Information to be requested from all CA17104 participants:

	
Indicate your Working Group(s) in COST Action17104:	**(WG1 and WG3)**
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Link to webpage with biography:	**http://www.szu.cz/seznam-publikaci and http://www.biomedic-plzen.cz/en/345-publications-projects-cooperation-publikace-projekty-spoluprace-18**

Link to webpage with group description:	**http://www.szu.cz/oddeleni-toxikogenomiky and http://www.biomedic-plzen.cz/en/220-laboratory-of-pharmacogenomics**

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Linkedin	**https://www.linkedin.com/in/radka-v%C3%A1clav%C3%ADkov%C3%A1-bb578982/**
Expertise relevant for this COST Action:	Gene expression profile, miRNA expression profile, genetic variability, NGS, Sanger sequecing, HRM analysis, DNA methylation, breast, ovarian, colorectal and pancreatic tumors, ABC and SLC transporters, metabolism and transport of taxanes, *in silico* prediction of clinical importance of genetic variations, cell cultures, *in vitro* studies
Available facilities to conduct work, relevant for this COST Action:	Handling and processing of solid tumor samples and blood samples, Isolation of DNA/RNA and proteins, PCR, Real Time PCR, NGS – DNA/RNA sequencing, Sanger sequencing, Affymetrix microarray analysis, Databases of clinical and pathological data of patients including type of response (good vs. poor responders, sensitive vs. resistant patients) Cell Culture, Flow Cytometry, xCELLigence real time cell analysis, MDR-reversal agents: Synthetic taxane analogs - Stony Brook taxanes
Matherials/Methods that could be shared with other members of this COST Action:	DNA/RNA, serum, plasma and protein samples of solid tumor patients and controls (breast, ovarian, colorectal, pancreatic carcinomas) characterized for the type of response to therapy, breast and ovarian cancer cell lines sensitive and resistant to

	Taxol, pancreatic carcinoma cell lines, *in vitro* techniques – flow cytometry, cytotoxicity, gene manipulation (e.g. siRNA knockdown, gene transfection), immunoblotting, gene expression profiles, miRNOm profiles and genetic variability analyses using real-time PCR, microarray analysis, NGS or direct sequencing Clinical and pathological data and databases, *in silico* tools for prediction of genetic biomarkers of MDR

NOTE: By submitting this form to the Grant Manager of CA17104, I agree that this information can be used within the scope of this COST Action (e.g. may be included on the webpage of CA17104).