3/69 ERAD pathway 7/380 protein catabolic process 8/181 response to endoplasmic reticulum stress 6/70 endoplasmic reticulum unfolded protein response
1/6 PERK-mediated unfolded protein response
8/114 response to topologically incorrect protein 0/9 regulation of translational initiation in response to stress 2/30 negative regulation of response to endoplasmic reticulum stress 3/59 regulation of response to endoplasmic reticulum stress 2/13 protein folding in endoplasmic reticulum
4/133 protein folding in endoplasmic reticulum
6/136 protein folding in endoplasmic reticulum
6/136 protein folding in endoplasmic reticulum
6/136 protein folding for endoplasmic reticulum
6/136 protein localization to endoplasmic reticulum
6/136 establishment of protein localization to endoplasmic reticulum
6/136 establishment of protein localization to endoplasmic reticulum
6/136 protein targeting to membrane
6/136 protein targeting to membrane
6/136 protein targeting to membrane
6/1376 protein to membrane
6/1376 protein localization to membrane 3/257 protein localization to membrane 5/144 phagocytosis 5/144 phagocytosis
2/35 defense response to virus
3/93 regulation of cell cycle G1/S phase transition
7/254 regulation of cell cycle phase transition
4/180 negative regulation of cell cycle process
10/454 regulation of cell cycle process
1/488 nositive negulation of cell cycle process 1/68 positive regulation of cell cycle phase transition 5/184 positive regulation of cell cycle process 1/65 regulation of mitotic sister chromatid segregation 8/438 regulation of mitotic cell cycle 1/98 regulation of chromosome segregation 2/275 regulation of chromosome organization 3/89 DNA integrity checkpoint 8/311 negative regulation of cell cycle 4/171 negative regulation of mitotic cell cycle 10/550 mitotic cell cycle 1/138 mitotic nuclear division 1/20 attachment of spindle microtubules to kinetochore 5/296 organelle fission 1/115 sister chromatid segregation 15/623 chromosome organization 4/195 chromosome segregation 0/146 spindle organization 2/376 microtubule cytoskeleton organization
0/87 mitotic spindle organization 0/42 mitotic spindle assembly 1/128 microtubule cytoskeleton organization involved in mitosis 0/85 spindle assembly
14/478 DNA metabolic process 10/300 DNA repair 10/300 DNA fepair 4/136 double-strand break repair 6/135 DNA recombination 14/451 cellular response to DNA damage stimulus 0/17 nucleotide–excision repair, DNA gap filling
0/22 DNA strand elongation
0/16 DNA strand elongation
1/45 Cell cycle DNA replication
1/45 Cell cycle DNA replication 2/96 DNA-dependent DNA replication 4/137 DNA replication 0/6 DNA unwinding involved in DNA replication 0/54 DNA geometric change 1/22 mismatch repair 1/7 regulation of DNA-dependent DNA replication initiation 177 tegulation of DNA replication
7/262 regulation of DNA replication
7/262 regulation of DNA metabolic process
3/50 regulation of DNA-dependent DNA replication
3/95 negative regulation of DNA metabolic process
1/15 chromatin remodeling at centromee
8/73 chromatin assembly or disassembly 2/22 centromere complex assembly 1/52 chromosome condensation
7/119 DNA packaging
7/170 DNA conformation change
1/12 heterochromatin organization involved in chromatin silencing 1/51 blastocyst development 2/43 nephron epithelium morphogenesis 14/578 tube morphogenesis 0/6 mesonephric tubule formation 2/53 kidney morphogenesis 0/11 regulation of mesonephros development 15/507 sensory organ development 0/41 artery development 11/281 cell fate commitment 1/38 osteoblast differentiation 11/330 reproductive system development 8/197 development of primary sexual characteristics 0/9 positive regulation of chondrocyte differentiation 1/22 regulation of chondrocyte differentiation 2/35 regulation of cartilage development 1/18 positive regulation of cartilage development 3/106 limb development 1/13 positive regulation of pathway–restricted SMAD protein phosphorylation 0/11 germ-band shortening 6/64 nerve development 0/9 mitochondrial electron transport, ubiquinol to cytochrome c 0/66 oxidative phosphorylation 3/149 energy derivation by oxidation of organic compounds 3/269 mitochondrion organization 1/59 lipoprotein metabolic process

p < 0.001 p < 0.01 p < 0.05