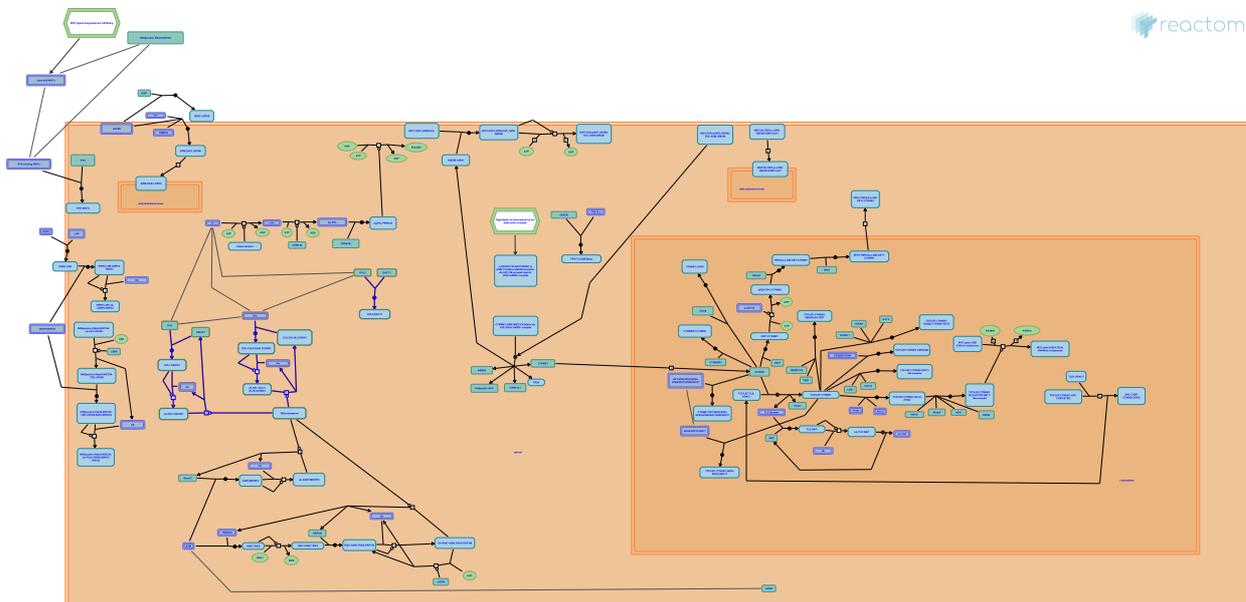


Degradation of DVL



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://creativecommons.org/licenses/by/4.0/).

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. [↗](#)

