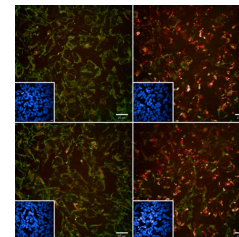


May 20, 2024 Version 3

# KAT8 compound inhibition inhibits the initial steps of PINK1-dependant mitophagy V.3

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**Protocol status:** Working

**We use this protocol and it's working**

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**Keywords:** KAT8, MG149, Parkinson's disease, mitophagy, autophagy, TMRM, mitoKeima

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## Abstract

It has recently been shown that KAT8, a genome-wide association study candidate risk gene for Parkinson's Disease, is involved in PINK1/Parkin-dependant mitophagy. The KAT8 gene encodes a lysine acetyltransferase and represents the catalytically active subunit of the non-specific lethal epigenetic remodelling complex. In the current study, we show that contrary to KAT5 inhibition, dual inhibition of KAT5 and KAT8 via the MG149 compound inhibits the initial steps of the PINK1-dependant mitophagy process. More specifically, our study shows that following mitochondrial depolarisation induced by mitochondrial toxins, MG149 treatment inhibits PINK1-dependant mitophagy initiation by impairing PINK1 activation, and subsequent phosphorylation of Parkin and ubiquitin. While this inhibitory effect of MG149 on PINK1-activation is potent, MG149 treatment in the absence of mitochondrial toxins is sufficient to depolarise the mitochondrial membrane, recruit PINK1 and promote partial downstream recruitment of the autophagy receptor p62, leading to an increase in mitochondrial delivery to the lysosomes. Altogether, our study provides additional support for KAT8 as a regulator of mitophagy and autophagy processes.

## Materials

### Mitochondrial toxins

Oligomycin (inhibitor of mitochondrial complex V) was purchased from Cayman Chemicals (11341) and from Sigma-Aldrich (O4876) Antimycin A (inhibitor of mitochondrial complex III) was purchased from Sigma-Aldrich (A8674)

### Antibodies used for immunoblotting


rabbit anti-phospho-ubiquitin (Ser65) (Cell Signaling, 37642, 1:1000)  
mouse anti-TIM23 (BD Biosciences, 611223, RRID:AB\_398755, 1:1000)  
mouse anti-TOM20 (Santa Cruz, sc-11415, RRID:AB\_2207533, 1:1000)  
mouse anti-GAPDH (Abcam, ab110305, RRID:AB\_10861081, 1:1000)  
rabbit anti-pParkin(Ser65) (Abcam/Michael J.Fox Foundation, MJF17, 1:1000)  
rabbit anti-MFN2 (Cell Signaling, 9482, 1:1000)  
mouse anti-OPA1 (BD Biosciences, 612607, 1:1000)  
rabbit anti-LC3B (Novus Biologicals, NB100-2220, 1:1000)  
IRDye 680LT donkey anti mouse (LI-COR Biosciences, 925-68022, RRID:AB\_2814906, 1:20000)  
IRDye 800CW donkey anti rabbit (LI-COR Biosciences, 925-32213, RRID:AB\_2715510, 1:20000)  
rabbit monoclonal anti-PINK1 antibody generated as described in the following manuscript: Sci Rep. 2015. DOI: <https://doi.org/10.1038/s41598-018-26949-6>

### Antibodies used for immunofluorescence

mouse anti TOM20 (Santa Cruz, sc-17764, RRID:AB\_628381 1:1000)  
rabbit anti phospho-ubiquitin (Ser65) (Cell Signaling, 37642, 1:1000)  
mouse anti-p62 (BD Biosciences, 610832, 1:1000)  
AlexaFluor 488 goat anti rabbit (Invitrogen, A11008, 6 RRID:AB\_143165, 1:2000)  
AlexaFluor 568 goat anti mouse (Invitrogen, A11004, 7 RRID:AB\_2534072, 1:2000)



## Cell Culture

- 1 Maintain cells in culture in a humidified 5% CO<sub>2</sub> incubator at  37 °C in Dulbecco's modified Eagle's medium (DMEM, Gibco, 11995-065) supplemented with 10% heat-inactivated foetal bovine serum (FBS, Gibco). Change cell medium every 3 days.

### Note

Parkin over-expressing (POE) SHSY5Y cells are a gift from H. Ardley (Ardley, H., *et al.*, 2003).

DOI: <https://doi.org/10.1091/mbc.e03-02-0078>

Mt-Keima POE SHSY5Y cells were a gift of C. Luft (Soutar, M., *et al.*, 2019).

