Ub-specific processing proteases

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. For more information see our license.

30/05/2020
**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**


Reactome database release: 72

This document contains 1 pathway and 40 reactions (see Table of Contents)
Ub-specific processing proteases (USPs) are the largest of the DUB families with more than 50 members in humans. The USP catalytic domain varies considerably in size and consists of six conserved motifs with N- or C-terminal extensions and insertions occurring between the conserved motifs (Ye et al. 2009). Two highly conserved regions comprise the catalytic triad, the Cys-box (Cys) and His-box (His and Asp/Asn) (Nijman et al. 2005, Ye et al. 2009, Reyes-Turcu & Wilkinson 2009). They recognize their substrates by interactions of the variable regions with the substrate protein directly, or via scaffolds or adapters in multiprotein complexes.

**Literature references**


**Editions**

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2015-04-16</td>
<td>Authored</td>
<td>Jupe, S.</td>
</tr>
<tr>
<td>2016-05-05</td>
<td>Edited</td>
<td>Jupe, S.</td>
</tr>
<tr>
<td>2016-05-16</td>
<td>Reviewed</td>
<td>Meldal, BH.</td>
</tr>
</tbody>
</table>
USP7 deubiquitinates TP53, MDM2, MDM4, FOXO4, PTEN

**Location:** Ub-specific processing proteases

**Stable identifier:** R-HSA-5689950