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Data Article

Data on interleukin (IL)-2- and IL-15-dependent changes in IL-2Rβ and IL-2Rγ complexes

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ABSTRACT

We provide detailed datasets from our analysis of the proteins that associate with IL-2Rβ and IL-2Rγ in T-cells stimulated with IL-2 or IL-15 compared with resting T-cells, as identified by SILAC-based quantitative proteomics. We also include quantitative data regarding site-specific phosphorylation events observed both in IL-2Rβ and IL-2Rγ. Moreover, we provide results demonstrating the specific protein recruitment capacity of four of those site-specific phosphorylations. The proteomics and phosphoproteomics data described in this article is associated with a research article entitled "Characterization of receptor-associated protein complex assembly in Interleukin (IL)-2- and IL-15-activated T-lymphocytes" (Osinalde et al., 2016 [1]). The mass spectrometry data have been deposited to the ProteomeEXchange Constorium with the identifier PXD002386.

Specifications Table

Subject area	*Immunology*
More specific subject area	*Protein-protein interaction, site-specific phosphorylation, phosphosite-dependent interaction*

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Type of data	*Mass Spectrometry (MS) data*
How data was acquired	*MS data was acquired in a Q-Exactive (Thermo) mass spectrometer and Velos Orbitrap MS system (Thermo).*
Data format	*Raw (*raw), excel files (.xlsx), figures*
Experimental factors	***For IL-2R interactome analyses:*** *Kit225 T-cells were grown in light (Arg0/Lys0), medium (Arg6/Lys4) and heavy (Arg10/Lys8) media. Differentially SILAC-labeled T-cells were kept unstimulated, treated with IL-2 or stimulated with IL-15, respectively prior to cell lysis.* ***For peptide pull-down analyses:*** *Kit225 T-cells were grown in light (Arg0/Lys0) and heavy (Arg10/Lys8) media.*
Experimental features	***For IL-2R interactome and phosphorylation analyses****, after stimulation, cells were lysed and protein extracts derived from the three different experimental conditions were combined and affinity-purified using specific antibodies against IL-2R beta or gamma subunits. Immune complexes were fractionated on a SDS-PAGE and in-gel digested using trypsin. Resulting peptides were either directly analyzed by LC-MS/MS or enriched in phosphorylated peptides using TiO_2 beads prior to MS analysis using a QE-Exactive MS instrument.* ***For peptide pull-down analyses,*** *differentially labeled cells were lysed and separately incubated with the unmodified and phosphorylated version of the peptide used as bait. Then precipitated proteins were on-bead digested with LysC and subsequently with trypsin and resulting peptides were analyzed by LC-MS/MS in a Velos Orbitrap MS system.*
Data source location	*Odense, Denmark*
Data accessibility	*Data are available in this article and deposited at ProteomeEXchange Constorium,* http://www.proteomexchange.org/.

Value of the data

- The study uncovers new IL-2- and IL-15-dependent interacting partners of IL-2Rβ and IL-2Rγ.
- This investigation provides unprecedented data regarding cytokine-dependent and –independent phosphorylation events occurring in IL-2R β and γ subunits.
- A large number of phosphosites corresponding to a wide range of proteins are reported.
- The data presented here underscores the capacity of certain cytokine-dependent phosphorylation sites localized on IL-2Rβ and IL-2Rγ to recruit downstream signaling molecules.
- Overall, the study provides novel insights into the early activation events following interleukin/receptor engagement in $CD4^+$ T-lymphocytes.

1. Data

The data in this article show the effect of IL-2 and IL-15 stimulation on the phosphorylation state and interacting partners of IL-2Rβ and IL-2Rγ. Data on the capacity of selected phosphorylations to serve as anchoring sites and recruit proteins are also presented. In all the experiments a SILAC-based approach was followed in combination with LC-MS/MS and subsequent bioinformatic analyses.

2. Experimental design, materials and methods

2.1. Cell culture

For mass spectrometry (MS)-based analysis, human leukemic Kit225 T-cells, which depend on IL-2 [2], were grown in RPMI deficient in arginine and lysine supplemented with 10% dyalized serum

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