



**Tiannan Guo**

**Kontakt**

Tiannan Guo

## Publikationen (6)

Zhu Y, Christiansen A, Fritz C, Rupp N, Poyet C, Rushing E, Weller M, Roth P, Haralambieva E, Hofer S, Chen C, Jochum W, Gao X, Teng X, Chen L, Zhong Q, Wild P, Aebersold R, Ljubicic J, Rutishauser D, Schmid M, Weiss T, Zhang Q, Sun R, Wang B, Yi X, Wu Z, Gao H, Cai X, Ruan G, Zhu T, Xu C, Lou S, Yu X, Gillet L, Blattmann P, Saba K, Fankhauser C, Guo T. High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. *Mol Oncol* 2019; 13:2305–2328.

Guo T, Aebersold R, Wild P, Poyet C, Saba K, Fankhauser C, Jochum W, Rueschoff J, Wagner U, Wong C, Charmpi K, Rupp N, Zhong Q, Li L, Beyer A. Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. *Life Sci Alliance* 2018; 1

Shao S, Guo T, Gross V, Lazarev A, Koh C, Gillessen Sommer S, Jörger M, Jochum W, Aebersold R. Reproducible Tissue Homogenization and Protein Extraction for Quantitative Proteomics Using MicroPestle-Assisted Pressure-Cycling Technology. *J Proteome Res* 2016; 15:1821–9.

Zhong Q, Poyet C, Blattner M, Soldini D, Moch H, Rubin M, Noske A, Rüschoff J, Haffner M, Jochum W, Perner S, Buhmann J, Rüschoff J, Guo T, Gabrani M, Schöffler P, Rechsteiner M, Liu Y, Fuchs T, Rupp N, Fankhauser C, Wild P. Image-based computational quantification and visualization of genetic alterations and tumour heterogeneity. *Sci Rep* 2016; 6:24146.

Shao S, Guo T, Koh C, Gillessen Sommer S, Jörger M, Jochum W, Aebersold R. Minimal sample requirement for highly multiplexed protein quantification in cell lines and tissues by PCT-SWATH mass spectrometry. *Proteomics* 2015; 15:3711–21.

Guo T, Jochum W, Jörger M, Gillessen Sommer S, Blum L, Collins B, Rosenberger G, Röst H, Wolski W, Gillet L, Koh C, Kouvonen P, Aebersold R. Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. *Nat Med* 2015; 21:407–13.

## Projekte (0)

Keine Resultate gefunden.

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