Table S2. GOrilla analysis of SILAC data. Most significantly affected biological processes, molecular functions and cellular components reported from GOrilla analysis (GO Ontology database released 2022-07-01, single ranked list, arbitrary cut-off)

Treatment		P-value	FDR	Enrichment
Upregulated				
	Biological process			
PDT	Regulation of transcription, DNA-templated	2.58E-17	2.87E-13	1.58
BLM	Small molecule biosynthetic process	1.78E-12	1.97E-8	2.42
BLM_{PCI}	Regulation of transcription by RNA Polymerase II	2.78E-19	3.02E-15	1.76
	Molecular function			
PDT	DNA binding	8.33E-19	2.4E-15	1.80
BLM	Identical protein binding	2.63E-9	7.58E-6	1.42
BLM_{PCI}	DNA binding	5.49E-19	1.55E-15	1.85
	Cellular component			
PDT	Nuclear part	3.67E-28	5.79E-25	1.39
BLM	Cytoplasm	4.53E-14	7.14E-11	1.31
BLM_{PCI}	Nuclear Part	8.54E-39	1.33E-35	1.44
Downregulated				
	Biological process			
PDT	small molecule biosynthetic process	6.13E-14	6.8E-10	2.88
BLM	rRNA metabolic process	1.44E-30	1.6E-26	3.44
BLM_{PCI}	nucleobase-containing small molecule biosynthetic process	6.72E-10	7.46E-6	2.97
	Molecular function			
PDT	translation factor activity, RNA binding	4.52E-12	1.3E-8	3.12
BLM	Nucleic acid binding	6.91E-25	1.99E-21	1.56
BLM_{PCI}	Catalytic activity	1.03E-8	2.98E-5	1.27
	Cellular component			
PDT	Cytosol	1.27E-28	2E-25	1.51
BLM	Nucleolus	1.26E-42	1.99E-39	2.56
BLM_{PCI}	Cytoplasmic part	2.87E-11	4.53E-8	1.14