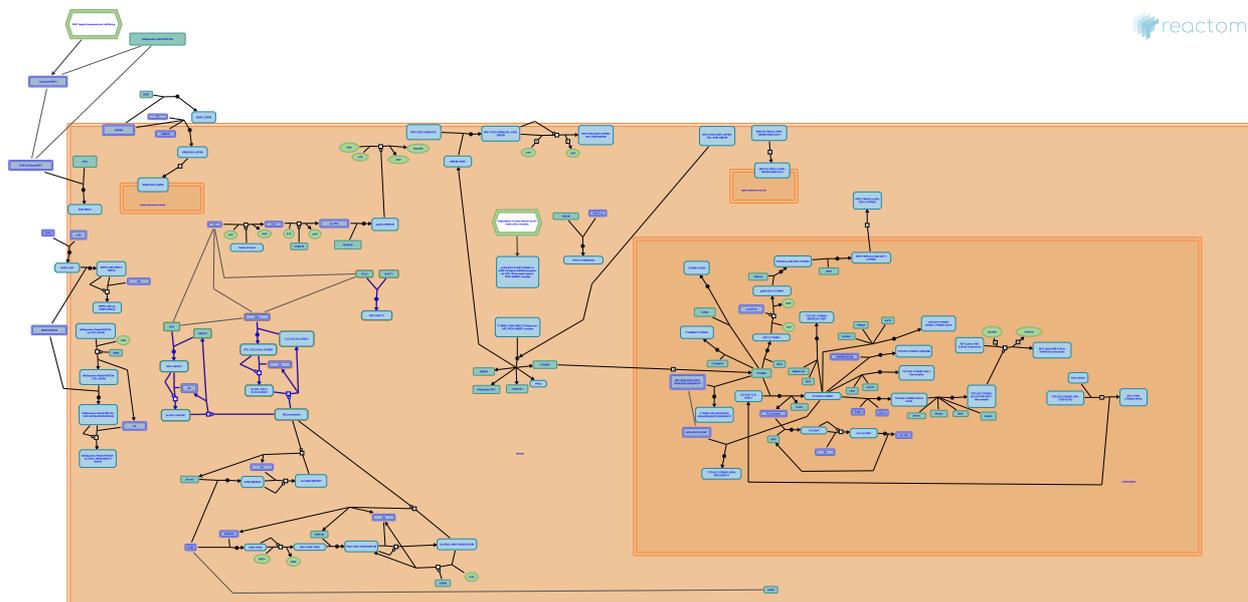
Reactome database release: 70

This document contains 1 pathway and 7 reactions ([see Table of Contents](#))

Degradation of DVL ↗

Stable identifier: R-MMU-4641258

Inferred from: [Degradation of DVL \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

DVL is bound by the CUL3:KLHL12:RBX1 ubiquitin ligase complex ↗

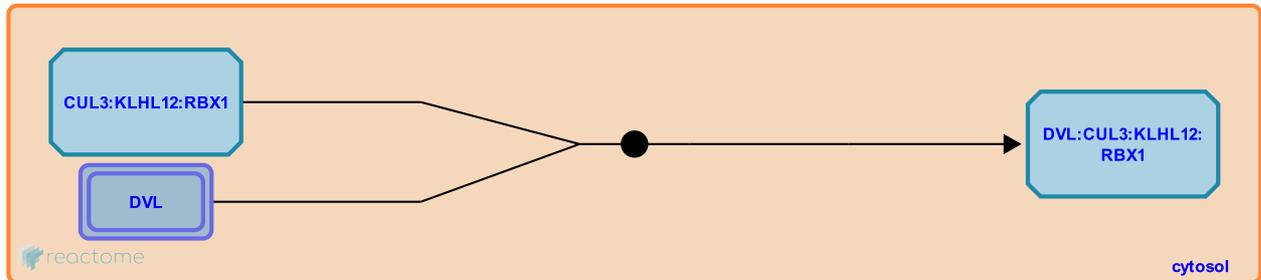
Location: [Degradation of DVL](#)

Stable identifier: R-MMU-1504213

Type: binding

Compartments: cytosol

Inferred from: [DVL is bound by the CUL3:KLHL12:RBX1 ubiquitin ligase complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [DVL is ubiquitinated by CUL3:KLHL12:RBX1](#)

DVL is ubiquitinated by CUL3:KLHL12:RBX1 ↗

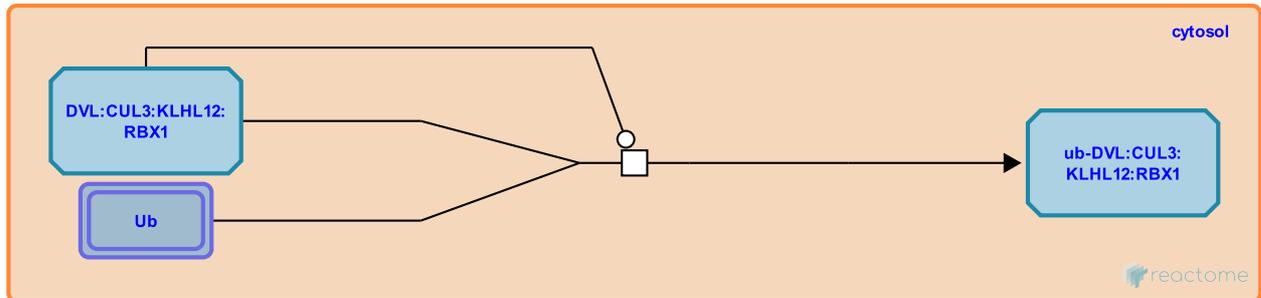
Location: [Degradation of DVL](#)