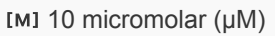

DOI: <https://doi.org/10.1080/15548627.2019.1603549>

PINK1-HA overexpressing SHSY5Y cells were a gift from E. Deas (Deas, E., *et al.*, 2011).

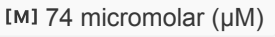
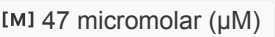
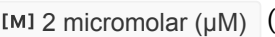
DOI: <https://doi.org/10.1093/hmg/ddq526>

- 2 Split cells at 75% to 90% confluency using  2 mL of Trypsin.

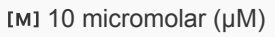
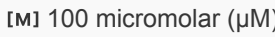


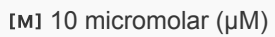
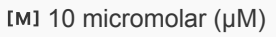


## Cell Treatment (Small Molecule Modulator and Mitophagy Induction)

- 3 Dilute each compound in DMSO to reach concentrations determined according to their speculated toxicity and IC<sub>50</sub>,  for NU9056 and  for MG149.

### Note

MG149 targets KAT5 and KAT8 with IC<sub>50</sub> values of  and  respectively; NU9056 targets KAT5 with an IC<sub>50</sub> value of  (Li, L., *et al.*, 2020).

DOI: <https://doi.org/10.1172/JCI131145>

- 4 Treat cells with DMSO,  NU9056, or  MG149 for  06:00:00 before collecting / fixing for downstream experiments. 
- 5 Treat cells with either DMSO or  oligomycin/  
 antimycin for  03:00:00 to induce mitophagy before collecting / fixing for downstream experiments. 

**Note**

Note that both small molecule modulator and O/A are often added to the same wells / cells to look at the impact of MG149 on mitophagy initiation.




**Mitochondrial Enrichment****2h 10m**

- 6 Incubate cells Overnight at -80 °C in mitochondrial homogenization buffer (250mM sucrose, 1mM EDTA, 10mM Tris (pH 7.4) supplemented with protease and phosphatase inhibitors).
- 7 Thaw, scrape into 1.5mL centrifuged tubes, and triturate 20x, keeping samples On ice .
- 8 Freeze tubes at -80 °C for 01:00:00 , then thaw On ice . 1h
- 9 Remove cell debris / non-lysed cells by centrifugation 1500 rcf, 4°C, 00:20:00 . 20m
- 10 Centrifuge the supernatant 12500 x g, 4°C, 00:20:00 to collect the mitochondrial enriched pellet (aka the mitochondrial fraction) and save the supernatant (aka the cytoplasmic fraction). 20m
- 11 Centrifuge the cytoplasmic fraction 12500 x g, 4°C, 00:20:00 to remove membrane contamination and wash the mitochondrial fraction twice in 500 µL of fractionation buffer ( 12500 x g, 4°C, 00:10:00 x 2) to remove cytoplasmic contaminants. 30m
- 12 Determine the relative ratios of sample differences for the mitochondrial enriched fraction using the protein concentration of the cytoplasmic fraction (BSA assay). Re-suspend the mitochondrial enriched pellet accordingly using 1x NuPAGE® LDS sample buffer supplemented with 10 mM dithiothreitol (DTT).
- 13 Sonicate the mitochondrial fraction (10 microns power amplitude for 2 x 10 seconds, "flick" in between) and heat to 70 °C for 00:10:00 . 10m

**Cell Lysis****1h 30m**





- 14 Lyse cells in whole-cell lysis buffer (50mM Tris (pH 7.4), 0.1mM EGTA, 1mM EDTA, 0.27M Sucrose, 1% triton-x-100, supplemented with protease and phosphatase inhibitors) On ice and incubated Overnight at -80 °C .



- 15 Centrifuge the lysates  1600 x g, 4 °C, 00:20:00 and protein quantify the supernatant by BSA assay. 20m
- 16 Make LDS preps with 10 mM dithiothreitol (DTT), and heat to  70 °C for  00:10:00 . 10m







## Western Blotting

1h 30m

- 17 Separate the LDS preps (either after cell lysis or mitochondrial enrichment) by SDS-PAGE and transfer them to nitrocellulose membrane.
- 18 Incubate the membrane  Overnight at  4 °C with primary antibodies diluted in 3% milk in PBS-Tween.
- 19 Wash and incubate the membrane for  01:00:00 at  Room temperature in secondary antibodies diluted in PBS-Tween. 1h
- 20 Detect the protein bands using Odyssey CLx LI-COR.



