

# p14ARF mutant does not translocate to the nucleus

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28/04/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## 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](#))

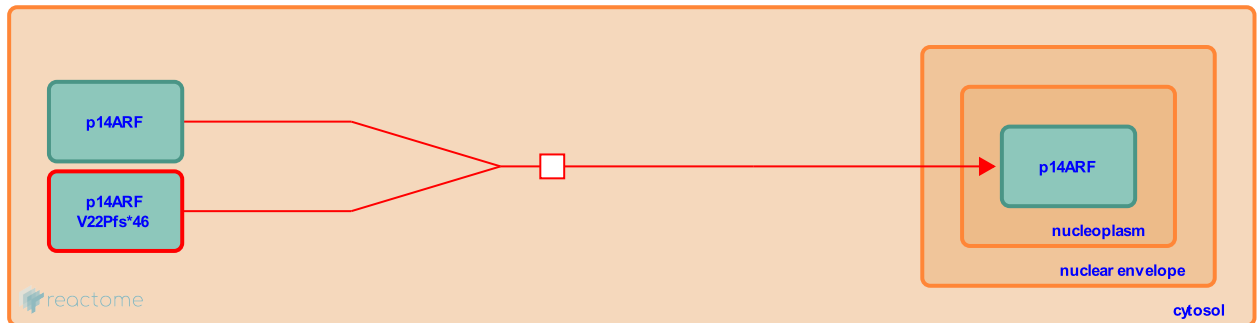
## p14ARF mutant does not translocate to the nucleus [↗](#)

**Stable identifier:** R-HSA-9646295

**Type:** transition

**Compartments:** cytosol

**Diseases:** cancer



A germline mutation affecting exon 1beta of the CDKN2A locus is associated with a familial melanoma syndrome. The mutation represents an insertion of 16 nucleotides (CGCCCCGCCGCGAGTG) between coding bases 60 and 61 in exon 1beta. This insertion results in a frameshift, starting at arginine codon at position 21 of p14ARF, with the first amino acid changed being valine at position 22, and ending with a premature stop codon at position 67. The mutant protein p14ARF V22Pfs\*46 (p14ARF 60ins16) is unable to translocate to the nucleus and stabilize TP53 (Rizos, Puig et al. 2001).

### Literature references

Puig, S., Milà, M., Darmanian, AP., Badenas, C., Kefford, RF., Rizos, H. et al. (2001). A melanoma-associated germline mutation in exon 1beta inactivates p14ARF. *Oncogene*, 20, 5543-7. [↗](#)

### Editions

2019-06-28	Authored	Orlic-Milacic, M.
2019-07-08	Reviewed	Rizos, H.
2019-07-16	Edited	Orlic-Milacic, M.
2019-08-12	Reviewed	Bennett, DC.
2019-08-14	Edited	Orlic-Milacic, M.