Stable identifier: R-MMU-1504190

Type: transition

Compartments: cytosol

Inferred from: [DVL is ubiquitinated by CUL3:KLHL12:RBX1 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [DVL is bound by the CUL3:KLHL12:RBX1 ubiquitin ligase complex](#)

Followed by: [Ubiquitinated DVL is degraded by the proteasome](#)

Ubiquitinated DVL is degraded by the proteasome ↗

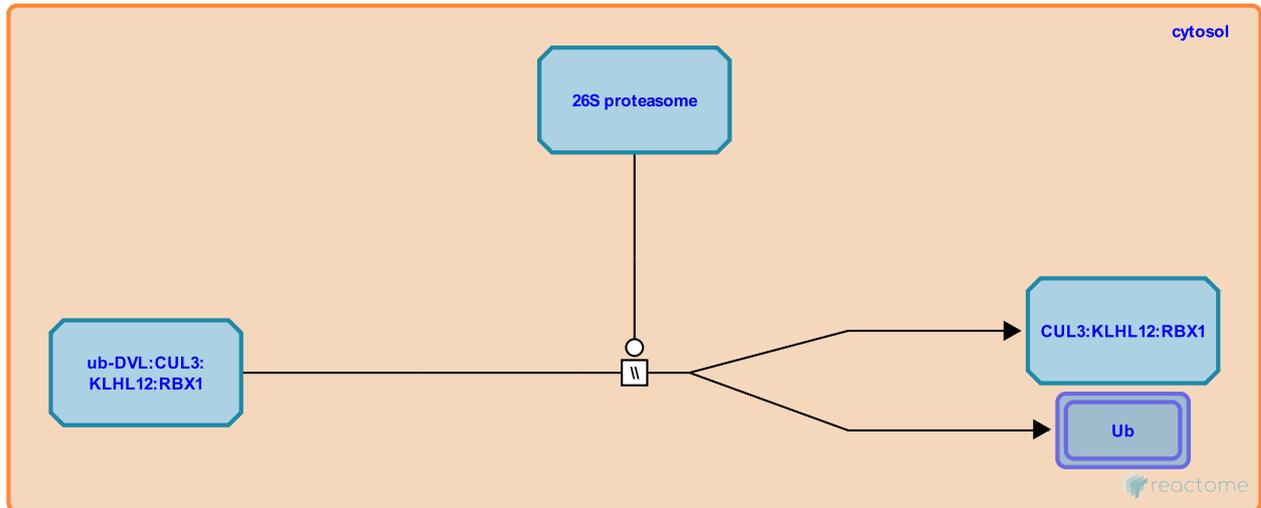
Location: [Degradation of DVL](#)

Stable identifier: R-MMU-1504193

Type: omitted

Compartments: cytosol

Inferred from: [Ubiquitinated DVL is degraded by the proteasome \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [DVL is ubiquitinated by CUL3:KLHL12:RBX1](#)

