

Significantly enriched (FDR<0.05) GO Biological process terms and groups in the list of 80 differential proteins (p<0.05 or 0.5>FC>2 between Control and Inoculated)								
GO ID	GO Term	Source	Term FDR	Group FDR	Enrichment score	GO groups	% Associated proteins	Number of proteins
GO:0072524	pyridine-containing compound metabolic process	BP	1.85E-04	1.29E-04	12.9	4	4.24	5.00
GO:0019362	pyridine nucleotide metabolic process	BP	2.07E-04	1.29E-04	12.9	4	4.50	5.00
GO:0006733	oxidoreduction coenzyme metabolic process	BP	2.09E-04	1.29E-04	12.9	4	4.00	5.00
GO:0046496	nicotinamide nucleotide metabolic process	BP	2.64E-04	1.29E-04	12.9	4	4.55	5.00
GO:0006739	NADP metabolic process	BP	5.49E-04	1.29E-04	12.9	4	8.33	3.00
GO:0006081	cellular aldehyde metabolic process	BP	2.07E-03	1.29E-04	12.9	4	4.05	3.00
GO:0046365	monosaccharide catabolic process	BP	3.34E-07	3.53E-04	11.5	6	44.44	4.00
GO:0019320	hexose catabolic process	BP	2.30E-05	3.53E-04	11.5	6	37.50	3.00
GO:0072524	pyridine-containing compound metabolic process	BP	1.85E-04	3.53E-04	11.5	6	4.24	5.00
GO:0005996	monosaccharide metabolic process	BP	1.96E-04	3.53E-04	11.5	6	4.35	5.00
GO:0019362	pyridine nucleotide metabolic process	BP	2.07E-04	3.53E-04	11.5	6	4.50	5.00
GO:0006733	oxidoreduction coenzyme metabolic process	BP	2.09E-04	3.53E-04	11.5	6	4.00	5.00
GO:0046496	nicotinamide nucleotide metabolic process	BP	2.64E-04	3.53E-04	11.5	6	4.55	5.00
GO:0019318	hexose metabolic process	BP	3.77E-04	3.53E-04	11.5	6	5.19	4.00
GO:0006739	NADP metabolic process	BP	5.49E-04	3.53E-04	11.5	6	8.33	3.00
GO:0006006	glucose metabolic process	BP	6.23E-04	3.53E-04	11.5	6	7.32	3.00
GO:0009135	purine nucleoside diphosphate metabolic process	BP	1.71E-03	3.53E-04	11.5	6	4.48	3.00
GO:0009185	ribonucleoside diphosphate metabolic process	BP	1.71E-03	3.53E-04	11.5	6	4.48	3.00
GO:0009179	purine ribonucleoside diphosphate metabolic process	BP	1.71E-03	3.53E-04	11.5	6	4.48	3.00
GO:0006757	ATP generation from ADP	BP	1.71E-03	3.53E-04	11.5	6	4.48	3.00
GO:0046031	ADP metabolic process	BP	1.71E-03	3.53E-04	11.5	6	4.48	3.00
GO:0006096	glycolytic process	BP	1.71E-03	3.53E-04	11.5	6	4.48	3.00
GO:0006165	nucleoside diphosphate phosphorylation	BP	2.00E-03	3.53E-04	11.5	6	4.17	3.00
GO:0009132	nucleoside diphosphate metabolic process	BP	2.06E-03	3.53E-04	11.5	6	4.00	3.00
GO:0046939	nucleotide phosphorylation	BP	2.07E-03	3.53E-04	11.5	6	4.05	3.00
GO:0043094	cellular metabolic compound salvage	BP	5.65E-04	5.90E-04	10.7	3	4.21	4.00
GO:0009853	photorespiration	BP	1.14E-03	5.90E-04	10.7	3	5.56	3.00
GO:0065004	protein-DNA complex assembly	BP	4.08E-04	9.43E-04	10.1	5	4.94	4.00
GO:0071824	protein-DNA complex subunit organization	BP	5.23E-04	9.43E-04	10.1	5	4.40	4.00
GO:0006334	nucleosome assembly	BP	6.23E-04	9.43E-04	10.1	5	7.32	3.00
GO:0031497	chromatin assembly	BP	9.81E-04	9.43E-04	10.1	5	6.12	3.00
GO:0034728	nucleosome organization	BP	1.03E-03	9.43E-04	10.1	5	5.88	3.00
GO:0006333	chromatin assembly or disassembly	BP	1.44E-03	9.43E-04	10.1	5	4.84	3.00
GO:0006323	DNA packaging	BP	1.45E-03	9.43E-04	10.1	5	4.92	3.00
GO:0034440	lipid oxidation	BP	1.14E-03	9.53E-04	10.0	1	5.56	3.00
GO:0034976	response to endoplasmic reticulum stress	BP	1.32E-03	9.79E-04	10.0	2	5.17	3.00

The leading term of each enriched group is that with the lowest term FDR (highest enrichment score), highlighted in bold and used to name the respective group.