

# PARK2 K63-Ubiquitinates SNCAIP

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## Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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## Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

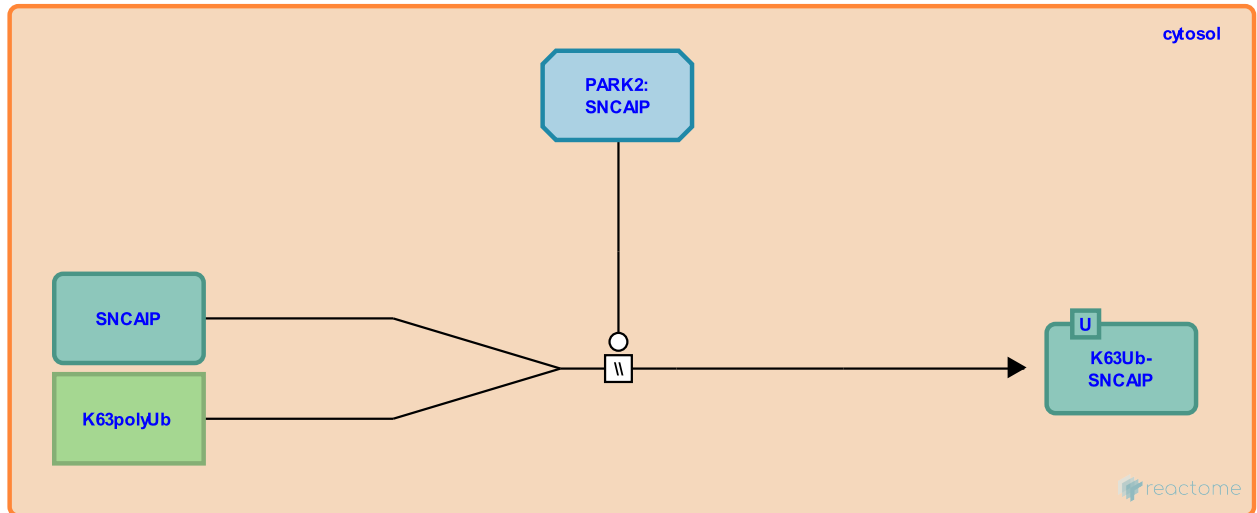
This document contains 1 reaction ([see Table of Contents](#))

## PARK2 K63-Ubiquitinates SNCAIP [↗](#)

**Stable identifier:** R-HSA-5667111

**Type:** omitted

**Compartments:** cytosol



SNCAIP is ubiquitinated by several different E3 ubiquitin-ligases, including Parkin (PARK2). PARK2 overexpression with SNCAIP in cell culture leads to the formation of protein aggregates (Chung et al. 2001). PARK2 preferentially mediates the addition of lysine-63 (K63)-linked polyubiquitination of SNCAIP (Lim et al. 2005). This leads to SNCAIP degradation only at an unusually high PARK2 to SNCAIP ratio (Lim et al. 2005). K63-linked ubiquitination may be a signal that leads to the degradation of inclusions by autophagy when the ubiquitin-proteasome system is dysfunctional (Lim et al. 2005, Tan et al. 2008).

### Literature references

Zhang, Y., Dawson, TM., Ross, CA., Dawson, VL., Lim, KL., Gao, J. et al. (2001). Parkin ubiquitinates the alpha-synuclein-interacting protein, synphilin-1: implications for Lewy-body formation in Parkinson disease. *Nat. Med.*, 7, 1144-50. [↗](#)

### Editions

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