## Immunofluorescence

4h 20m

- 21 Fix cells with 4% Paraformaldehyde (PFA, Sigma-Aldrich) for  00:20:00 at  Room temperature . 20m
- 22 Remove PFA solution, block and permeabilize the cells with a mix of 10% FBS, 0.25% Triton X-100 in PBS for  01:00:00 at  Room temperature . 1h
- 23 Immunostain the cells with pUb(Ser65) and TOM20 primary antibodies diluted in 10% FBS/PBS for  02:00:00 at  Room temperature . 2h

### Note

rabbit anti-pUb(Ser65) (Cell Signaling, 37642) and mouse anti-TOM20 (Santa Cruz, sc-17764) primary antibodies are both added at a 1:1000 dilution in 10% FBS/PBS.

- 24 Wash wells three times using PBS 1X and incubate with secondary antibodies for  01:00:00 at  Room temperature , before washing again three times using PBS 1X. 1h

**Note**

AlexaFluor 568 anti-mouse, 488 anti-rabbit secondary antibodies, and Hoechst 33342 (Thermo Scientific) are all added at a 1:2000 dilution in 10% FBS/PBS.

- 25 Image cells on the Opera Phenix (Perkin Elmer), acquiring confocal z-stacks for multiple fields of view across 3 individual wells per experimental condition, using the 40X water objective.

**Note**

Analyse images using Columbus 2.8 analysis system (Perkin Elmer) to measure the integrated intensity of pUb(Ser65) within the whole cell.

For visualisation purposes, select brightness and contrast settings on control and apply the same settings to all other conditions.

**Measuring Mitochondrial Membrane Potential using TMRM**

40m

- 26 Seed POE-SHSY4Y cells in a 96-well CellCarrier Ultra plate.
- 27 Incubate live cells in [M] 25 nanomolar (nM) Tetramethylrhodamine, Methyl Ester, Perchlorate (TMRM) (Sigma Aldrich) diluted in cell media for ⌚ 00:40:00 at 🌡️ 37 °C and 4% CO<sub>2</sub>.
- 28 Image cells on the Opera Phenix (PerkinElmer) at 🌡️ 37 °C and 4% CO<sub>2</sub>, acquiring confocal z-stacks for multiple fields of view across 3 individual wells per experimental condition using the 40X water objective.

40m


**Note**

Analyse images using the Columbus 2.8 analysis system (Perkin Elmer) to measure the TMRM signal intensity of maximum intensity projections.

**Measuring Mitochondrial Delivery to Lysosomes using mitoKeima Reporter**

40m

- 29 Seed mt-Keima expressing POE SHSY5Y cells in a 96-well CellCarrier Ultra plate and treat them according to desired conditions (MG149, NU9056, O/A as described in ➡️ [go to step #3](#) ).
- 30 Before imaging, replace cell media with phenol-free DMEM + 10% FBS containing the treatments previously administered ➡️ , and adding Hoechst 33342 (1:10000) to stain the nuclei.

- 31 Image cells immediately on the Opera Phenix (PerkinElmer) at  37 °C with 5% CO<sub>2</sub>, acquiring multiple single-plane fields of view, using the 63X water objective.

#### Note

Analyse images in using the Columbus 2.8 analysis system (Perkin Elmer) to measure the mitophagy index.

To analyse:

- Identify cells using the Hoechst 33342 channel, before measuring the area of the cytoplasmic and lysosomal mitoKeima
- Calculate the mitophagy index = the ratio between the total area of lysosomal mitochondria and the total area of mitoKeima (cytoplasmic + lysosomal areas) per well.

## RT-qPCR

- 32 Extract total RNA from cells using the Monarch Total RNA Miniprep Kit (New England Bioscience) with inclusion of the optional on-column DNase treatment.
- 33 Reverse transcribe RNA with SuperScript™ IV reverse transcriptase and random hexamers (Invitrogen).
- 34 Dilute the cDNA product then subject to quantitative real-time PCR (qPCR) using Power SYBR™ Green Master Mix (Applied Biosystems) and gene specific primer pairs on a QuantStudio™ 7 Flex Real-Time PCR System (Applied Biosystems).

A	B	C	D
	<b>Sequence 5'-3'</b>		
<b>Gene Target</b>	<b>Forward</b>	<b>Reverse</b>	<b>Product Size / bp</b>
<i>RPL 18A</i>	CCCACAACATGTACCGGGAA	TCTTGGAGTCGTGGAAGTGC	180
<i>PINK1</i>	GTGGAACATCTCGGCAGGTT	CCTCTCTTGGATTTTCTGTAAGTGAC	129

List of primer pairs used for RT-qPCR of target genes

- 35 Calculate relative mRNA expression levels using the  $2^{-\Delta\Delta C_t}$  method and *RPL 18A* as the housekeeping gene.

