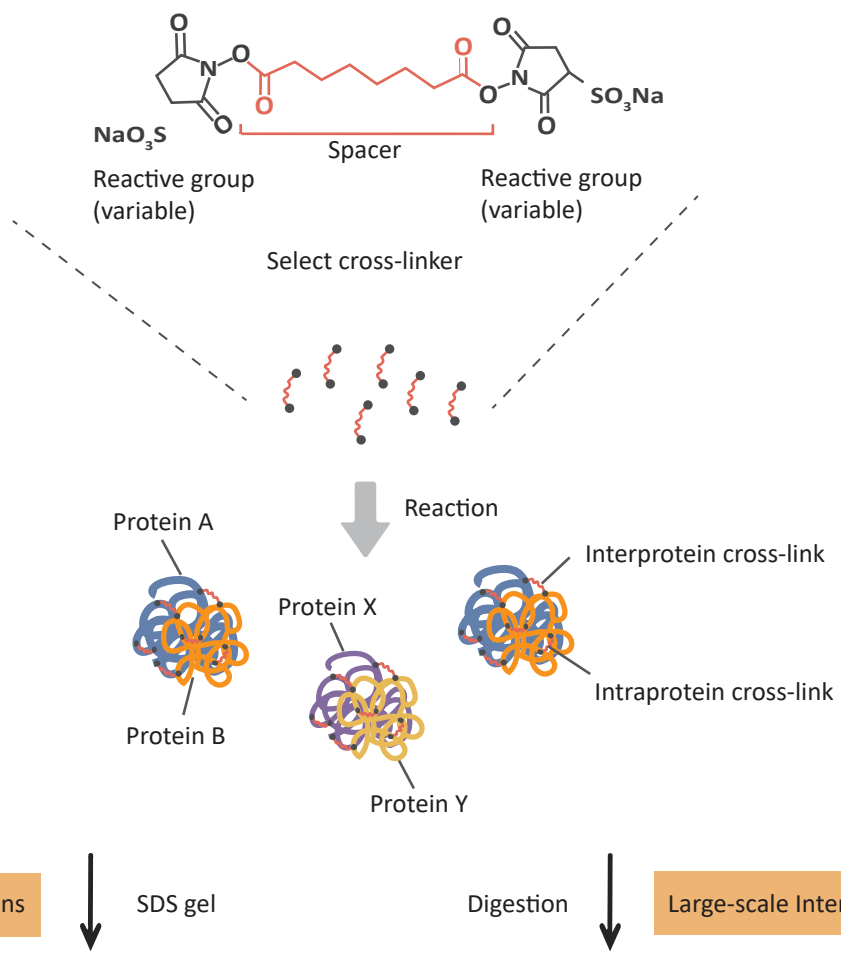
Creative Proteomics

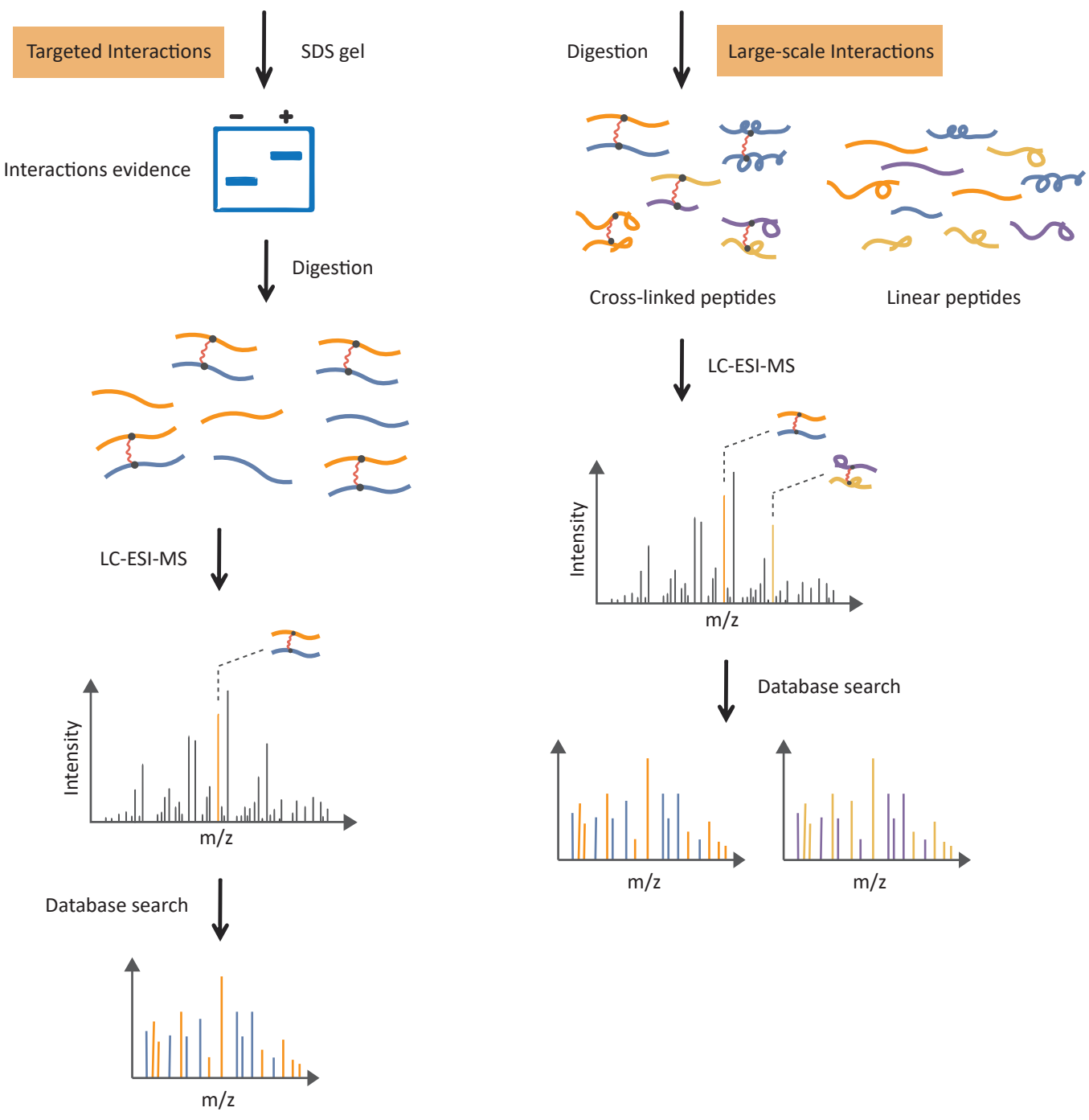
PROTEIN INTERACTION ANALYSIS

Crosslinking and Label Transfer

CROSSLINKING PROTEIN INTERACTION ANALYSIS

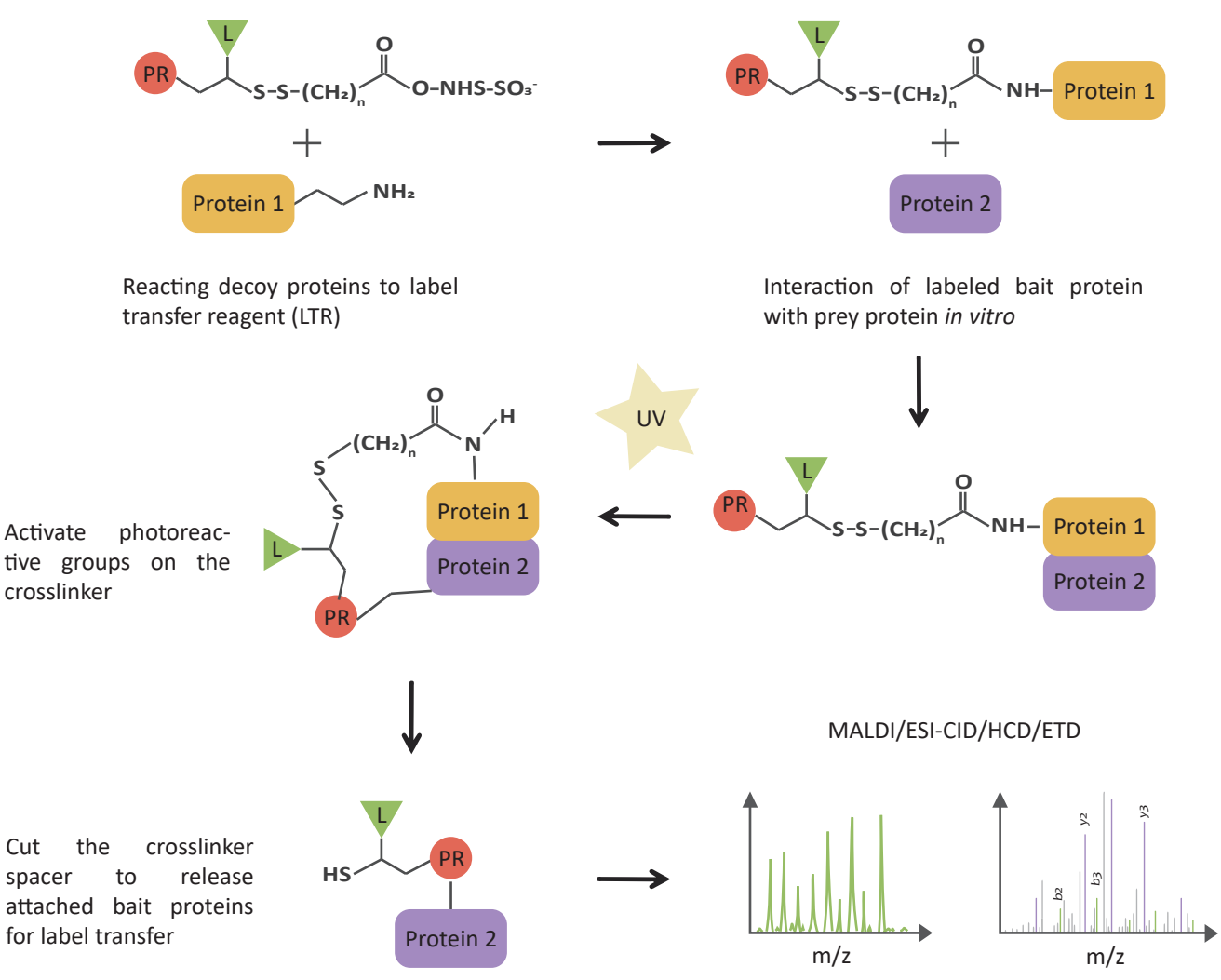
Under physiological condition, most protein-protein interactions are transient, and happen in a very short duration, increasing the difficulties to study them. Crosslinking reagents, or crosslinkers, provide the analytical solution to capture protein-protein complexes by covalently binding them together as they interact and freezing even transient, weak interactions for consequent isolation and characterization.





LABEL TRANSFER PROTEIN INTERACTION ANALYSIS

The label transfer approach incorporates crosslinking methodology to study protein-protein interactions by labeling proteins that interact with a protein of interest. This method can be used to discover novel interactions, confirm putative interactions suggested by other techniques, and investigate protein complexes. In addition, the label transfer method can detect weak or transient protein interactions that often fail to detect by co-immunoprecipitation, or pull-down method.



CHARACTERISTICS

Protein Crosslinking

1. Ability to detect weak or transient protein interactions
2. *In vivo* cross-linking: interactions between proteins can be captured in their natural environment. However, this method cannot strictly control the reaction conditions. If multiple proteins have functional groups that specifically react with the cross-linking agent, the cross-linking agent will react with the multiple proteins.
3. *In vitro* cross-linking: strictly control more reaction conditions for specific cross-linking reaction. But lack of physiological conditions.
4. Multiple protein cross-linking methods, including chemical cross-linking, enzymatic cross-linking, and photoprotein cross-linking

Label Transfer

1. Ability to detect weak or transient protein interactions
2. Can be used to purify and detect prey proteins
3. Most LTRs can directly label specific protein domains, but they are generally not suitable for mapping protein-protein interaction networks because homing molecules attached to cross-linking agents usually only direct cross-linking to the binding domain.