, rotate gently for 1 hr, R.T.
- 163 · save the rest of the Lysis as Input
- 164 · Remove sup by magnet (up to 5 min) and save as Flow Through
- 165 · Wash 3X with 500 uL R.T. Wash buffer (can save these washes)
- 166 · for the last wash, transfer beads and wash to a new tube (optional if you're using Lo-bind tubes)

- 167 · Remove sup from last wash and resuspend in ~90 uL 1X DB with rough mixing (vortex, pipetting), then heat block 10 min
- 168 · Magnetize 5 min to collect beads and save sup as Eluate
- 169 · Add 1/3 volume of 4X DB to Input and Flow Through and heat 95 C for 5 min
- 170 · Proceed to gel electrophoresis Gel electrophoresis and immune-blotting
- 171 - This protocol was developed for use with the LI-COR system for protein detection Set-up
- 172 - Set up electrophoresis cell with 10% gels by manufacturer's instructions
- 173 - Fill cell with RB and flush wells with a plastic transfer pipet.
- 174 - Invert samples by hand to mix, and ensure all samples are at the bottom of tubes by briefly centrifuging
- 175 - Load wells with equal amounts of protein (Option 1) or equal volumes (Options 2 and
- 176 and molecular weight standard (4-5 uL).
- 177 o Note: We load 15-25 uL eluate and 10 uL Input

- 178 - For empty lanes, load approx. equal volume of 1X DB. Running
- 179 - Run samples through stacking gel (85 V, 20-40 min)
- 180 - Run samples through 10% gel (125 V, until front has reached bottom of gel, usually ~70 min) Transfer
- 181 - Remove gels from electrophoresis cell and construct transfer cassettes with PVDF membranes according to manufacturer's instructions
- 182 - Place the cassettes in the transfer cell and fill cell with Transfer buffer and icepack
- 183 - place the cell in a basin
- 184 - Fill basin with ice around cell
- 185 - Run transfer for 60-70 min, 100 V Membrane processing and total protein stain
- 186 - Dry membrane between filter paper in the dark for at least 45 min
- 187 o Note: this is most important for small proteins

- 188    o   Note: can be a stopping point for several days
  
- 189    -   Rehydrate membrane in MetOH
  
- 190    -   Wash in ddWater
  
- 191    -   Wash in 1X TBS 2 min
  
- 192    -   Stain total protein, 5 min, R.T., with REVERT 700 Total Protein Stain
  
- 193    -   Wash membrane 2x 30 sec with REVERT wash buffer
  
- 194    -   Image total protein on LICOR
  
- 195    o   Note: can cut the membrane based on total stain if desired
  
- 196    -   Wash off total stain with REVERT Reversal (up to 10 min, R.T.)
  
- 197    -   Rinse in ddWater   Immuno-labeling
  
- 198    -   Block membranes in EveryBlot buffer, 5 min, R.T. with rocking

- 199 - Incubate in vacuum packs with primary antibodies in EveryBlot overnight at 4 C. See materials and methods for concentrations of antibodies used.
- 200 - Wash with TBST 4x 5 min
- 201 - Incubate with secondary antibody 1:20,000 in TrueBlack antibody diluent with 0.2% TWEEN and 1:1000 10% SDS for up to 1 hr
- 202 - Wash with TBST 4x 5 min
- 203 - Wash 1X with TBS to clear TWEEN
- 204 - Wash 1X with water
- 205 - Image Quantification
- 206 - For quantification of knockdown (Option 1)
- 207 o Use ImageStudio software to draw rectangles around total protein in each lane of Total Protein image and subtract background
- 208 o Then add rectangles to outline p62 bands and subtract background

- 209    o   Transfer intensity measurements to Excel
  
- 210    o   Calculate p62 expression relative to total protein for each experiment
  
- 211    -   For quantification of p62 enrichment from GFP-NEMO immuno-precipitation
  
- 212    o   Use ImageStudio to add rectangles around input/cytosolic p62 and eluted p62
  
- 213    o   Transfer intensity measurements with background subtracted to Excel
  
- 214    o   Calculate p62 eluted relative to input amounts
  
- 215    o   Calculate elution/input quantity relative one condition
  
- 216    §   Note: we found it necessary to perform this secondary normalization due to variability across replicates. In our case, we normalized results from each condition to the EGFP-NEMO + AntA/OligA results