Phosphorylation of LAT by p-SYK

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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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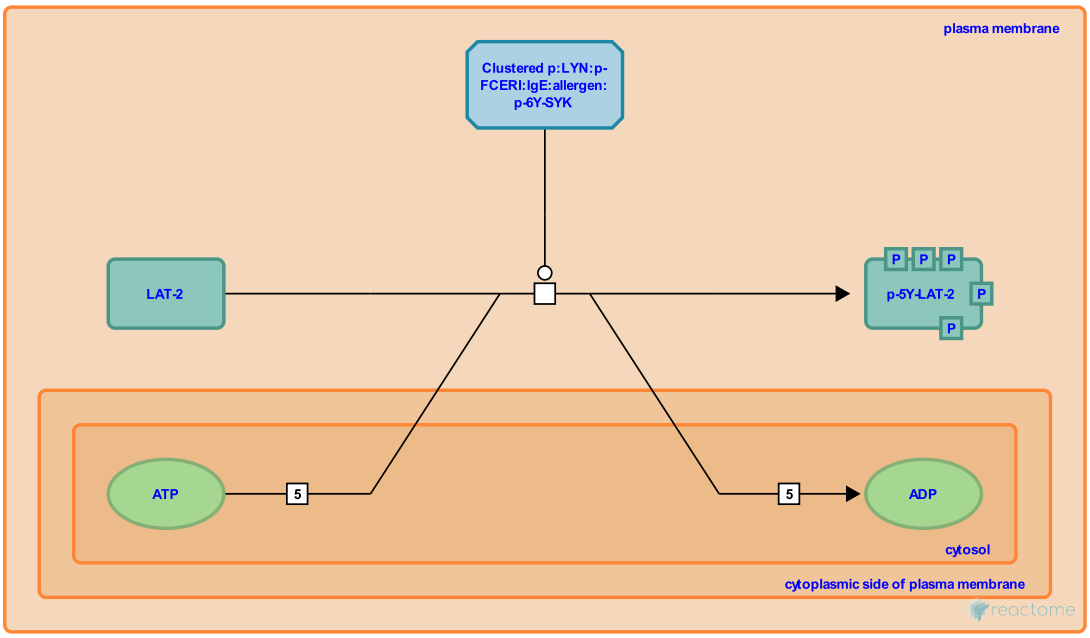
Stable identifier: R-HSA-2730843

Type: transition

Compartments: plasma membrane, cytosol



LAT is palmitoylated and membrane-associated adaptor protein. It rapidly becomes tyrosine-phosphorylated upon receptor engagement. LAT has nine conserved tyrosine residues of which five have been shown to undergo phosphorylation (Y127, Y132, Y171, Y191 and Y226). Src family kinases, SYK and ZAP-70 efficiently phosphorylate LAT on these tyrosine residues (Jiang & Cheng 2007, Paz et al. 2001). Phosphorylation of LAT creates binding sites for the Src homology 2 (SH2) domain proteins PLC-gamma1, GRB2 and GADS, which indirectly bind SOS, VAV, SLP-76 and ITK (Wange 2000).

Literature references

Samelson, LE., Irvin, BJ., Abraham, RT., Dick, CJ., Leibson, PJ., Billadeau, DD. et al. (1999). Cutting edge: a role for the adaptor protein LAT in human NK cell-mediated cytotoxicity. *J. Immunol., 162*, 2453-6. ↗

Abo, A., Wang, S., Lu, X., Paz, PE., Stokoe, D., Clarke, H. (2001). Mapping the Zap-70 phosphorylation sites on LAT (linker for activation of T cells) required for recruitment and activation of signalling proteins in T cells. *Biochem. J., 356*, 461-71. ↗

Jiang, Y., Cheng, H. (2007). Evidence of LAT as a dual substrate for Lck and Syk in T lymphocytes. *Leuk Res, 31*, 541-5. ↗

Editions

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