## Statistical Analysis



- 36 Use a minimum of 3 biological replicates for each experiments (N numbers shown in legends refer to the number of replicate experiments).
- For each imaging experiments, calculate the mean values of every condition from a minimum of 3 technical replicates.
  - Normalise intensity and integrated density measurements to control conditions.
- 37 Subject data to a two-way ANOVA with Dunnett's post-hoc analysis for multiple comparisons unless stated otherwise.
- Express data as the mean  $\pm$  standard deviation (SD) from replicate experiments.
  - Set statistical significance at a p-value of  $<0.05$ .

**Note**

Use GraphPad Prism 6 (La Jolla, California, USA) for statistical analyses and graph production.  
(Present data with error bars showing mean  $\pm$  standard deviation (SD) from replicate experiments).

## Measuring p62 recruitment to the OMM and mitochondrial delivery to lysosomes using mitoSRAI

3h

- 38 Seed mitoSRAI POE SHSY5Y cells in a 96-well CellCarrier Ultra plate and treat them according to desired conditions (MG149, NU9056, O/A as described in [⇒ go to step #3](#) ).
- 39 Fix cells as described in [⇒ go to step #21 to 22](#)
- 40 Immunostain the cells with p62 primary antibodies diluted in 10% FBS/PBS for [🕒 02:00:00](#) at [🌡 Room temperature](#) .

2h

**Note**

mouse anti-SQSTM1/p62 (Abcam, ab56416) primary antibody added at a 1:1000 dilution in 10% FBS/PBS.

- 41 Wash wells three times using PBS 1X and incubate with secondary antibodies for [🕒 01:00:00](#) at [🌡 Room temperature](#) , before washing again three times using PBS 1X.

1h

**Note**

AlexaFluor 568 anti-mouse secondary antibodies, and draql5 (Thermo Scientific) are all added at a 1:2000 dilution in 10% FBS/PBS.



- 42 Image cells on the Opera Phenix (Perkin Elmer), acquiring confocal z-stacks for multiple fields of view across 3 individual wells per experimental condition, using the 63X water objective.

**Note**

Analyse images using Columbus 2.8 analysis system (Perkin Elmer) to measure the SRAI mitophagy index

- corresponds to the ratio between the area of lysosomal mitochondria (corresponding to the total YPet negative TOLLES area) and the total mitochondrial area (corresponding to the total TOLLES area) per well.

Analyse images using Columbus 2.8 analysis system (Perkin Elmer) to measure p62 recruitment to the mitochondria using TOLLES as a mitochondrial marker

- calculated as the ratio of p62 signal intensity inside vs. outside TOLLES

For visualisation purposes, select brightness and contrast settings on control and apply the same settings to all other conditions.

## Generating PINK1 KO POE SH-SY5Y cell line

- 43 PINK1 was functionally knocked out from the POE SH-SY5Y cell line through CRISPR-Cas9 editing by adapting previously published protocols (DOI: [10.15252/emmm.202013579](https://doi.org/10.15252/emmm.202013579))

**Note**

Single guide RNA (sgRNA) sequences targeting Exon 1 of PINK1 (NM\_032409) were designed using the Horizon Discovery CRISPR Design Tool (<https://horizondiscovery.com/en/ordering-and-calculation-tools/crispr-design-tool>)

A	B	C	D
SgRNA ID	5'-3' sgRNA Sequence (PAM)	5'-3' Forward ssDNA Oligo with BbSI Overhang	5'-3' Reverse ssDNA Oligo with BbSI Overhang
<b>PINK1_Seq1</b>	CGCCACCATGGCGGTGCGAC(AGG)	caccgCGCCACCATGGCGGTGCGAC	aaacGTCGCACCGCCATGGTGGCGc
<b>PINK1_Seq2</b>	ACCGGGCGCGGAGCCTCGCA(GGG)	caccgACCGGGCGCGGAGCCTCGCA	aaacTGCGAGGCTCCGCGCCCGGTc

5'-3' Forward and Reverse ssDNA sequences generated (Sigma Aldrich) inclusive of 5' overhangs suitable for cloning into BbSI digested pSpCas9(BB)-2A-GFP plasmid

**Note****Materials:**

pSpCas9(BB)-2A-GFP Addgene plasmid no. 48138 was a gift from Feng Zhang; (RRID:Addgene\_48138)  
IRDye 800CW donkey anti-rabbit secondary (LI-COR Biosciences, 925-32213, RRID:AB\_2715510, 1:2000)  
pUb(Ser65) (CST, 62802, RRID:AB\_2799632, 1:1000)

