

# Strep-tag® and One-STrEP-tag for Protein-protein Interaction Analysis

IBA GmbH

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Protein-protein interactions (PPI) govern almost all important processes in living organisms. Thus, their rapid and accurate determination and investigation is a major challenge in life sciences. With four different determination systems based on *Strep-tag*®II and One-STrEP-tag, we provide optimal solutions for in vivo protein-protein interaction analysis.

## Materials

**One-STrEP Set** (Cloning and Purification Kit for Mammalia and *Escherichia coli*)

**One-TAP Set** (Cloning and Purification Kit for Mammalia and *E. coli*)

**Two-TAP Set** (Cloning and Purification Kit for Mammalia and *E. coli*)

**Spine Set** (Cloning and Purification Kit for *E. coli*)

## Methods

The **One-STrEP** system is recommended for getting started. It needs one tag and one

purification step only. Due to its excellent performance, this method yields a favorable signal-to-noise ratio in most cases. Mild elution and fast washing allow the isolation of even weakly interacting preys.

In case the One-STrEP system provides sub-optimal data, the **One-TAP** system extends the options of the One-STrEP system since it adds a second independent purification step yet with the same tag. Two different purification steps may better discriminate specific from nonspecific binding but bear the risk of losing weakly interacting partners.

The **Two-TAP** system is recommended only as an option in case of unsatisfying data with the

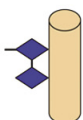
One-STrEP or One-TAP approach and not as first choice starting point.

In addition to these non-covalent capture methods of potential preys, **SPINE** adds the possibility to covalently link the preys to its bait by formaldehyde cross-linking. This linkage is achieved in the living organism enabling a time resolved snapshot of interacting proteins. SPINE is currently validated in prokaryotes only but its adaptation to mammalian system is under way.

## StarGate for Bait Cloning

This novel cloning system is the perfect tool for efficient screening and fast identification of the optimal tag for PPI investigation with a given bait. Once the bait is cloned into a **Donor Vector**, a large selection of **Acceptor Vectors** for its expression with different tag arrangements in the desired host is available.

Address correspondence to IBA GmbH Headquarters, Rudolf-Wissell-Strasse 28, 37079 Göttingen, Germany; Tel.: Europe +49 551 50672-0, USA +1 877 422 4624; info@iba-go.com, www.iba-go.com.

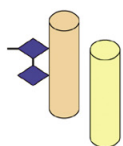


Recommended method to start

**One-STrEP**  
one tag  
one column

- only one tag
- even weakly interacting preys are isolated

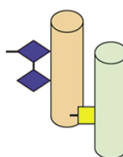
(Juntilla et al., Proteomics 2005)



Recommended in case of background with One-STrEP method

**One-TAP**  
one tag  
two columns

- two purification steps with only one tag increase signal:noise ratio
- recommended for high-affinity PPI

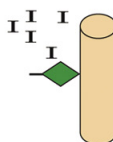


Alternative option only if One-TAP performs insufficiently

**Two-TAP**  
two tags  
two columns

- improved purification procedure for FLAG®-users with two tags
- improvement of original TAP procedure

(Gloeckner et al., Proteomics 2007)



Reversible cross-linking in vivo with formaldehyde

**SPINE**  
one tag  
one column  
formaldehyde

- only one tag
- time-resolved map of interacting proteins possible

(Herzberg et al., Proteomics 2007)