Impact of Delayed Freezing on Protein Profiles in Clinical Tissues

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The European consortium SPIDIA (www.spidia.eu) systematically addresses the impact of pre-analytical factors on the molecular portrait of clinical samples.

The aim of this subproject was to characterize protein and phosphoprotein profiles in human tissue samples during the pre-analytical phase as basis for novel Technical Specifications (CEN/TS).

Experimental Results: Amounts of proteins and phospho-proteins in tissues can change during the pre-analytical phase.

Standardization activity: CEN/TS documents for protein analysis in frozen tissues are being developed.

SPIDIA’s ways to exploit scientific results

Publication → IP → Standard

Time course experiment

\begin{figure}[h]
\centering
\begin{tikzpicture}
\begin{axis}[
    width=\textwidth,
    height=4cm,
    ybar,
    bar width=10pt,
    y dir=reverse,
    yticklabel style={/pgf/number format/1000 sep=,xxx},
    symbolic x coords={0, 30, 60, 180},
    xtick=data,
    nodes near coords, nodes near coords align=center,
]
\addplot coordinates {(0, 3) (30, 5) (60, 7) (180, 8)} node [above] \text{p-p44/42-MAPK};
\addplot coordinates {(0, 1) (30, 3) (60, 2) (180, 1)} node [above] \text{GAPDH};
\end{axis}
\end{tikzpicture}
\end{figure}

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