CSF2RA:CSF2RB binds SFTPs

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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. ↗

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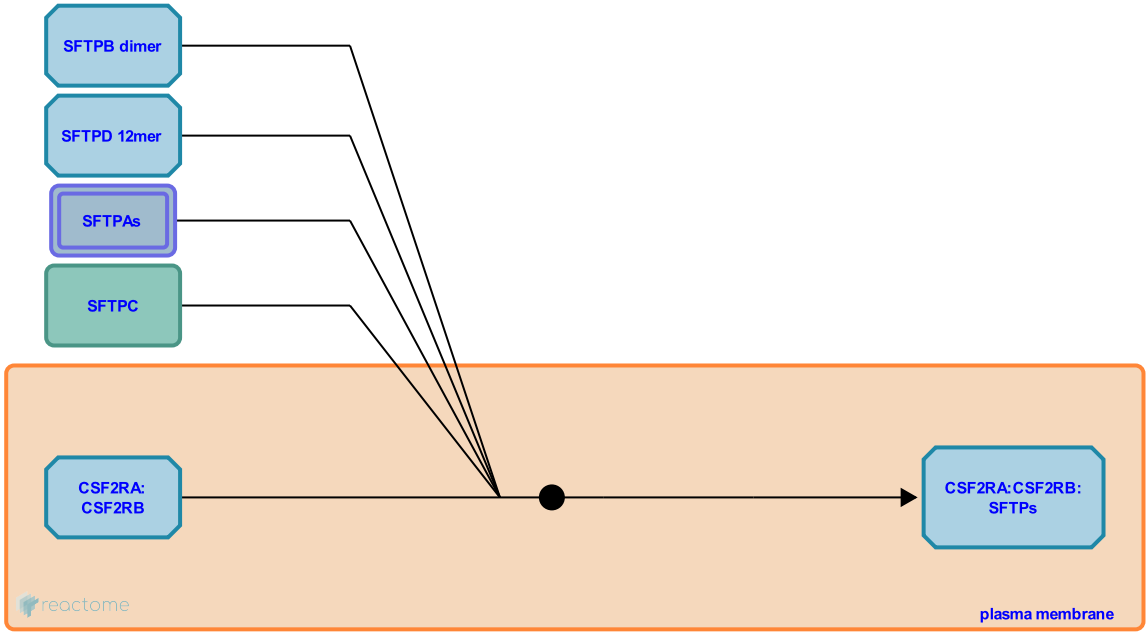
Stable identifier: R-HSA-5686335

Type: binding

Compartments: plasma membrane, extracellular region



Surfactant catabolism by alveolar macrophages plays a small but critical part in surfactant recycling and metabolism. Upon ligand binding, granulocyte-macrophage colony-stimulating factor receptor (GM-CSF), a heterodimer of alpha (CSF2RA) and beta (CSF2RB) subunits (Hansen et al. 2008), initiates a signalling process that not only induces proliferation, differentiation and functional activation of hematopoietic cells but can also determine surfactant uptake into alveolar macrophages and its degradation via clathrin-coated vesicles. The exact mechanism of surfactant degradation in macrophages is poorly understood (Jain et al. 2005, Ikegami 2006). GM-CSF-deficiency can result in pulmonary alveolar proteinosis (PAP), a lung disease characterised by surfactant accumulation and lipid-engorged alveolar macrophages (Carey & Trapnell 2010).

Literature references

Ikegami, M. (2006). Surfactant catabolism. *Respirology, 11*, S24-7.

Fisher, AB., Jain, D., Bates, SR., Dodia, C. (2005). Pathways for clearance of surfactant protein A from the lung. *Am. J. Physiol. Lung Cell Mol. Physiol., 289*, L1011-8.

Carey, B., Trapnell, BC. (2010). The molecular basis of pulmonary alveolar proteinosis. *Clin. Immunol., 135*, 223-35.

Guthridge, M., Stomski, FC., Ramshaw, H., McClure, BJ., Lopez, AF., Powell, J. et al. (2008). The structure of the GM-CSF receptor complex reveals a distinct mode of cytokine receptor activation. *Cell, 134*, 496-507.

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