SESN1,2,3 bind overoxidized PRDX1

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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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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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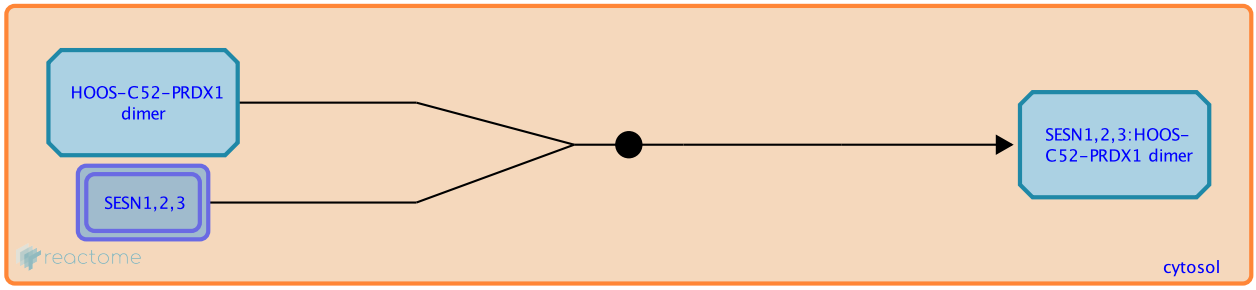
Stable identifier: R-HSA-5631903

Type: binding

Compartments: cytosol



Sestrins (SESN1, SESN2 and likely SESN3) bind overoxidized PRDX1, in which the catalytic cysteine C52 has been converted to cysteine-sulfinic acid. Among all peroxiredoxins, PRDX1 is the most abundant member of the PRDX family. The major function is to protect cells against reactive oxygen species (ROS), thus impacting on cell proliferation and survival (Gong et al. 2015). While several reports state that sestrins reduce overoxidized PRDX1 to the catalytically active homodimer (Budanov et al. 2004, Papadia et al. 2008, Essler et al. 2009), there are conflicting reports claiming that sestrins do not possess cysteine sulfinyl reductase activity (Woo et al. 2009).

Literature references

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Editions

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