DVL1 is bound by the HECT ubiquitin ligase HECW1 ↗

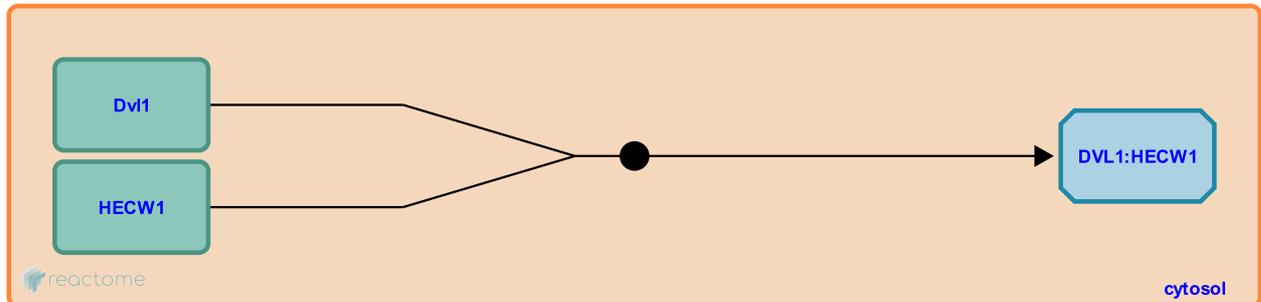
Location: [Degradation of DVL](#)

Stable identifier: R-MMU-4641155

Type: binding

Compartments: cytosol

Inferred from: [DVL1 is bound by the HECT ubiquitin ligase HECW1 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [DVL1 is ubiquitinated by HECW1](#)

DVL1 is ubiquitinated by HECW1 ↗

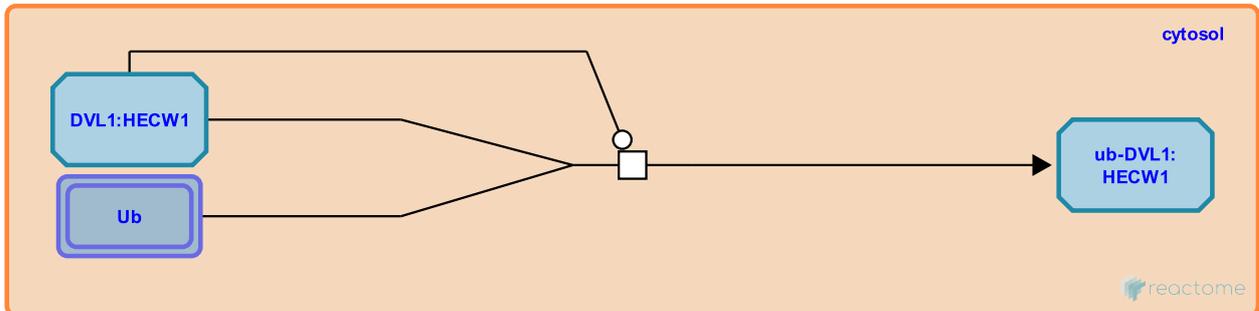
Location: [Degradation of DVL](#)

Stable identifier: R-MMU-4641159

Type: transition

Compartments: cytosol

Inferred from: [DVL1 is ubiquitinated by HECW1 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [DVL1 is bound by the HECT ubiquitin ligase HECW1](#)

Followed by: [Ubiquitinated DVL1 is degraded by the proteasome](#)

