Cell Selection & Expansion

For research use only

Protocol

Cell isolation with Strep-Tactin® Magnetic Microbeads

for PBMCs or other single cell suspensions

1. REQUIRED REAGENTS

Cat. no.	Product	Required/total cells		
		1 x 10^7	1 x 10^8	1 x 10^9
6-5510-050	Strep-Tactin® Magnetic Microbeads, 750 µl	15 µl	150 µl	1500 µl
	Protein of choice fused to a Twin-Strep-tag®	1 µg*	10 µg*	100 µg*
6-6325-001	Biotin stock solution, 100 mM, 1 ml	100 µl	150 µl	600 µl
6-6320-085	10x Buffer CI, 85 ml 10x PBS containing 10 mM EDTA and 5% BSA	3-4 ml	6-7 ml	18-19 ml

*Amounts refer to a 50 kDa protein

2. INITIAL PREPARATIONS

2.1. Reagent preparation

Volumes are suitable for isolating target cells out of **up to 1 x 10^7** PBMCs. For higher cell numbers, protein and Strep-Tactin® Magnetic Microbead volumes should be upscaled linearly according to total cell numbers (e.g., for 5 x 10^7 cells use 5x indicated Fab-Strep volume). Adapt other volumes according to **Table 1.**

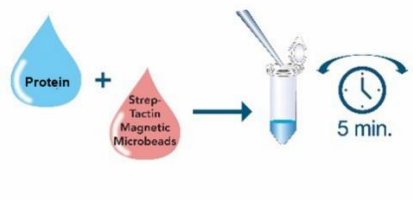
Cell labeling and isolation (3.1. and **3.2.) has to be performed at 4 °C.** Please make sure that all reagents and cells are accordingly refrigerated before starting the protocol. **The subsequent removal of reagents and washing (3.3** and **3.4) has to be performed at room temperature.**

2.1.1. Prepare 1x Buffer CI by diluting stock with ddH_2O.

2.1.2. Optional: Wash Strep-Tactin® Magnetic Microbeads before use to remove sodium azide. Add **1 ml** Buffer CI to required volume of microbeads (see 2.1.4.). Mix carefully and separate beads from buffer using a magnet. Discard supernatant and resuspend magnetic microbeads in Buffer CI (initial volume as in 2.1.4.).

2.1.3. Dilute your Twin-Strep-tag® fusion protein to a concentration of **50 µg/ml** with Buffer CI.

Titration of optimal isolation conditions might be necessary. The following instructions are an example for isolating cells with a **50 kDa** protein fused to a Twin-Strep-tag®.



2.1.4. Mix **20 µl** Twin-Strep-tag® fusion protein (2.1.3.) with **15 µl** Strep-Tactin® Magnetic Microbeads (vortex before pipetting!) in an Eppendorf tube. Incubate under constant gentle agitation for **5 min** (up to 24 h) at **4 °C**.

2.1.5. Prepare 1 mM Biotin Elution Buffer by diluting **100 µl** of 100 mM Biotin stock solution in **10 ml** Buffer CI. Mix thoroughly. Keep at **room temperature**.

2.2. Sample preparation

Prepare **1 x 10^7** PBMCs in **30 µl** Buffer CI. Buffer CI volume should be upscaled linearly for higher cell numbers (e.g., use 5x 30 µl Buffer CI for 5 x 10^7 total cells). Cells should be cooled down to **4 °C** before starting the protocol.

Table 1: Recommended volumes & tube sizes for different cell numbers

Starting cell number	Recommended tube size [**ml**]	Resuspension volume [**ml**]	Total Biotin Elution Buffer [**ml**]	3.3.1. [**ml**]
≤ 1 x 10^7	15	5	10	5
≤ 1 x 10^8	15	10	15	7.5
≤ 1 x 10^9	50	30	60	30

3. PROTOCOL

3.1. Cell labeling

Perform all steps at **4 °C.**

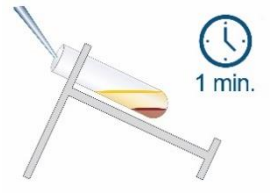
3.1.1. Add PBMCs to the pre-incubated protein-Microbead preparation (2.1.4.) and mix thoroughly by gentle pipetting.

3.1.2. Incubate for **10 min** under gentle constant agitation, e.g. on a roller mixer, to prevent cells from sedimentation. Continue with 3.2.1.

3.2. Magnetic cell isolation

Perform all steps at **4 °C.**

3.2.1. Add the incubated cells to **5 ml** Buffer CI. Mix thoroughly by gentle pipetting.



3.2.2. Incubate the tube on a magnet for **1 min**, remove entire supernatant carefully.

3.2.3. Resuspend cells in **5 ml** Buffer CI. Incubate the tube on a magnet for **1 min** (see 3.2.2.), remove entire supernatant carefully.

