SHPRH binds monoUb-K164-PCNA, RAD6:RAD18, UBE2V2:Ub:UBE2N

May, B., Myung, K.

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.

22/07/2024

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. ↗

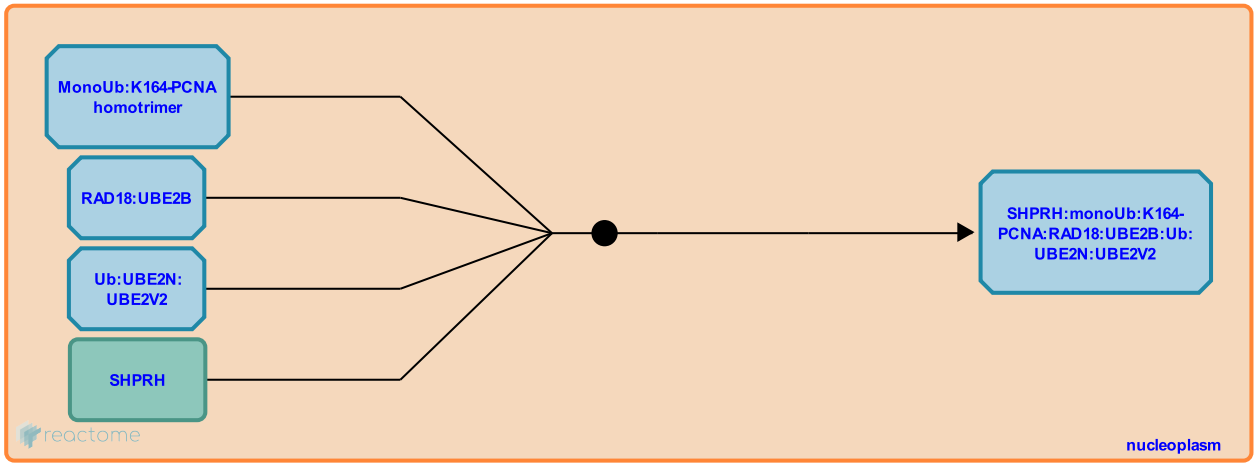
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

SHPRH binds monoUb-K164-PCNA, RAD6:RAD18, UBE2V2:Ub:UBE2N ↗

Stable identifier: R-HSA-8943007

Type: binding

Compartments: nucleoplasm



At stalled replication forks, the E3 ubiquitin ligase SHPRH interacts with PCNA monoubiquitinated at lysine-164 (monoUb-K164-PCNA), the RAD18:UBE2B complex (RAD18:RAD6 complex), and the Ub:UBE2N:UBE2V2 complex (UBC13:MMS2 complex with ubiquitin conjugated to UBC13) (Unk et al. 2006, Motegi et al. 2006, Motegi et al. 2008).

Literature references

Roest, HP., Ding, H., Motegi, A., Myung, K., Markowitz, SD., Wu, X. et al. (2008). Polyubiquitination of proliferating cell nuclear antigen by HLTF and SHPRH prevents genomic instability from stalled replication forks. *Proc. Natl. Acad. Sci. U.S.A., 105*, 12411-6. ↗

Haracska, L., Hurwitz, J., Blastyák, A., Bermudez, V., Prakash, L., Fatyol, K. et al. (2006). Human SHPRH is a ubiquitin ligase for Mms2-Ubc13-dependent polyubiquitylation of proliferating cell nuclear antigen. *Proc. Natl. Acad. Sci. U.S.A., 103*, 18107-12. ↗

Motegi, A., Myung, K., Markowitz, SD., Sood, R., Liu, PP., Moinova, H. (2006). Human SHPRH suppresses genomic instability through proliferating cell nuclear antigen polyubiquitination. *J. Cell Biol., 175*, 703-8. ↗

Editions

2016-10-22	Authored, Edited	May, B.
2017-01-11	Edited, Reviewed	Myung, K.