Ubiquitinated DVL1 is degraded by the proteasome ↗

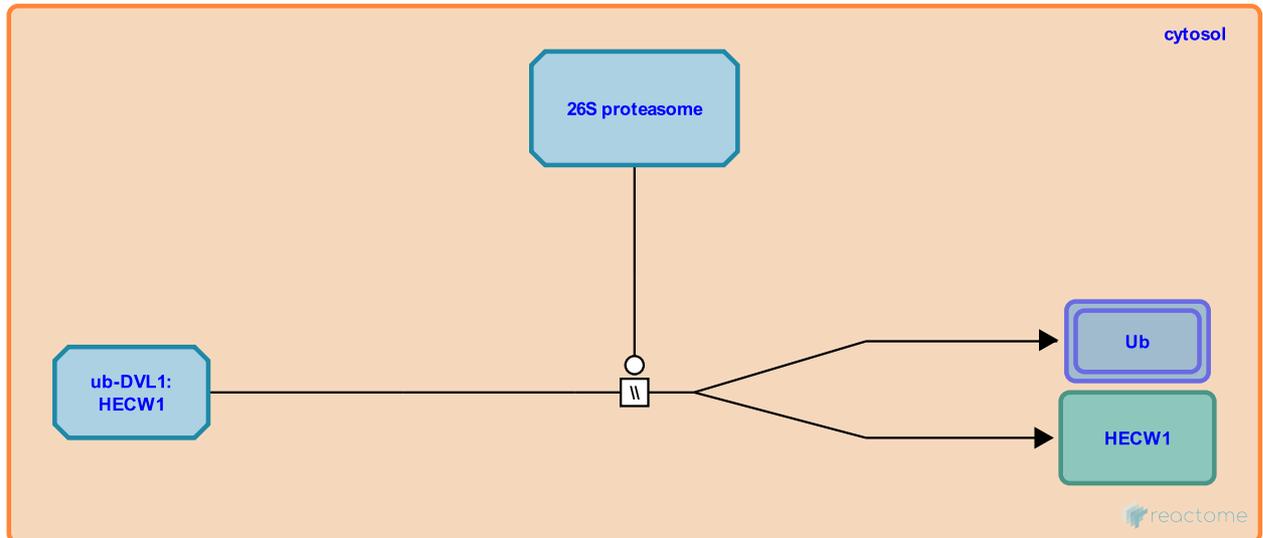
Location: [Degradation of DVL](#)

Stable identifier: R-MMU-4641260

Type: omitted

Compartments: cytosol

Inferred from: [Ubiquitinated DVL1 is degraded by the proteasome \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [DVL1 is ubiquitinated by HECW1](#)

DACT1 binds DVL2 ↗

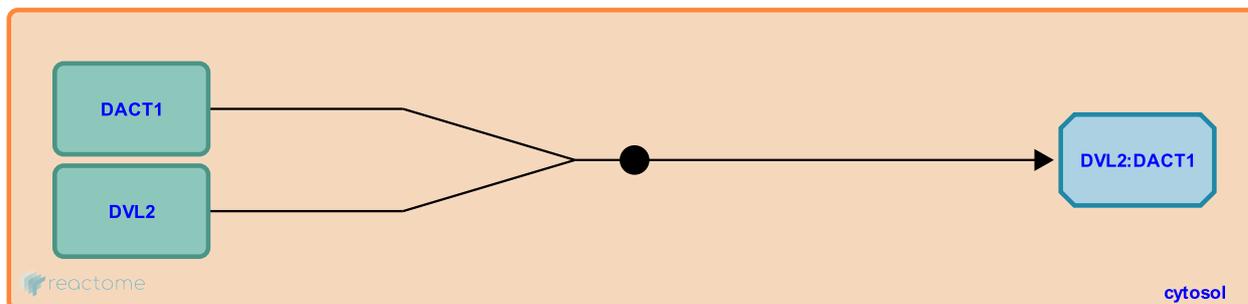
Location: [Degradation of DVL](#)

Stable identifier: R-MMU-4641147

Type: binding

Compartments: cytosol

Inferred from: [DACT1 binds DVL2 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Table of Contents

Introduction	1
⚡ Degradation of DVL	2
↳ DVL is bound by the CUL3:KLHL12:RBX1 ubiquitin ligase complex	3
↳ DVL is ubiquitinated by CUL3:KLHL12:RBX1	4
↳ Ubiquitinated DVL is degraded by the proteasome	5
↳ DVL1 is bound by the HECT ubiquitin ligase HECW1	6
↳ DVL1 is ubiquitinated by HECW1	7
↳ Ubiquitinated DVL1 is degraded by the proteasome	8
↳ DACT1 binds DVL2	9
Table of Contents	10