

IL6 binds IL6R-2

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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

- 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: 88

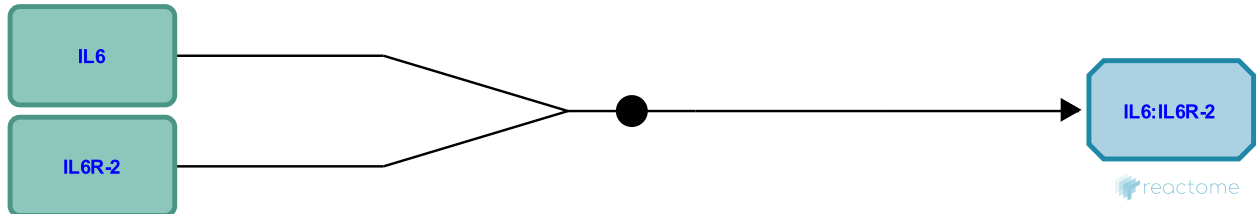
This document contains 1 reaction ([see Table of Contents](#))

IL6 binds IL6R-2 [↗](#)

Stable identifier: R-HSA-1067640

Type: binding

Compartments: extracellular region



The short, soluble form of Interleukin-6 receptor alpha (IL6R-2, sIL6R), like the longer membrane-associated form IL6R, binds circulating Interleukin-6 (IL6). IL6R-2 is generated by limited proteolysis of the longer membrane associated form and by translation of an alternatively spliced mRNA. The IL6:IL6R-2 dimer can associate with the IL6 receptor signaling beta subunit IL6ST (gp130) and stimulate cells that do not express IL6R, a process termed trans-signaling. IL6ST is expressed in many cell types that do not express IL6R (Rose-John et al. 2006).

Literature references

Matsuda, T., Kishimoto, T., Taga, T., Yamasaki, K., Hirano, T., Hibi, M. et al. (1989). Interleukin-6 triggers the association of its receptor with a possible signal transducer, gp130. *Cell*, 58, 573-81. [↗](#)

Editions

2010-12-10	Edited	Jupe, S.
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