

# Association of APOBEC3G:Vif with the Cul5-SCF complex

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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

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Reactome database release: 77

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

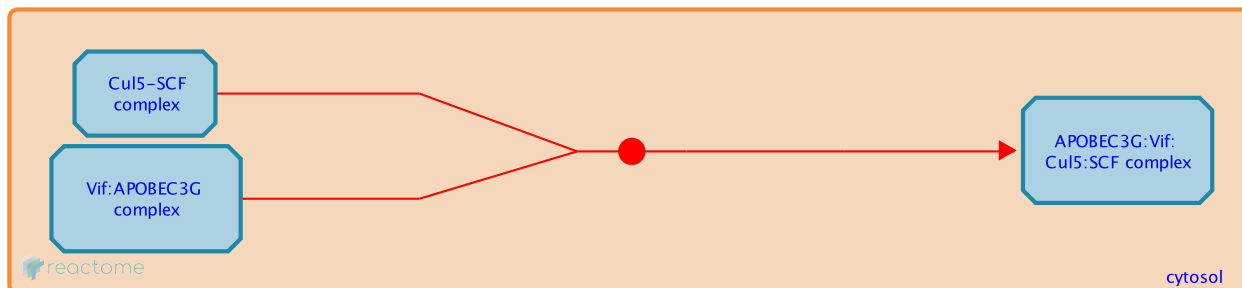
## Association of APOBEC3G:Vif with the Cul5-SCF complex [↗](#)

**Stable identifier:** R-HSA-180555

**Type:** binding

**Compartments:** cytosol

**Diseases:** Human immunodeficiency virus infectious disease



The interaction between Vif and the E3 ubiquitin ligase complex (Cullin5, Elongin B and Elongin C, and Rbx1) takes place through direct binding of the SOCS box motif in the viral protein Vif to the host protein Elongin C. Moreover, a conserved HCCH motif in Vif allows binding to Cullin 5.

### Literature references

Yu, X., Yu, Y., Liu, B., Luo, K., Kong, W., Mao, P. et al. (2003). Induction of APOBEC3G ubiquitination and degradation by an HIV-1 Vif-Cul5-SCF complex. *Science*, 302, 1056-60. [↗](#)

### Editions

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