**Order: 2006**

**Manuscript: RNF43 inhibits WNT5A-driven signaling and suppresses melanoma invasion and resistance to the targeted therapy**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8550759/>

Data are available via ProteomeXchange ([Deutsch et al., 2020](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8550759/#bib39)) with identifier PXD020478 in the PRIDE database ([Perez-Riverol et al., 2019](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8550759/#bib132)). The analysis of the mass spectrometric RAW data files was carried out using the MaxQuant software (version 1.6.2.10) using default settings unless otherwise noted. MS/MS ion searches were done against modified cRAP database (based on <http://www.thegpm.org/crap>) containing protein contaminants like keratin, trypsin, etc., and UniProtKB protein database for Homo sapiens (<ftp://ftp.uniprot.org/pub/databases/uniprot/current_release/knowledgebase/reference_proteomes/Eukaryota/UP000005640_9606.fasta.gz>; downloaded 19.8.2018, version 2018/08, number of protein sequences 21,053). Oxidation of methionine and proline, deamidation (N, Q) and acetylation (protein N-terminus) as optional modification, carbamidomethylation (C) as fixed modification, and trypsin/P enzyme with two allowed miss cleavages was set. Peptides and proteins with FDR threshold <0.01 and proteins having at least one unique or razor peptide were considered only. Match between runs was set among all analyzed samples. Protein abundance was assessed using protein intensities calculated by MaxQuant. Protein intensities reported in proteinGroups.txt file (output of MaxQuant) were further processed using the software container environment (<https://github.com/OmicsWorkflows>, [Kristina, 2021](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8550759/#bib91)), version 3.7.2 a. Processing workflow is available upon request. Briefly, it covered (1) removal of decoy hits and contaminant protein groups, (2) protein group intensities log2 transformation, (3) LoessF normalization, (4) imputation by the global minimum, and (5) differential expression using LIMMA statistical test. Prior to volcano plot plotting, suspected BirA\* binders were filtered out (proteins identified by at least two peptides in both technical replicates of particular BirA\* sample, and present in more than three samples). Volcano plot was created in R using ggplot2 and ggrepel R packages by R version 3.6.1. Proteins with an adjusted p-value < 0.05 and log fold change >1 were further subjected to gene ontology tools, considering only the first ID of majority protein IDs: g:Profiler online tool (<https://biit.cs.ut.ee/gprofiler/gost>, version e98\_eg45\_p14\_ce5b097; [Raudvere et al., 2019](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8550759/#bib141)) was used and selected GO terms were highlighted. RNF43 interactors from BioID assay are listed in [Figure 1—source data 1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8550759/#fig1sdata1), and the results obtained by g:Profiler are presented in [Figure 1—source data 2](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8550759/#fig1sdata2).