Proportionally controlled proteins	
Enrichment Score: 15.722412271963268	
[erm	FDR
GO:0018198~peptidyl-cysteine modification	3.219E-13
GO:0018197~peptidyl-aspartic acid modification	3.219E-13
GO:0018339~peptidyl-L-beta-methylthioaspartic acid biosynthetic process from peptidyl-aspartic acid	3.219E-13
50.0010000 peptidyr-E-beta-metryttinoaspartie acid biosynthetic process from peptidyr-aspartie acid	0.213L-13
Enrichment Score: 5.177276313087028	
- Term	FDR
GO:0044271~nitrogen compound biosynthetic process	0.00
GO:0046394~carboxylic acid biosynthetic process	0.01
GO:0016053~organic acid biosynthetic process	0.01
GO:0009309~amine biosynthetic process	0.02
GO:0008652~cellular amino acid biosynthetic process	0.05
nrichment Score: 5.0019785746451575	
erm	FDR
GO:0007049~cell cycle	0.00
GO:0051301~cell division	0.02
GO:0007059~chromosome segregation	0.15
Enrichment Score: 3.7902178093615957	
Ferm	FDR
GO:0042330~taxis	4.03E-4
GO:0007610~behavior	4.03E-4
GO:0007626~locomotory behavior	4.03E-4
GO:0048870~cell motility	0.20
GO:0001539~ciliary or flagellar motility	0.20
GO:0051674~localization of cell	0.20
GO:0006928~cell motion	0.22
GO:0043064~flagellum organization	4.11
GO:0030030~cell projection organization	10.53
GO:0009296~flagellum assembly	73.89
GO:0030031~cell projection assembly	90.39
Enrichment Score: 3.136632364510789	
erm	FDR
GO:0006790~sulfur metabolic process	0.04
GO:0009070~serine family amino acid biosynthetic process	0.29
GO:0044272~sulfur compound biosynthetic process	0.56
GO:0009069~serine family amino acid metabolic process	0.70
GO:0000097~sulfur amino acid biosynthetic process	0.70
GO:0000096~sulfur amino acid metabolic process	2.11
GO:0019344~cysteine biosynthetic process	8.05
GO:0006534~cysteine metabolic process	22.87
Enrichment Score: 2.968167724937097	
Ferm	FDR
GO:0006418~tRNA aminoacylation for protein translation	0.02
GO:0043038~amino acid activation	0.02
GO:0043039~tRNA aminoacylation	0.02
GO:0006399~tRNA metabolic process	0.04
60:0034660~ncRNA metabolic process	0.14
60:0009451~RNA modification	2.42
GO:0006400~tRNA modification	53.53
GO:0008033~tRNA processing	87.59
GO:0034470~ncRNA processing	87.90
GO:0006396~RNA processing	89.71