

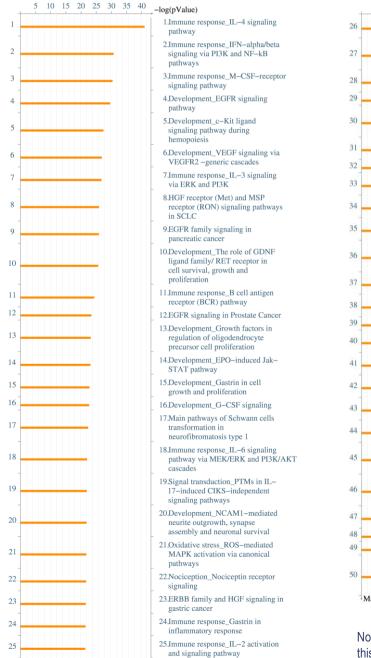
PamChip® Peptide Phosphosites: **Canonical Pathways and Network Objects**

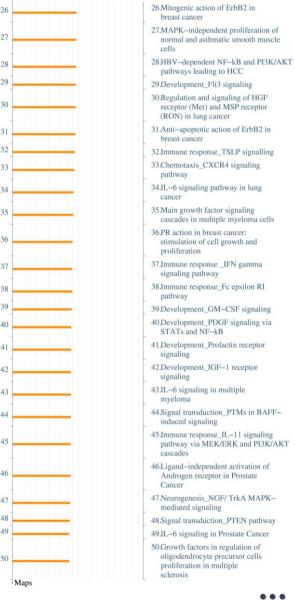
Peptides on PamChip (PTK 86402 and STK 87102) can be phosphorylated by a number of kinases which are represented in signaling cascades in pathways. Some basic information is shown about how we interpret the PamChip data (pathway profiles).

5 10 15 20 25 30 35 40

Deriving information for Pathways containing PamChip kinase substrates

The 13 amino acid peptide sequences on the PamChip are derived from Kinase substrates which are a part of several canonical pathways. The UniPROT accession numbers of these substrates are imported to Thomson Reuters Metacore GeneGO pathway analysis tool. Canonical pathway maps represent a set of signalling and metabolic maps covering the human signalling pathways in a comprehensive way. All maps are created by Thomson Reuters scientists by a high quality manual curation process based on published peer reviewed literature. Experimental data is visualized on the maps as blue (for downregulation) and red (upregulation) histograms (page 2). Enrichment analysis consists of matching the Kinase Substrate UniPROT IDs with functional ontologies in MetaCore. The probability of a random intersection between a set of IDs in the target list with ontology entities is estimated in p value of hypergeometric intersection. The lower p value means higher relevance of the entity to the dataset, which shows in higher rating for the entity. Here we show the Top 50 canonical pathway maps that contain the Kinase substrates on the PTK (86402) and ST (87102) PamChips.



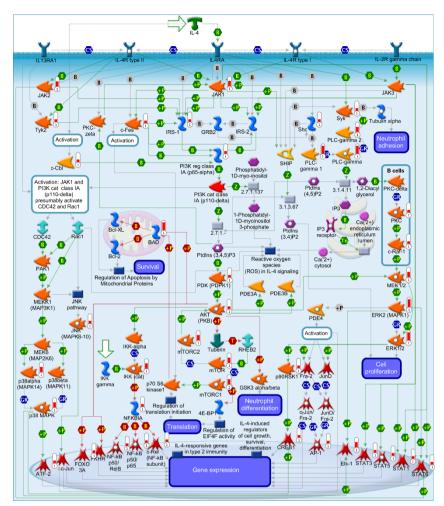


-log(pValue)

Note: here $-\log_{10}(p)$ is shown, the higher this value, the more the significance.



Examples of select pathways are shown



Immune response_IL-4 signaling pathway

Development_EGFR signalling pathway

Note: Presence of a histogram next to a network object indicates the kinasesubstrate protein with 1 or more phosphosites on the PamChip (related to height).