- 44 A subconfluent 6-well dish of POE SH-SY5Ys were transfected with 1  $\mu$ g of each PINK1\_Seq1 and PINK1\_Seq2 sgRNA encoding pSpCas9(BB)-2A-GFP plasmid using lipofectamine 3000 (Invitrogen)
- 45 24 h post-transfection cells were trypsinised and subjected to fluorescence-activated cell sorting and clonal selection of GFP-positive cells: isolated clones were expanded and phenotypically screened for clones which did not show pUb(Ser65) signal after 1.5 h O/A treatment
- 46 Confluent wells of a 96-well were prepared for immunofluorescence staining of pUb(Ser65) with IRDye 800CW donkey anti-rabbit secondary
- 47 gDNA was extracted from a positive clone using the Wizard Genomic DNA Purification Kit (Promega) and subjected to whole genome sequencing (Novogene) which revealed homozygous 22 bp deletion and frameshift in exon 1 of PINK1 (c.156\_177delGGGCGCGGAGCCTCGCAGGGTC, p.A54Sfs\*46).

**Generating mitoSRAI POE SH-SY5Y cell line**

- 48 MitoSRAI cDNA was first PCR amplified from mitoSRAI\_pcDNA3 with inclusion of 5' EcoRI and 3' NotI restriction sites
- 49 The PCR product was cloned into pLVX-EF1 $\alpha$ -IRES-Puro using EcoRI and NotI restriction sites to generate pLVX-EF1 $\alpha$ -mitoSRAI-IRES-Puro.

**Note****Material:**

mitoSRAI\_pcDNA3: provided by the RIKEN BRC through the National BioResource Project of the MEXT, Japan; cat. RDB18223  
pLVX-EF1 $\alpha$ -IRES-Puro: Clontech, Takara Bio, 631988  
pMD2.G (Addgene plasmid no. 12259, RRID:Addgene\_12259) and pCMVR8.74 (Addgene plasmid #22036, RRID:Addgene\_22036) were gifts from Didier Trono

- 50 Lenti-X 293 T HEK cells cultured in DMEM 10% FBS media were transfected with pMD2.G, pCMVR8.74 and pLVX-EF1 $\alpha$ -mitoSRAI-IRES-Puro at a 1:1:2 molar mass ratio using Lipofectamine 3000 (Invitrogen)



- 51 The next day, a full media change was performed using DMEM 10% FBS and cells cultured for further 24
- 52 The lentivirus containing media was collected and diluted 1:2 with DMEM 10% FBS before filtering through 0.44 µm PES filters
- 53 1 × 10<sup>6</sup> POE SHSY5Ys were reverse transduced with the 1:2 lentivirus supernatant dilution in the presence of 10 µg/mL polybrene (Sigma Aldrich)
- 54 Bulk populations of cells stably expressing mitoSRAI were established through selection with 1 µg/mL puromycin (M P BIOMEDICALS UK)  
Puromycin was maintained during routine culture but withdrawn when seeding for experimental assays.

## Protocol references

Ardley HC, Scott GB, Rose SA, Tan NG, Markham AF, Robinson PA. Inhibition of proteasomal activity causes inclusion formation in neuronal and non-neuronal cells overexpressing Parkin. *Mol Biol Cell*. 2003 Nov;14(11):4541-56. doi: <https://doi.org/10.1091/mbc.e03-02-0078>. Epub 2003 Aug 22. PMID: 12937272; PMCID: PMC266771.

Soutar MPM, Kempthorne L, Annuario E, Luft C, Wray S, Ketteler R, Ludtmann MHR, Plun-Favreau H. FBS/BSA media concentration determines CCCP's ability to depolarize mitochondria and activate PINK1-PRKN mitophagy. *Autophagy*. 2019 Nov;15(11):2002-2011. doi: <https://doi.org/10.1080/15548627.2019.1603549>. Epub 2019 May 7. PMID: 31060423; PMCID: PMC6844515.

Deas E, Plun-Favreau H, Gandhi S, Desmond H, Kjaer S, Loh SH, Renton AE, Harvey RJ, Whitworth AJ, Martins LM, Abramov AY, Wood NW. PINK1 cleavage at position A103 by the mitochondrial protease PARL. *Hum Mol Genet*. 2011 Mar 1;20(5):867-79. doi: <https://doi.org/10.1093/hmg/ddq526>. Epub 2010 Dec 6. PMID: 21138942; PMCID: PMC3033179.