Cell Communication and Signaling BioMed Central

Meeting abstract

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A comprehensive map of the IL-1R signalling network

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from 12th Joint Meeting of the Signal Transduction Society (STS). Signal Transduction: Receptors, Mediators and Genes
Weimar, Germany. 29–31 October 2008

Published: 26 February 2009

Cell Communication and Signaling 2009, **7**(Suppl 1):A25 doi:10.1186/1478-811X-7-S1-A25

This abstract is available from: http://www.biosignaling.com/content/7/S1/A25

The interleukin-1 (IL-1) signalling pathway represents a paradigm for all IL-1 family cytokines (IL-1A, IL-1B, IL-18, IL-33, IL1F5 to IL1F10) as well as for the toll-like-receptor-induced pathways. Research on IL-1 signalling for more than 20 years has generated a large body of experimental data, which are scattered across many different publications. No signal transduction map exists that covers comprehensively this huge knowledge on IL-1-activated effector molecules. We attempted to improve the publicly accessible IL-1 signalling map currently deposited in Netpath http://www.netpath.org/pathways. This map contains 36 molecules and information for a total of 89 reactions including physical interactions, catalytic reactions (e.g. phosphorylations) and subcellular distributions. Netpath includes data from experimental results reported in 46 publications. We created an extended version that now contains 140 molecules and 245 reactions taken from original data out of 146 selected publications. In addition to visualization of molecules involved in IL-1 signal transduction this map enables direct access to the scientific evidence that was used to build up the map. Subsequently we imported the map into GenMAPP, Version 2.1 and mapped mRNA expression data from a time course experiment of human KB cells that were stimulated for 0.5, 1, 3, 16 and 24 h with 10 ng/ml IL-1alpha. This analysis revealed that several interconnected parts of the IL-1 signalling network are co-induced or co-repressed during stimulation. By treating the cells with 50 μM PD 98059 we were able to map the part of the IL-1-signalling network that responds to ERK-inhibition at the level of mRNA. In summary, this type of knowledge-based curated data base serves not only to sort and to store data from biochemical, cell biological and molecular biology experiments but may also help to depict nodes of signal transduction that can be used to design new hypothesis-driven experiments.