3.2.4. Repeat step 3.2.3. once. Continue with step 3.3.1.

3.3. Removal of magnetic microbeads

Perform all steps at **room temperature.**

3.3.1. Resuspend cells in **5 ml** Biotin Elution Buffer (2.1.5.). Mix by thoroughly by pipetting and incubate for **5 min** at **room temperature** on a roller mixer.

3.3.2. Incubate the tube on a magnet for **1 min**, collect entire supernatant carefully and transfer it to a new collection tube.

3.3.3. Repeat steps 3.3.1. and 3.3.2. once.

3.3.4. Pool the supernatants and collect cells by centrifugation **(400 x g, 6 - 10 min).**

Remove supernatant and resuspend cells in appropriate buffer or medium for further applications.

If further removal of magnetic microbeads is needed (e.g. for further positive enrichment steps), proceed to step **3.4**.

3.4. Removal of remaining magnetic microbeads

Perform all steps at **room temperature.**

3.4.1. Discard supernatant carefully. Resuspend cell pellet in **5 ml** Buffer CI and incubate for **5 min** under agitation (e.g. on a roller mixer) at **room temperature**.

3.4.2. Place tube back on the magnet (to remove any potential residual beads) and incubate for **3 min**.

3.4.3. After incubation, transfer supernatant to a **new tube** and centrifuge cells for **6 – 10 min at 400 x g.**

3.4.4. Remove supernatant and resuspend cells in appropriate buffer or medium for further applications.

To perform further positive isolation or depletion steps, please start the protocol once more at **3.1.**

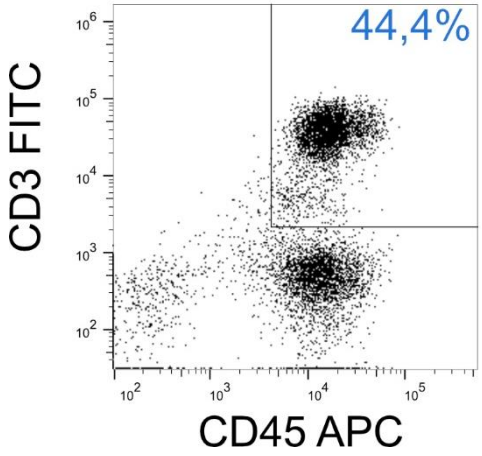
4. TROUBLESHOOTING

Low yield	*Option 1:* Titrate the ratio between Twin-Strep-tag® fusion protein and Strep-Tactin® Magnetic Microbeads for different cell numbers. *Option 2:* Increase incubation time of cells with protein-Microbead mix (3.1.2.). *Option 3:* Make sure that you carefully remove supernatants during incubation on the magnet (3.2.) without disrupting the binding of the microbeads to the magnet. *Option 4:* Check for biotin contamination in your samples.
Low purity	Increase number of washing steps (3.2.)
Microbead contamination	Make sure that you carefully remove supernatants during incubation on the magnet (3.3. and 3.4.) without disrupting the binding of the microbeads to the magnet.
High amount of cell death	Make sure that you always work at the recommended temperatures.

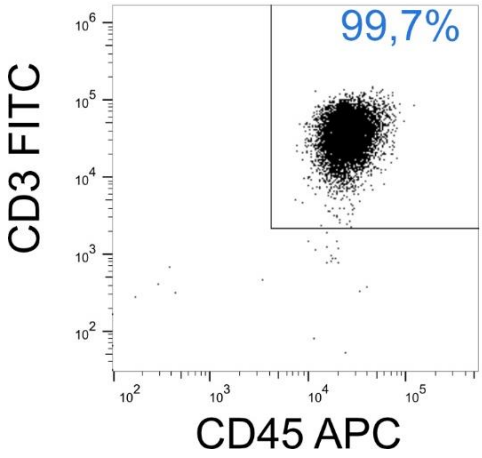
5. EXAMPLE DATA

Isolation of CD3⁺ T cells from PBMCs using a Fab Fragment against CD3 fused to a Twin-Strep-tag®. Unlysed cells were stained with CD3-FITC (OKT-3) / CD45-APC (2D1) and analyzed by flow cytometry (CytoFlex, BC). Dead cells were excluded from the analysis using DAPI staining. Doublet and debris discrimination were performed using different FSC/SSC signals.

Before isolation



After isolation



Watch this How-to video to see an exemplary isolation

https://www.youtube.com/watch?v=Er-HVYXIuH8

Check our Downloads page

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for the latest version of this protocol

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If you have any questions, please contact

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We are here to help!

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