Supplementary Table S1 Manual GO Annotations for Validation Proteins

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| Uniprot ID | Ontology | Accession | Name |
| Q13608 | BP | GO:0050821 | protein stabilization |
| Q13608 | BP | GO:0007031 | peroxisome organization |
| Q13608 | MF | GO:0016887 | ATP hydrolysis activity |
| Q13608 | MF | GO:0005524 | ATP binding |
| Q13608 | MF | GO:0044877 | protein-containing complex binding |
| Q13608 | CC | GO:0005777 | peroxisome |
| Q13608 | CC | GO:0005778 | peroxisomal membrane |
| P55072 | BP | GO:0016567 | protein ubiquitination |
| P55072 | BP | GO:0036503 | ERAD pathway |
| P55072 | BP | GO:0016236 | macroautophagy |
| P55072 | BP | GO:0042981 | regulation of apoptotic process |
| P55072 | BP | GO:1901224 | positive regulation of non-canonical NF-kappaB signal transduction |
| P55072 | BP | GO:0031334 | positive regulation of protein-containing complex assembly |
| P55072 | BP | GO:0006974 | DNA damage response |
| P55072 | BP | GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process |
| P55072 | BP | GO:0090263 | positive regulation of canonical Wnt signaling pathway |
| P55072 | BP | GO:0032436 | positive regulation of proteasomal ubiquitin-dependent protein catabolic process |
| P55072 | BP | GO:0006914 | autophagy |
| P55072 | BP | GO:0045732 | positive regulation of protein catabolic process |
| P55072 | BP | GO:0034605 | cellular response to heat |
| P55072 | BP | GO:0045184 | establishment of protein localization |
| P55072 | BP | GO:0006302 | double-strand break repair |
| P55072 | MF | GO:0016887 | ATP hydrolysis activity |
| P55072 | CC | GO:0048471 | perinuclear region of cytoplasm |
| P55072 | CC | GO:0034774 | secretory granule lumen |
| P55072 | CC | GO:1904813 | ficolin-1-rich granule lumen |
| P55072 | CC | GO:0000502 | proteasome complex |
| P55072 | CC | GO:0010494 | cytoplasmic stress granule |
| P55072 | CC | GO:0035578 | azurophil granule lumen |
| P55072 | CC | GO:0035861 | site of double-strand break |
| P55072 | CC | GO:0005811 | lipid droplet |
| P54784 | BP | GO:0043007 | maintenance of rDNA |
| P54784 | BP | GO:0030466 | silent mating-type cassette heterochromatin formation |
| P54784 | BP | GO:0006270 | DNA replication initiation |
| P54784 | BP | GO:0006267 | pre-replicative complex assembly involved in nuclear cell cycle DNA replication |
| P54784 | MF | GO:0016887 | ATP hydrolysis activity |
| P54784 | MF | GO:0003682 | chromatin binding |
| P54784 | MF | GO:0031491 | nucleosome binding |
| P54784 | MF | GO:0005524 | ATP binding |
| P54784 | MF | GO:0003688 | DNA replication origin binding |
| P54784 | CC | GO:0005656 | nuclear pre-replicative complex |
| P54784 | CC | GO:0031261 | DNA replication preinitiation complex |
| P54784 | CC | GO:0005664 | nuclear origin of replication recognition complex |
| P40341 | BP | GO:0006465 | signal peptide processing |
| P40341 | BP | GO:0065003 | protein-containing complex assembly |
| P40341 | MF | GO:0016887 | ATP hydrolysis activity |
| P40341 | MF | GO:0005524 | ATP binding |
| P40341 | CC | GO:0005743 | mitochondrial inner membrane |