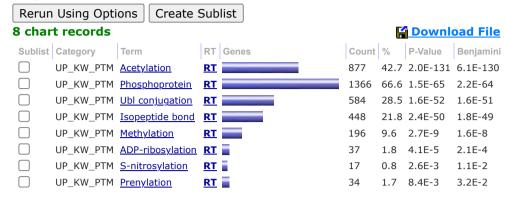**National Institutes of Health**
*DAVID Bioinformatics*

## Functional Annotation Chart

[Help and Manual](#)

**Current Gene List: condition_specific_gene_list**
**Current Background: Homo sapiens**
**2052 DAVID IDs**

**Options**

Rerun Using Options | Create Sublist

**8 chart records**

📥 **Download File**

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---|---|---|---|---|---|---|---|---|
| ☐ | UP_KW_PTM | Acetylation | **RT** | ▬▬▬ | 877 | 42.7 | 2.0E-131 | 6.1E-130 |
| ☐ | UP_KW_PTM | Phosphoprotein | **RT** | ▬▬▬▬ | 1366 | 66.6 | 1.5E-65 | 2.2E-64 |
| ☐ | UP_KW_PTM | Ubl conjugation | **RT** | ▬▬ | 584 | 28.5 | 1.6E-52 | 1.6E-51 |
| ☐ | UP_KW_PTM | Isopeptide bond | **RT** | ▬▬ | 448 | 21.8 | 2.4E-50 | 1.8E-49 |
| ☐ | UP_KW_PTM | Methylation | **RT** | ▬ | 196 | 9.6 | 2.7E-9 | 1.6E-8 |
| ☐ | UP_KW_PTM | ADP-ribosylation | **RT** | ▪ | 37 | 1.8 | 4.1E-5 | 2.1E-4 |
| ☐ | UP_KW_PTM | S-nitrosylation | **RT** | ▪ | 17 | 0.8 | 2.6E-3 | 1.1E-2 |
| ☐ | UP_KW_PTM | Prenylation | **RT** | ▪ | 34 | 1.7 | 8.4E-3 | 3.2E-2 |

426 gene(s) from your list are not in the output.

Please [cite DAVID](#) within any publication that makes use of any methods inspired by **DAVID**.