ATP metabol process	lic anaphase-promoti complex-depende catabolic process	ng ubiquitin–depend nt protein cataboli process	protein	mRNA splicing, via spliceosome	regulation of alternative mRN splicing, via spliceosome	MRNA cis splicing, via spliceosome	positive regulation of transcription by RNA polymerase II	mitotic cell cycle	G2/M transition of mitotic cell cycle	intracellular protein transport	vesicle-mediated transport	mitotic spindle assembly	cilium movement involved in cell motility	
CTP biosynthetic process	ubiquitin–dependent ERAD pathway	histone H4-K5 acetylation	histone H4–K8 acetylation	·	elongation by RNA	on transcription circadia	on regulation of mRNA splicing.		phase transition  phase transition  cell cycle cell cycle cell cycle	protein transport		spinose cytoskeleton Spinose cytoskeleton Spinose cytoskeleton Spinose cytoskeleton  reg latic of polymerization or		
histone H4-K16 acetylation	biosyr Atic process  metak	GTP Synthetic process	proton motive force–driven ATP synthesis		transcription by RNA	A-templated elongation by R polymerase I	nuclear–transcribed mRNA catabolic process, nonsense–mediated	meiotic reg	f mitotic cell cycle phase transition  regulation of G2/M transition of mitotic cell cycle cycle phase transition positive regulation of mitotic cycle	to membrane,	negative regulation of protein localization to plasma membrane	axoneme assembly	depolymerization microtubule bundle formation spindle	
protein peptidyl-prolyl isomerization	prot K11-li	ein nked peptidyl-se	proton motive force–driven mitochondrial ATP synthesis protein			spliceosomal snRNP assembly regulation of mRNA	mRNA catabolic process regulation of	negative regulation of	cell cycle  cell cycle  cellul  negative regulation of	canonical Wnt signaling	response to UV-C	prote	organization  protein  refulding	
DNA replication	metabolic K48 process ubiqu	rotein DNA -linked biosynth uitination proce	N-linked hetic glycosylation	mRNA processing	mRNA regulation mRNA	positive stability spliceosoma complex iceosome assembly	DNA-templated transcription    positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	DN negati transcription regulat	polymerase II regulation of	to DNA	to DNA base-excision repair		folding perone cofact. dependent protein refolding regulation of	
fork processing protein	protein kinase activity pro	F-dependent roteasomal iitin-dependent tein catabolic process	omal regulation of ubiquitin protein ligase activity	chromatin respirat chair	ory clathrin	nucleosome disassembly organizat		of DN  -ptempla stabilization transcri apopt	cellul respons	cellular processed to hydroxyurea cymulus	rotein nsport, ER to ytosol	regulation regulation	J	
translational elongation	proteasomal protein catabolic ro	DNA pplication h	rotein mitochondrial translational termination istone H3-K4 trimethylation		assembly assembly		ubunit  nesis  transcription-compe SSU-rRNA onic rRNA SU-rRNA,	regulati	negative regulation of phosphatase NADH	nitochondri electron totransport, OH to ubiqu	oxygen species metabolic	chromo segreg	some.	